

cgt taagccctct taggaatcat gaa
1005
Arg

Ala Glu Asp Leu His Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln
 260 265 270

Glu Val Leu Tyr Asn Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His
 275 280 285

Gly Gln Asp Ala Val Arg
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<210> 675
 <211> 601
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(601)
 <223> RXN02027

<400> 675
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tcgtcgtacc cctccgaaaa taacgggttat ccttagattt atg agc caa act aag 115
 Met Ser Gln Thr Lys
 1 5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163
 Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu
 10 15 20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211
 Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr
 25 30 35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259
 Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val
 40 45 50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307
 Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu
 55 60 65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355
 Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp
 70 75 80 85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403
 Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly
 90 95 100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451
 Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe
 105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499
 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile
 120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547
 Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly

135	140	145	
gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac	595		
Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp			
150	155	160	165
gat atc			601
Asp Ile			

<210> 676
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 676
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 Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala
 35 40 45
 Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp
 50 55 60
 Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu
 65 70 75 80
 Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val
 85 90 95
 Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro
 100 105 110
 Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys
 115 120 125
 Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg
 130 135 140
 Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn
 145 150 155 160
 Gly Glu Ile Arg Asp Asp Ile
 165

<210> 677
 <211> 595
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(595)
 <223> FRXA02027

<400> 677

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 Met Ser Gln Thr Lys
 1 5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163
 Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu
 10 15 20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211
 Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr
 25 30 35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259
 Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val
 40 45 50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307
 Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu
 55 60 65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355
 Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp
 70 75 80 85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403
 Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly
 90 95 100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451
 Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe
 105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499
 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile
 120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547
 Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly
 135 140 145

gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595
 Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp
 150 155 160 165

<210> 678

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 678

Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg
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Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile
 20 25 30

Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala

35	40	45
Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp		
50	55	60
Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu		
65	70	75
Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val		
85	90	95
Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro		
100	105	110
Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys		
115	120	125
Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg		
130	135	140
Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn		
145	150	155
Gly Glu Ile Arg Asp		
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<210> 679

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00106

<400> 679

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Met Ile Gly Ala Ile
1 5
tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
10 15 20
tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
25 30 35
cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
40 45 50
ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
55 60 65
gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355

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Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
 70 75 80 85
 tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
 Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
 90 95 100
 gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
 Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
 105 110 115
 ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
 Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
 120 125 130
 tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
 Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
 135 140 145
 atc aag gtt taaggagcaa acaacatgag caa 579
 Ile Lys Val
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<210> 680

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 680

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 Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
 20 25 30
 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
 35 40 45
 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
 50 55 60
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
 65 70 75 80
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
 85 90 95
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
 100 105 110
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
 115 120 125
 Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
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 Lys Phe Gln Arg Tyr Ile Lys Val
 145 150

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 <211> 1044
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1021)
 <223> RXN01321

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acttagacct gacttagtgt gggaaaattt ccagggtaga atg caa cga atg acc 115
 Met Gln Arg Met Thr
 1 5

ccg agt tct cct gaa gtt cgt aat cgt ccg agc gct gcg cct gaa gag 163
 Pro Ser Ser Pro Glu Val Arg Asn Arg Pro Ser Ala Ala Pro Glu Glu
 10 15 20

cgt cag ttt gtg ctc act ttt ggc tgc cct gac tcc act gga att gtg 211
 Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp Ser Thr Gly Ile Val
 25 30 35

gcg aag ttg tgc tgc ttc cta gct gag cgt ggg ggt tgg att act gag 259
 Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly Gly Trp Ile Thr Glu
 40 45 50

gct gga tat ttc acg gat cct gat tgc aat tgg ttc ttt act cgt cag 307
 Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp Phe Phe Thr Arg Gln
 55 60 65

gcg att cgc gct gag tgc att gat acc acg att gag cag ttg cgg gag 355
 Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile Glu Gln Leu Arg Glu
 70 75 80 85

gag ttc gct ccg ctt gcg gag gag ttc ggc ccg agg gct aag tgg agt 403
 Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro Arg Ala Lys Trp Ser
 90 95 100

ttc act gac act gcg cag gtg aag aag gct gtg ttg ttg gtg tct aag 451
 Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val Leu Leu Val Ser Lys
 105 110 115

gag ggc cac tgc ttg cac gat ttg tta ggt cgt gtg gct gag aat gat 499
 Glu Gly His Cys Leu His Asp Leu Leu Gly Arg Val Ala Glu Asn Asp
 120 125 130

tat ccg atg gaa gtt gtt gcg gtt gtg ggt aac cat gag aac ttg cgt 547
 Tyr Pro Met Glu Val Val Ala Val Val Gly Asn His Glu Asn Leu Arg
 135 140 145

tat att gcg gag aac cat aat gtt ccg ttt ttc cat gtg ccg ttt cct 595
 Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe His Val Pro Phe Pro
 150 155 160 165

aag gat gcg gtt ggt aag cgg aag gcg ttt gac cag gtc gct gag att 643
 Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile
 170 175 180

gtg aat ggt tat gat ccg gat gcg att gtt ttg gct cgt ttt atg cag 691
 Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln
 185 190 195

att ttg ccg ccg gat ttg tgt gag atg tgg gct ggt cgt gtg ttg aat 739
 Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn
 200 205 210

att cat cac agt ttc ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat 787
 Ile His His Ser Phe Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His
 215 220 225

cag gcg tat agc cgt ggt gtg aag ttg att ggt gcg acc tgc cat tat 835
 Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr
 230 235 240 245

gcg act ggg gat ctg gat gat ggt ccg atc att gag cag gat gtt att 883
 Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile
 250 255 260

cgt gtg acg cat aag gat acg ccg act gag atg cag cgt ttg ggc cgc 931
 Arg Val Thr His Lys Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg
 265 270 275

gat gcg gag aag cag gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag 979
 Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu
 280 285 290

gac cgg gtg ctg gtt tac ggt aac cgc acg gtt gtc ttt gat
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 Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val Val Phe Asp
 295 300 305

taaggctttt tgcttttcga cgc
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<210> 682
 <211> 307
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 682
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 20 25 30

Ser Thr Gly Ile Val Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly
 35 40 45

Gly Trp Ile Thr Glu Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp
 50 55 60

Phe Phe Thr Arg Gln Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile
 65 70 75 80

Glu Gln Leu Arg Glu Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro
 85 90 95

Arg Ala Lys Trp Ser Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val
 100 105 110
 Leu Leu Val Ser Lys Glu Gly His Cys Leu His Asp Leu Leu Gly Arg
 115 120 125
 Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn
 130 135 140
 His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe
 145 150 155 160
 His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp
 165 170 175
 Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu
 180 185 190
 Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala
 195 200 205
 Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly
 210 215 220
 Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly
 225 230 235 240
 Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile
 245 250 255
 Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met
 260 265 270
 Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu
 275 280 285
 Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val
 290 295 300
 Val Phe Asp
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<210> 683
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (23)..(559)
 <223> FRXA01321

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 gtt gcg gtt gtg ggt aac cat gag aac ttg cgt tat att gcg gag aac 100
 Val Ala Val Val Gly Asn His Glu Asn Leu Arg Tyr Ile Ala Glu Asn
 15 20 25

cat aat gtt ccg ttt ttc cat gtg ccg ttt cct aag gat gcg gtt ggt 148
 His Asn Val Pro Phe Phe His Val Pro Phe Pro Lys Asp Ala Val Gly
 30 35 40

aag cgg aag gcg ttt gac cag gtc gct gag att gtg aat ggt tat gat 196
 Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile Val Asn Gly Tyr Asp
 45 50 55

ccg gat gcg att gtt ttg gct cgt ttt atg cag att ttg ccg ccg gat 244
 Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln Ile Leu Pro Pro Asp
 60 65 70

ttg tgt gag atg tgg gct ggt cgt gtg ttg aat att cat cac agt ttc 292
 Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn Ile His His Ser Phe
 75 80 85 90

ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat cag gcg tat agc cgt 340
 Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg
 95 100 105

ggt gtg aag ttg att ggt gcg acc tgc cat tat gcg act ggg gat ctg 388
 Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr Ala Thr Gly Asp Leu
 110 115 120

gat gat ggt ccg atc att gag cag gat gtt att cgt gtg acg cat aag 436
 Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile Arg Val Thr His Lys
 125 130 135

gat acg ccg act gag atg cag cgt ttg ggc cgc gat gcg gag aag cag 484
 Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln
 140 145 150

gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag gac cgg gtg ctg gtt 532
 Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu Asp Arg Val Leu Val
 155 160 165 170

tac ggt aac cgc acg gtt gtc ttt gat taaggctttt tgcttttcga 579
 Tyr Gly Asn Arg Thr Val Val Phe Asp
 175

cgc 582

<210> 684

<211> 179

<212> PRT

<213> Corynebacterium glutamicum

<400> 684

Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn
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His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe
 20 25 30

His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp
 35 40 45

Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu
 50 55 60

Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala
 65 70 75 80
 Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly
 85 90 95
 Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly
 100 105 110
 Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile
 115 120 125
 Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met
 130 135 140
 Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu
 145 150 155 160
 Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val
 165 170 175

Val Phe Asp

<210> 685
 <211> 975
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(952)
 <223> RXA00461

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 Val Thr Ala Ile Lys 5
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 ctt gat gga aac tta tac cgc ggg gaa att ttc gcc gac ttg gaa cag 163
 Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe Ala Asp Leu Glu Gln 20
 10 15
 cgc gtt gct gcg ttg aag gag aaa ggg att gtg ccg ggg ctt gcc acc 211
 Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val Pro Gly Leu Ala Thr 35
 25 30
 gtg ctg gtg ggt gat gac cca gcg agc cac tct tac gtg aag atg aag 259
 Val Leu Val Gly Asp Asp Pro Ala Ser His Ser Tyr Val Lys Met Lys 50
 40 45
 cat cgt gac tgt gag cag att ggt gtg aac tcg atc cgt aag gat ctg 307
 His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser Ile Arg Lys Asp Leu 65
 55 60
 cct gct gat gtc acg cag gaa gag ctt ttc gct gtc atc gat gaa ctg 355
 Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala Val Ile Asp Glu Leu

70	75	80	85	
aac aac gat gat tct tgc act ggt tac att gtg cag ctt cct ttg cct	Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val Gln Leu Pro Leu Pro	403		
	90 95 100			
aag cac ttg gac gaa aac gct gtg ctg gag cgc att gat cca gct aag	Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg Ile Asp Pro Ala Lys	451		
	105 110 115			
gat gct gat ggc ctg cac cct gta aac ctg ggc aag ctt gtg ctc aac	Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly Lys Leu Val Leu Asn	499		
	120 125 130			
gag cca gct cca ctg cca tgc acc ccg aat ggt tcc atc agc ttg ttg	Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly Ser Ile Ser Leu Leu	547		
	135 140 145			
cgt cgt ttc ggc gtt gag ctt gat ggc gcg aag gtt gtt gtc att ggc	Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys Val Val Val Ile Gly	595		
	150 155 160 165			
cgt ggc gtc acc gtt ggt cgc cca att ggc ctg atg ctg acc cgc cgt	Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu Met Leu Thr Arg Arg	643		
	170 175 180			
tcc gag aac tcc acg gtt act ttg tgc cac act ggc acg aag gat ctg	Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr Gly Thr Lys Asp Leu	691		
	185 190 195			
gct gcg gag acc cgt gcg gct gac gtc atc att gct gca gct ggt cag	Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile Ala Ala Ala Gly Gln	739		
	200 205 210			
ccg cac atg ctg acc gca gac atg gtc aag cca ggc gca gcg gtg ctc	Pro His Met Leu Thr Ala Asp Met Val Lys Pro Gly Ala Ala Val Leu	787		
	215 220 225			
gat gtc ggc gtc tcc cgc aag gac ggc aag ttg ctt ggc gac gtc cac	Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu Leu Gly Asp Val His	835		
	230 235 240 245			
ccc gac gtg tgg gaa gtc gcc ggc gcg gtc tca cca aac cca ggc ggc	Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser Pro Asn Pro Gly Gly	883		
	250 255 260			
gtt ggc cct ctg acc cgt gca ttc ttg gtg cac aat gtt gtc gag cgc	Val Gly Pro Leu Thr Arg Ala Phe Leu Val His Asn Val Val Glu Arg	931		
	265 270 275			
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<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 686

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 20 25 30
 Pro Gly Leu Ala Thr Val Leu Val Gly Asp Asp Pro Ala Ser His Ser
 35 40 45
 Tyr Val Lys Met Lys His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser
 50 55 60
 Ile Arg Lys Asp Leu Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala
 65 70 75 80
 Val Ile Asp Glu Leu Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val
 85 90 95
 Gln Leu Pro Leu Pro Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg
 100 105 110
 Ile Asp Pro Ala Lys Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly
 115 120 125
 Lys Leu Val Leu Asn Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly
 130 135 140
 Ser Ile Ser Leu Leu Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys
 145 150 155 160
 Val Val Val Ile Gly Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu
 165 170 175
 Met Leu Thr Arg Arg Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr
 180 185 190
 Gly Thr Lys Asp Leu Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile
 195 200 205
 Ala Ala Ala Gly Gln Pro His Met Leu Thr Ala Asp Met Val Lys Pro
 210 215 220
 Gly Ala Ala Val Leu Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu
 225 230 235 240
 Leu Gly Asp Val His Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser
 245 250 255
 Pro Asn Pro Gly Gly Val Gly Pro Leu Thr Arg Ala Phe Leu Val His
 260 265 270
 Asn Val Val Glu Arg Ala Glu Lys Leu Ala Gly Leu
 275 280

<210> 687

<211> 711

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(688)

<223> RXA01514

<400> 687

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 Val Asp Asn His Ala
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gca gtt cgc gag ttc gat gag gag cgc gca aca gct gcg att cgt gag 163
 Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr Ala Ala Ile Arg Glu
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ttg ctc atc gct gtg ggt gag gat cca gat cgc gaa ggc ctg ttg gaa 211
 Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg Glu Gly Leu Leu Glu
 25 30 35

acc cca gct cga gtg gct agg gcg tac aag gaa act ttc gcg ggt ctg 259
 Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu Thr Phe Ala Gly Leu
 40 45 50

cat gag gat ccc acc act gtg ctg gag aag acg ttc tct gag ggc cat 307
 His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr Phe Ser Glu Gly His
 55 60 65

gaa gag ttg gtt ctg gtt cgt gag atc ccg att tac tcc atg tgt gag 355
 Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile Tyr Ser Met Cys Glu
 70 75 80 85

cac cac ttg gtg ccg ttc ttt ggc gtg gcg cac att ggt tac att ccg 403
 His His Leu Val Pro Phe Phe Gly Val Ala His Ile Gly Tyr Ile Pro
 90 95 100

ggt aag tcc ggc aag gtg act ggc ctg tcc aag ctg gcg cgt tta gcg 451
 Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys Leu Ala Arg Leu Ala
 105 110 115

gat atg ttt gct aag cga cct cag gtt cag gag cgc ttg acc tcc caa 499
 Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu Arg Leu Thr Ser Gln
 120 125 130

att gcg gat gct ctc gtc gaa aag ctt gat gcc cag gcc gtg gcc gtg 547
 Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala Gln Ala Val Ala Val
 135 140 145

gtg att gaa gct gag cac ctg tgc atg gcc atg cgc gga atc cgt aag 595
 Val Ile Glu Ala Glu His Leu Cys Met Ala Met Arg Gly Ile Arg Lys
 150 155 160 165

cct ggt gct gtg acc acg acg tct gcg gtg cgc ggc ggt ttt aag aac 643
 Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg Gly Gly Phe Lys Asn
 170 175 180

aac gct gcc tcc cgc gct gag gtg ttc tcc ctg att cgg ggg cac 688
 Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu Ile Arg Gly His
 185 190 195

taaataaacg tatectcttt gac 711

<210> 688
 <211> 196
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 688
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 35 40 45
 Thr Phe Ala Gly Leu His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr
 50 55 60
 Phe Ser Glu Gly His Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile
 65 70 75 80
 Tyr Ser Met Cys Glu His His Leu Val Pro Phe Phe Gly Val Ala His
 85 90 95
 Ile Gly Tyr Ile Pro Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys
 100 105 110
 Leu Ala Arg Leu Ala Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu
 115 120 125
 Arg Leu Thr Ser Gln Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala
 130 135 140
 Gln Ala Val Ala Val Val Ile Glu Ala Glu His Leu Cys Met Ala Met
 145 150 155 160
 Arg Gly Ile Arg Lys Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg
 165 170 175
 Gly Gly Phe Lys Asn Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu
 180 185 190
 Ile Arg Gly His
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<210> 689
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(490)
 <223> RXA01516

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gaa	ctt	aaa	ggc	ctt	gaa	tgc	ttc	gga	cac	cac	ggg	gtg	ttc	gac	ttt	163					
Glu	Leu	Lys	Gly	Leu	Glu	Cys	Phe	Gly	His	His	Gly	Val	Phe	Asp	Phe						
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gaa	aaa	gag	caa	ggc	cag	ccc	ttc	att	gtg	gat	gtc	acc	tgc	tgg	atg	211					
Glu	Lys	Glu	Gln	Gly	Gln	Pro	Phe	Ile	Val	Asp	Val	Thr	Cys	Trp	Met						
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Asp	Phe	Asp	Ala	Ala	Gly	Ala	Ser	Asp	Asp	Leu	Ser	Asp	Thr	Val	Asp						
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tac	ggc	gcg	ttg	gca	ttg	ttg	gtt	gct	gaa	atc	gtg	gaa	ggc	cca	tcc	307					
Tyr	Gly	Ala	Leu	Ala	Leu	Leu	Val	Ala	Glu	Ile	Val	Glu	Gly	Pro	Ser						
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agg	gat	ttg	atc	gag	acg	gtg	gcc	acg	gaa	tct	gcg	gat	gct	gtg	atg	355					
Arg	Asp	Leu	Ile	Glu	Thr	Val	Ala	Thr	Glu	Ser	Ala	Asp	Ala	Val	Met						
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gct	aaa	ttt	gat	gcg	ctt	cat	gcg	gtg	gaa	gta	acc	atc	cat	aag	ccc	403					
Ala	Lys	Phe	Asp	Ala	Leu	His	Ala	Val	Glu	Val	Thr	Ile	His	Lys	Pro						
				90					95					100							
aaa	gca	ccg	atc	cca	cgt	act	ttt	gct	gac	gtc	gcg	gtg	gtt	gcc	cga	451					
Lys	Ala	Pro	Ile	Pro	Arg	Thr	Phe	Ala	Asp	Val	Ala	Val	Val	Ala	Arg						
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cgt	tcc	agg	aaa	tcc	atg	gct	gct	gga	agg	agc	aac	gcc	taatg	catgc		500					
Arg	Ser	Arg	Lys	Ser	Met	Ala	Ala	Gly	Arg	Ser	Asn	Ala									
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<210> 690

<211> 130

<212> PRT

<213> Corynebacterium glutamicum

<400> 690

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Gly Val Phe Asp Phe Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp
20 25 30

Val Thr Cys Trp Met Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu
35 40 45

Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile
50 55 60

Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser
65 70 75 80

Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val
85 90 95

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val
 100 105 110

Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser
 115 120 125

Asn Ala
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<210> 691

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(952)

<223> RXA01515

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 Met Asn Val Ser Ser
 1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr
 10 15 20

gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg 211
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala
 25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp
 40 45 50

gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser
 55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala
 70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala
 90 95 100

gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451
 Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu
 105 110 115

gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val
 120 125 130

tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547

Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln
 135 140 145
 gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595
 Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp
 150 155 160 165
 gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643
 Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile
 170 175 180
 gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691
 Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp
 185 190 195
 cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739
 Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile
 200 205 210
 ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787
 Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp
 215 220 225
 cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala
 230 235 240 245
 gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His
 250 255 260
 gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg
 265 270 275
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 Ser Gly Gly Thr His His Gly
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<210> 692

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 692

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 Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly
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 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val
 50 55 60
 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys
 65 70 75 80


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                                         Met Ser Ser Leu Pro
                                           1           5

gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag      163
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys
                10                        15                      20
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ggt gcg aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc	211
Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val	
25 30 35	
att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc	259
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly	
40 45 50	
ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca	307
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro	
55 60 65	
atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt	355
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val	
70 75 80 85	
gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca	403
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala	
90 95 100	
acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag	451
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln	
105 110 115	
gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg	499
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly	
120 125 130	
gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg	547
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val	
135 140 145	
gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt	595
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg	
150 155 160 165	
gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc	643
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe	
170 175 180	
ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag	691
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu	
185 190 195	
gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat	739
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp	
200 205 210	
ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc	787
Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly	
215 220 225	
acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt	835
Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe	
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cgc gtg cat gaa gtt gcg gaa acc	859
Arg Val His Glu Val Ala Glu Thr	
250	

<210> 694
 <211> 253
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 694

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Ser	Phe	Tyr	Asp	Lys	Gly	Ala	Thr	Phe	Glu	Asp	Thr	Ala	Ala	Leu	Asn
			20					25					30		
Arg	Ala	Ala	Glu	Val	Ile	Glu	Gln	Gly	Ala	Gly	Ile	Val	Asp	Ile	Gly
		35					40					45			
Gly	Val	Lys	Ala	Gly	Pro	Gly	Asp	Phe	Val	Ser	Ala	Glu	Glu	Glu	Ile
	50					55					60				
Asp	Arg	Val	Val	Pro	Ile	Ile	Ala	Ala	Val	Arg	Glu	Arg	Phe	Pro	Asp
65					70					75				80	
Ile	Asp	Ile	Ser	Val	Asp	Thr	Trp	Arg	Ala	Ser	Val	Ala	Asp	Val	Ala
				85					90					95	
Val	Ala	His	Gly	Ala	Thr	Leu	Ile	Asn	Asp	Thr	Trp	Ala	Gly	His	Asp
			100					105					110		
His	Glu	Leu	Val	Gln	Val	Ala	Gly	Gln	His	Lys	Val	Gly	Tyr	Val	Cys
		115					120					125			
Ser	His	Thr	Gly	Gly	Val	Ile	Pro	Arg	Thr	Arg	Pro	Tyr	Arg	Val	His
	130					135					140				
Phe	Asp	Asp	Ile	Val	Ala	Asp	Val	Ile	Thr	Glu	Thr	Thr	Lys	Leu	Ala
145					150					155				160	
Glu	Gln	Ala	Val	Arg	Ala	Gly	Val	Pro	Glu	Glu	Arg	Val	Phe	Ile	Asp
				165					170					175	
Pro	Thr	His	Asp	Phe	Gly	Lys	Asn	Thr	Phe	His	Gly	Leu	Glu	Leu	Leu
			180					185					190		
Arg	Arg	Ile	Asp	Glu	Val	Val	Ala	Thr	Gly	Trp	Pro	Val	Leu	Met	Ala
		195					200					205			
Leu	Ser	Asn	Lys	Asp	Phe	Ile	Gly	Glu	Thr	Leu	Glu	Arg	Gly	Val	Asp
	210					215					220				
Lys	Arg	Val	Ala	Gly	Thr	Leu	Ala	Ala	Thr	Ala	Trp	Ala	Ala	Ala	Arg
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Gly	Val	Ala	Ala	Phe	Arg	Val	His	Glu	Val	Ala	Glu	Thr			
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00106

<400> 695

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 Met Ile Gly Ala Ile
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tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
 Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
 10 15 20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
 Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
 25 30 35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
 Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
 40 45 50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
 Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
 55 60 65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355
 Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
 70 75 80 85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
 Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
 90 95 100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
 Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
 105 110 115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
 Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
 120 125 130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
 Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
 135 140 145

atc aag gtt taaggagcaa acaacatgag caa 579
 Ile Lys Val
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<210> 696

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 696

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 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
 35 40 45
 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
 50 55 60
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
 65 70 75 80
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
 85 90 95
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
 100 105 110
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
 115 120 125
 Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
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 Lys Phe Gln Arg Tyr Ile Lys Val
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<210> 697
 <211> 1556
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1533)
 <223> RXA00989

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 gat gac atc acc gta ggc gat gtc acg ttg ggc gag act gga ctg tct 96
 Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser
 20 25 30
 ttg ccc atc gat ctc gcc ggt gag gta gaa gca cct gcc tcc gag gag 144
 Leu Pro Ile Asp Leu Ala Gly Glu Val Glu Ala Pro Ala Ser Glu Glu
 35 40 45
 atc acc caa gaa gat ttg ctg cgc ctt gcc cag gtg gaa gca gag ttg 192
 Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu
 50 55 60
 gat caa cgt tgg ttg gaa acc aaa att gat ccc act ttc cga cgc atg 240
 Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met
 65 70 75 80
 agc tac atg atg gat ctc atg ggc caa cca cag aat tcc ttc cca gca 288
 Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala

85								90				95				
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Ile	His	Val	Ala	Gly	Thr	Asn	Gly	Lys	Thr	Ser	Thr	Thr	Arg	Met	Ile	
			100					105					110			
gag	tcg	ttg	ctg	cgc	gca	ttc	cac	cgc	cgc	acc	ggc	cgg	acc	acc	agc	384
Glu	Ser	Leu	Leu	Arg	Ala	Phe	His	Arg	Arg	Thr	Gly	Arg	Thr	Thr	Ser	
		115					120					125				
ccg	cac	ctg	cag	ctg	gta	acc	gaa	cgc	atc	gcg	att	gat	ggc	aag	ccc	432
Pro	His	Leu	Gln	Leu	Val	Thr	Glu	Arg	Ile	Ala	Ile	Asp	Gly	Lys	Pro	
	130					135					140					
atc	cac	ccg	cgt	gat	ttc	gtg	cgg	atc	tac	gaa	gag	att	aag	ccc	tac	480
Ile	His	Pro	Arg	Asp	Phe	Val	Arg	Ile	Tyr	Glu	Glu	Ile	Lys	Pro	Tyr	
145					150					155					160	
atg	gag	atg	acc	gac	gcc	tgg	tca	gag	gcc	gag	ggc	gga	ccg	aag	atg	528
Met	Glu	Met	Thr	Asp	Ala	Trp	Ser	Glu	Ala	Glu	Gly	Gly	Pro	Lys	Met	
				165				170					175			
agc	aag	ttt	gag	gca	ctc	gtg	gcc	ctc	gct	tac	gca	ggc	ttt	gcc	gac	576
Ser	Lys	Phe	Glu	Ala	Leu	Val	Ala	Leu	Ala	Tyr	Ala	Gly	Phe	Ala	Asp	
			180				185						190			
gct	cct	gtt	gac	gtc	gcc	gtc	gtt	gag	gtt	ggc	ctt	ggc	gga	cgc	tgg	624
Ala	Pro	Val	Asp	Val	Ala	Val	Val	Glu	Val	Gly	Leu	Gly	Gly	Arg	Trp	
		195					200					205				
gat	gcc	act	aac	gtg	atc	aac	gca	gct	gtt	tcc	gtg	atc	acc	ccg	gtg	672
Asp	Ala	Thr	Asn	Val	Ile	Asn	Ala	Ala	Val	Ser	Val	Ile	Thr	Pro	Val	
	210					215					220					
ggc	atg	gac	cac	gtg	gat	cgc	ctg	ggc	aac	acc	att	ggc	gaa	atc	gct	720
Gly	Met	Asp	His	Val	Asp	Arg	Leu	Gly	Asn	Thr	Ile	Gly	Glu	Ile	Ala	
225					230					235					240	
ggc	gaa	aag	gcc	ggc	atc	atc	aag	gct	cgt	cct	gca	tct	gag	gat	ggc	768
Gly	Glu	Lys	Ala	Gly	Ile	Ile	Lys	Ala	Arg	Pro	Ala	Ser	Glu	Asp	Gly	
			245				250						255			
acc	gag	cct	gag	ggc	aac	gtt	gtc	atc	gtg	ggc	aag	cag	gag	cca	gaa	816
Thr	Glu	Pro	Glu	Gly	Asn	Val	Val	Ile	Val	Gly	Lys	Gln	Glu	Pro	Glu	
			260				265						270			
gca	atg	aac	gtg	att	ctg	cag	caa	gcc	gtg	gac	gtg	gac	gca	gct	gtt	864
Ala	Met	Asn	Val	Ile	Leu	Gln	Gln	Ala	Val	Asp	Val	Asp	Ala	Ala	Val	
		275				280						285				
gct	cgt	ttg	aac	atg	gaa	ttc	ggc	gtg	gtg	gaa	tcc	gcc	att	gcc	gtt	912
Ala	Arg	Leu	Asn	Met	Glu	Phe	Gly	Val	Val	Glu	Ser	Ala	Ile	Ala	Val	
	290					295					300					
ggc	gga	cag	cag	ctc	acc	ctg	aag	ggc	ttg	ggc	ggc	gaa	tac	acc	gac	960
Gly	Gly	Gln	Gln	Leu	Thr	Leu	Lys	Gly	Leu	Gly	Gly	Glu	Tyr	Thr	Asp	
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1008																
Ile	Phe	Leu	Pro	Leu	Ser	Gly	Ala	His	Gln	Ala	Asp	Asn	Ala	Ala	Val	

325								330				335			
gct ctc gca gca gtg gaa gca ttt ttc ggt gca tcc gcc gga cgc cca															
1056															
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ttg gat atc gac acg gtg cgc gaa ggc ttc gca caa gtt cag tcc cca															
1104															
Leu	Asp	Ile	Asp	Thr	Val	Arg	Glu	Gly	Phe	Ala	Gln	Val	Gln	Ser	Pro
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ggt cgc ctc gag cgc ctg cgc tct gca cca acc gtg ttc atc gac gca															
1152															
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385					390					395					400
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1248															
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				405					410					415	
aag gat gcc cgc ggc atc ttg gaa tca ctt gag cca tac ctg cat gaa															
1296															
Lys	Asp	Ala	Arg	Gly	Ile	Leu	Glu	Ser	Leu	Glu	Pro	Tyr	Leu	His	Glu
		420						425					430		
att gtg tgc acc cag act gcc tca gag cgc gca ttg gac gca tac gat															
1344															
Ile	Val	Cys	Thr	Gln	Thr	Ala	Ser	Glu	Arg	Ala	Leu	Asp	Ala	Tyr	Asp
		435					440					445			
tta gct gaa tat gct cga gag atc tac ggc gat gag cgt gtg cac gtc															
1392															
Leu	Ala	Glu	Tyr	Ala	Arg	Glu	Ile	Tyr	Gly	Asp	Glu	Arg	Val	His	Val
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caa gaa gat ctt gct ggc gcg gta gaa ctc gct att gaa cta gca gaa															
1440															
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gac acc gat gta cag tcc gga tca ggt gtt gtg atc acc ggt tca atc															
1488															
Asp	Thr	Asp	Val	Gln	Ser	Gly	Ser	Gly	Val	Val	Ile	Thr	Gly	Ser	Ile
				485					490					495	
gtg acc gcc ggc gat gcg cgc acg ctg ttt gga aag gaa cct gca															
1533															
Val	Thr	Ala	Gly	Asp	Ala	Arg	Thr	Leu	Phe	Gly	Lys	Glu	Pro	Ala	
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 <213> Corynebacterium glutamicum

<400> 698

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Leu	Pro	Ile	Asp	Leu	Ala	Gly	Glu	Val	Glu	Ala	Pro	Ala	Ser	Glu	Glu
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Ile	Thr	Gln	Glu	Asp	Leu	Leu	Arg	Leu	Ala	Gln	Val	Glu	Ala	Glu	Leu
	50					55					60				
Asp	Gln	Arg	Trp	Leu	Glu	Thr	Lys	Ile	Asp	Pro	Thr	Phe	Arg	Arg	Met
65					70					75					80
Ser	Tyr	Met	Met	Asp	Leu	Met	Gly	Gln	Pro	Gln	Asn	Ser	Phe	Pro	Ala
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Ile	His	Val	Ala	Gly	Thr	Asn	Gly	Lys	Thr	Ser	Thr	Thr	Arg	Met	Ile
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Glu	Ser	Leu	Leu	Arg	Ala	Phe	His	Arg	Arg	Thr	Gly	Arg	Thr	Thr	Ser
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Pro	His	Leu	Gln	Leu	Val	Thr	Glu	Arg	Ile	Ala	Ile	Asp	Gly	Lys	Pro
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Met	Glu	Met	Thr	Asp	Ala	Trp	Ser	Glu	Ala	Glu	Gly	Gly	Pro	Lys	Met
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Ser	Lys	Phe	Glu	Ala	Leu	Val	Ala	Leu	Ala	Tyr	Ala	Gly	Phe	Ala	Asp
			180					185					190		
Ala	Pro	Val	Asp	Val	Ala	Val	Val	Glu	Val	Gly	Leu	Gly	Gly	Arg	Trp
		195					200					205			
Asp	Ala	Thr	Asn	Val	Ile	Asn	Ala	Ala	Val	Ser	Val	Ile	Thr	Pro	Val
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Gly	Met	Asp	His	Val	Asp	Arg	Leu	Gly	Asn	Thr	Ile	Gly	Glu	Ile	Ala
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Ala	Met	Asn	Val	Ile	Leu	Gln	Gln	Ala	Val	Asp	Val	Asp	Ala	Ala	Val
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Ile	Phe	Leu	Pro	Leu	Ser	Gly	Ala	His	Gln	Ala	Asp	Asn	Ala	Ala	Val
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Ala	Leu	Ala	Ala	Val	Glu	Ala	Phe	Phe	Gly	Ala	Ser	Ala	Gly	Arg	Pro
			340					345					350		
Leu	Asp	Ile	Asp	Thr	Val	Arg	Glu	Gly	Phe	Ala	Gln	Val	Gln	Ser	Pro
	355						360					365			
Gly	Arg	Leu	Glu	Arg	Leu	Arg	Ser	Ala	Pro	Thr	Val	Phe	Ile	Asp	Ala
370						375					380				
Ala	His	Asn	Pro	His	Gly	Ala	Ala	Ala	Leu	Gly	Ala	Ala	Leu	Asp	Arg
385					390					395					400
Asp	Phe	Glu	Phe	Arg	Arg	Leu	Ile	Gly	Val	Ile	Gly	Val	Leu	Cys	Asp
				405					410					415	
Lys	Asp	Ala	Arg	Gly	Ile	Leu	Glu	Ser	Leu	Glu	Pro	Tyr	Leu	His	Glu
			420					425					430		
Ile	Val	Cys	Thr	Gln	Thr	Ala	Ser	Glu	Arg	Ala	Leu	Asp	Ala	Tyr	Asp
		435					440					445			
Leu	Ala	Glu	Tyr	Ala	Arg	Glu	Ile	Tyr	Gly	Asp	Glu	Arg	Val	His	Val
	450					455					460				
Gln	Glu	Asp	Leu	Ala	Gly	Ala	Val	Glu	Leu	Ala	Ile	Glu	Leu	Ala	Glu
465					470					475					480
Asp	Thr	Asp	Val	Gln	Ser	Gly	Ser	Gly	Val	Val	Ile	Thr	Gly	Ser	Ile
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Val	Thr	Ala	Gly	Asp	Ala	Arg	Thr	Leu	Phe	Gly	Lys	Glu	Pro	Ala	
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<211> 600

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(577)

<223> RXA01517

<400> 699

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 Met His Ala Val Leu
 1 5

tcc atc ggt tcc aac atg gat gat cgc tac gcg ctg ctc aac aca gtg 163
 Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala Leu Leu Asn Thr Val

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Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser				
	25	30	35	
acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg				259
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val				
	40	45	50	
ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc				307
Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly				
	55	60	65	
caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg				355
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly				
	70	75	80	85
cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa				403
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu				
	90	95	100	
gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct				451
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala				
	105	110	115	
tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat				499
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp				
	120	125	130	
gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat				547
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp				
	135	140	145	
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Pro Thr Asp Ile Glu Gly Val Thr Lys Ile				
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gca				600
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Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu				
	35	40	45	
Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu				
	50	55	60	
Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg				
	65	70	75	80

Val	Arg	Lys	Trp	Gly	Pro	Arg	Thr	Leu	Asp	Val	Asp	Ile	Val	Gln	Ile
				85					90					95	
Ile	Lys	Asp	Gly	Glu	Glu	Ile	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Thr	Leu
			100					105					110		
Pro	His	Pro	Trp	Ala	Trp	Gln	Arg	Ala	Phe	Val	Leu	Ile	Pro	Trp	Leu
		115					120					125			
Glu	Ala	Glu	Pro	Asp	Ala	Val	Leu	His	Gly	Thr	Thr	Ile	Ala	Glu	His
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<223> RXA00579
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Met Arg Val Leu Ile
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Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu
10 15 20

gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata 211
Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile
25 30 35

gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac 259
Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His
40 45 50

gcc ggc gtt gcg gct gat ttt ggt atc tgt gca ggc gtc att gag cgt 307
Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg
55 60 65

gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg 355
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala
70 75 80 85

ttg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg gtc cac ggt	403
Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly	
90 95 100	

gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc 451
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile
105 110 115

cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc	499
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg	
120 125 130	
ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc	547
Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile	
135 140 145	
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Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His	
150 155 160 165	
ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc	643
Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe	
170 175 180	
ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att	691
Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile	
185 190 195	
ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat	739
Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His	
200 205 210	
tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt	787
Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu	
215 220 225	
ggt gat gcc agc ggt cct ctc gca gcg aca aaa acc cat aat gtc ggc	835
Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly	
230 235 240 245	
gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca	883
Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser	
250 255 260	
ggt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt	931
Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly	
265 270 275	
tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt	979
Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser	
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1027	
Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu	
295 300 305	
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1075	
Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe	
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Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro	
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 Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr
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 Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser
 360 365 370

tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc
 1267
 Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala
 375 380 385

cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat
 1315
 Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr
 390 395 400 405

ggt gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg
 1363
 Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro
 410 415 420

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 Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro
 425 430 435

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 Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu
 440 445 450

atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg
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 Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu
 455 460 465

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 Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro
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 1603
 Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr
 490 495 500

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 Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser
 505 510 515

ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt
 1699
 Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly
 520 525 530

gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct
 1747
 Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala
 535 540 545

cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc
 1795
 Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly
 550 555 560 565

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 1843
 Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn
 570 575 580

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg
 1891
 His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro
 585 590 595

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 1939
 Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn
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 615 620

<210> 702
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<400> 702
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 35 40 45
 Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala
 50 55 60
 Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly
 65 70 75 80
 His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro
 85 90 95
 Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly
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 Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser
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Met	Val	Ala	Thr	Arg	Leu	Pro	Glu	Ser	Leu	Lys	Ala	Thr	Ala	Thr	Ser	130	135	140	
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Gly	Val	Gln	Phe	His	Pro	Glu	Ser	Ile	Gly	Gly	Gln	Phe	Gly	His	Gln	165	170	175	
Ile	Ile	Lys	Asn	Phe	Leu	Asn	Leu	Ala	Arg	Thr	Tyr	Arg	Trp	Gln	Leu	180	185	190	
Thr	Glu	Lys	Thr	Ile	Pro	Leu	Ser	Val	Asp	Ser	Ala	Ala	Val	Phe	Glu	195	200	205	
Thr	Phe	Phe	Ala	His	Ser	Ser	His	Ala	Phe	Trp	Leu	Asp	Asp	Ala	Gln	210	215	220	
Gly	Thr	Ser	Tyr	Leu	Gly	Asp	Ala	Ser	Gly	Pro	Leu	Ala	Arg	Thr	Lys	225	230	235	240
Thr	His	Asn	Val	Gly	Glu	Gly	Asp	Phe	Phe	Thr	Trp	Leu	Lys	Glu	Asp	245	250	255	
Leu	Ala	Ala	Asn	Ser	Val	Ala	Pro	Gly	Gln	Gly	Phe	Arg	Leu	Gly	Trp	260	265	270	
Val	Gly	Tyr	Val	Gly	Tyr	Glu	Leu	Lys	Ala	Glu	Ala	Gly	Ala	Arg	Ala	275	280	285	
Ala	His	Thr	Ser	Ser	Leu	Pro	Asp	Ala	His	Leu	Ile	Phe	Ala	Asp	Arg	290	295	300	
Ala	Ile	Ala	Val	Glu	Ser	Asp	Gln	Val	Arg	Leu	Leu	Ala	Leu	Gly	Glu	305	310	315	320
Gln	Asp	Glu	Trp	Phe	Glu	Glu	Thr	Ile	Lys	Lys	Leu	His	Asn	Leu	Val	325	330	335	
Ala	Pro	Arg	Ile	Pro	Ala	Ser	Gly	His	Leu	Ala	Leu	Gln	Val	Arg	Asp	340	345	350	
Ser	Lys	Asp	Glu	Tyr	Leu	Asp	Lys	Ile	Arg	Arg	Ala	Gln	Glu	Leu	Ile	355	360	365	
Thr	Arg	Gly	Glu	Ser	Tyr	Glu	Ile	Cys	Leu	Thr	Thr	Lys	Leu	Gln	Gly	370	375	380	
Thr	Thr	Asp	Val	Ala	Pro	Leu	Ala	Ala	Tyr	Leu	Ala	Leu	Arg	Gly	Ala	385	390	395	400
Asn	Pro	Thr	Ala	Tyr	Gly	Ala	Tyr	Leu	Gln	Leu	Gly	Asp	Thr	Ser	Ile	405	410	415	
Leu	Ser	Ser	Ser	Pro	Glu	Arg	Phe	Ile	Thr	Ile	Asp	Ser	Ala	Gly	Tyr	420	425	430	
Val	Glu	Ser	Lys	Pro	Ile	Lys	Gly	Thr	Arg	Pro	Arg	Gly	Arg	Thr	Ala	435	440	445	
Gln	Glu	Asp	Gln	Glu	Ile	Ile	Ala	Glu	Leu	Arg	Ser	Asn	Pro	Lys	Asp				

450	455	460
Arg Ala Glu Asn Leu Met 465	Ile Val Asp Leu Val 470	Arg Asn Asp Leu Ala 475 480
Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val 485		490 495
Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu 500		505 510
Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly 515		520 525
Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp 530		535 540
Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr 545		550 555 560
Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu 565		570 575
Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu 580		585 590
Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser 595		600 605
Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro 610		615 620

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<211> 747

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(724)

<223> RXA00958

<400> 703

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ccattgcgct tgctgctggt tccactttgg aggtcatccg atg aca cac gtt gtt 115
Met Thr His Val Val
1 5

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163
Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe
10 15 20

gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211
Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val
25 30 35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259
Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly
40 45 50

cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307
 Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
 55 60 65
 aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
 Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala
 70 75 80 85
 ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403
 Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His
 90 95 100
 ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451
 Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro
 105 110 115
 gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499
 Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile
 120 125 130
 cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547
 Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val
 135 140 145
 gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595
 Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile
 150 155 160 165
 ggt gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643
 Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly
 170 175 180
 ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691
 Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile
 185 190 195
 ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744
 Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
 200 205
 tca 747

<210> 704

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 704

Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn
 1 5 10 15
 Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg
 20 25 30
 Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile
 35 40 45
 Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met
 50 55 60

Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys
65 70 75 80

Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro
85 90 95

Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala
100 105 110

Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro
115 120 125

Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His
130 135 140

Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr
145 150 155 160

Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp
165 170 175

Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro
180 185 190

Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
195 200 205

<210> 705

<211> 1266

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1243)

<223> RXA02790

<400> 705

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agggaatttt cccaggatga accaaatccg aaaccgccgg atg gag ccc gtc tac 115
Met Glu Pro Val Tyr
1 5

gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile
10 15 20

ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211
Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg
25 30 35

acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259
Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val
40 45 50

gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa	307
Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu	
55 60 65	
gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc	355
Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser	
70 75 80 85	
aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag	403
Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln	
90 95 100	
gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac	451
Glu Gln Met Asn Ala Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp	
105 110 115	
aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac	499
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp	
120 125 130	
gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc	547
Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile	
135 140 145	
gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag	595
Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu	
150 155 160 165	
gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc	643
Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val	
170 175 180	
cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag	691
Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys	
185 190 195	
cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc	739
Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser	
200 205 210	
aac gac gcc cag gga atc ctc acc gat ctg atc acg cga tca gca aac	787
Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn	
215 220 225	
cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt	835
His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu	
230 235 240 245	
act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca	883
Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu Ile Glu Arg Glu Ala	
250 255 260	
cca gca gga gat ttt gat aag gtc gcc cgc gtc atc ttg aac cgt ctc	931
Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu	
265 270 275	
gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg	979
Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu	
280 285 290	

tct gaa caa gaa gta gca acc acc gac gaa gac cgt cag acc gtc acc
1027
Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp Arg Gln Thr Val Thr
295 300 305

cca tgg aac act tac gcc atg gac ggc ctg cca caa acc ccc atc gcc
1075
Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala
310 315 320 325

gca gta tcc acc gaa gca ctc caa gcc atg gaa aac cct gca gaa gga
1123
Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu Asn Pro Ala Glu Gly
330 335 340

aac tgg ctg tac ttt gtc acc atc gac acc gat gga acc acc gtg ttc
1171
Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp Gly Thr Thr Val Phe
345 350 355

aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac
1219
Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile Glu Gln Ala Leu Asn
360 365 370

agt ggc gtt cta gac agc aac cga taaggatcag cgaataaaat tgg
1266
Ser Gly Val Leu Asp Ser Asn Arg
375 380

<210> 706

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 706

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Ile Ala Ser Leu Ile Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val
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Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly
35 40 45

Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu
50 55 60

Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe
65 70 75 80

Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly
85 90 95

Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Val Ser Ala
100 105 110

Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly
115 120 125

Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly
 130 135 140

Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn
 145 150 155 160

Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro
 165 170 175

Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg
 180 185 190

Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr
 195 200 205

Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile
 210 215 220

Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala
 225 230 235 240

Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu
 245 250 255

Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val
 260 265 270

Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr
 275 280 285

Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp
 290 295 300

Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro
 305 310 315 320

Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu
 325 330 335

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp
 340 345 350

Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile
 355 360 365

Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg
 370 375 380

<210> 707

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00106

<400> 707

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gctacgatcc acacccattg atccgcggca aggtcgccgt atg atc ggt gcg att 115
 Met Ile Gly Ala Ile
 1 5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
 Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
 10 15 20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
 Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
 25 30 35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
 Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
 40 45 50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
 Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
 55 60 65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355
 Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
 70 75 80 85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
 Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
 90 95 100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
 Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
 105 110 115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
 Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
 120 125 130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
 Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
 135 140 145

atc aag gtt taaggagcaa acaacatgag caa 579
 Ile Lys Val
 150

<210> 708

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 708

Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp
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Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
 20 25 30

Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
 35 40 45

Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
 50 55 60
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
 65 70 75 80
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
 85 90 95
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
 100 105 110
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
 115 120 125
 Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
 130 135 140
 Lys Phe Gln Arg Tyr Ile Lys Val
 145 150

<210> 709
 <211> 2599
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2599)
 <223> RXN02198

<400> 709
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 Met Ser Thr Ser Val
 1 5
 act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
 Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
 10 15 20
 ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
 25 30 35
 caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
 Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
 40 45 50
 tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307
 Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
 55 60 65
 cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355
 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
 70 75 80 85
 ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt 403
 Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg

90				95				100								
tgc	cgt	gag	ctt	gcc	tac	aag	ggc	act	gca	gtg	gct	agg	gaa	gtg	gct	451
Cys	Arg	Glu	Leu	Ala	Tyr	Lys	Gly	Thr	Ala	Val	Ala	Arg	Glu	Val	Ala	
			105					110					115			
gat	gag	atg	ggg	ccg	ggc	cga	aac	ggc	atg	cgg	cgt	ttc	gtg	gtt	ggt	499
Asp	Glu	Met	Gly	Pro	Gly	Arg	Asn	Gly	Met	Arg	Arg	Phe	Val	Val	Gly	
		120					125					130				
tcc	ctg	gga	cct	gga	acg	aag	ctt	cca	tcg	ctg	ggc	cat	gca	ccg	tat	547
Ser	Leu	Gly	Pro	Gly	Thr	Lys	Leu	Pro	Ser	Leu	Gly	His	Ala	Pro	Tyr	
	135					140					145					
gca	gat	ttg	cgt	ggg	cac	tac	aag	gaa	gca	gcg	ctt	ggc	atc	atc	gac	595
Ala	Asp	Leu	Arg	Gly	His	Tyr	Lys	Glu	Ala	Ala	Leu	Gly	Ile	Ile	Asp	
150					155				160						165	
ggt	ggt	ggc	gat	gcc	ttt	ttg	att	gag	act	gct	cag	gac	ttg	ctt	cag	643
Gly	Gly	Gly	Asp	Ala	Phe	Leu	Ile	Glu	Thr	Ala	Gln	Asp	Leu	Leu	Gln	
				170				175						180		
gtc	aag	gct	gcg	gtt	cac	ggc	gtt	caa	gat	gcc	atg	gct	gaa	ctt	gat	691
Val	Lys	Ala	Ala	Val	His	Gly	Val	Gln	Asp	Ala	Met	Ala	Glu	Leu	Asp	
			185					190					195			
aca	ttc	ttg	ccc	att	att	tgc	cac	gtc	acc	gta	gag	acc	acc	ggc	acc	739
Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val	Glu	Thr	Thr	Gly	Thr	
		200				205						210				
atg	ctc	atg	ggt	tct	gag	atc	ggt	gcc	gcg	ttg	aca	gcg	ctg	cag	cca	787
Met	Leu	Met	Gly	Ser	Glu	Ile	Gly	Ala	Ala	Leu	Thr	Ala	Leu	Gln	Pro	
	215					220					225					
ctg	ggt	atc	gac	atg	att	ggt	ctg	aac	tgc	gcc	acc	ggc	cca	gat	gag	835
Leu	Gly	Ile	Asp	Met	Ile	Gly	Leu	Asn	Cys	Ala	Thr	Gly	Pro	Asp	Glu	
230					235				240						245	
atg	agc	gag	cac	ctg	cgt	tac	ctg	tcc	aag	cac	gcc	gat	att	cct	gtg	883
Met	Ser	Glu	His	Leu	Arg	Tyr	Leu	Ser	Lys	His	Ala	Asp	Ile	Pro	Val	
				250				255						260		
tcg	gtg	atg	cct	aac	gca	ggt	ctt	cct	gtc	ctg	ggt	aaa	aac	ggt	gca	931
Ser	Val	Met	Pro	Asn	Ala	Gly	Leu	Pro	Val	Leu	Gly	Lys	Asn	Gly	Ala	
			265					270					275			
gaa	tac	cca	ctt	gag	gct	gag	gat	ttg	gcg	cag	gcg	ctg	gct	gga	ttc	979
Glu	Tyr	Pro	Leu	Glu	Ala	Glu	Asp	Leu	Ala	Gln	Ala	Leu	Ala	Gly	Phe	
		280				285						290				
gtc	tcc	gaa	tat	ggc	ctg	tcc	atg	gtg	ggt	ggt	tgt	tgt	ggc	acc	aca	
1027																
Val	Ser	Glu	Tyr	Gly	Leu	Ser	Met	Val	Gly	Gly	Cys	Cys	Gly	Thr	Thr	
	295					300					305					
cct	gag	cac	atc	cgt	gcg	gtc	cgc	gat	gcg	gtg	ggt	ggt	ggt	cca	gag	
1075																
Pro	Glu	His	Ile	Arg	Ala	Val	Arg	Asp	Ala	Val	Val	Gly	Val	Pro	Glu	
310					315					320					325	

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 1123
 Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln
 330 335 340

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc
 1171
 Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr
 345 350 355

tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc
 1219
 Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg
 360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc
 1267
 Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly
 375 380 385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt
 1315
 Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly
 390 395 400 405

gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc
 1363
 Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr
 410 415 420

gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg
 1411
 Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu
 425 430 435

cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt
 1459
 Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu
 440 445 450

gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac
 1507
 Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp
 455 460 465

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag
 1555
 Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys
 470 475 480 485

cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag
 1603
 Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln
 490 495 500

gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac
 1651
 Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp
 505 510 515

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac
1699
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp
520 525 530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat
1747
Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp
535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca
1795
Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro
550 555 560 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac
1843
Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn
570 575 580

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1939
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro
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1987
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Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln
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Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile
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Thr	Ala	Leu	Gln	Pro	Leu	Gly	Ile	Asp	Met	Ile	Gly	Leu	Asn	Cys	Ala			
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 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
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 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
 690 695 700
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 705 710 715 720
 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala

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Gly	Asp	Val	His	Asp	Ile	Gly	Lys	Asn	Leu	Val	Asp	Ile	Ile	Leu	Ser	
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Asp

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 Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
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Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg	
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Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala	
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Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr	
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Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala	
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 760 765 770

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 775 780 785

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Asp	Ile	Ala	Asp	Arg	Cys	Arg	Glu	Leu	Ala	Tyr	Lys	Gly	Thr	Ala	Val	100	105	110
Ala	Arg	Glu	Val	Ala	Asp	Glu	Met	Gly	Pro	Gly	Arg	Asn	Gly	Met	Arg	115	120	125
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Gln	Asp	Leu	Leu	Gln	Val	Lys	Ala	Ala	Val	His	Gly	Val	Gln	Asp	Ala	180	185	190
Met	Ala	Glu	Leu	Asp	Thr	Phe	Leu	Pro	Ile	Ile	Cys	His	Val	Thr	Val	195	200	205
Glu	Thr	Thr	Gly	Thr	Met	Leu	Met	Gly	Ser	Glu	Ile	Gly	Ala	Ala	Leu	210	215	220
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Val	Gly	Val	Pro	Glu	Gln	Glu	Thr	Ser	Thr	Leu	Thr	Lys	Ile	Pro	Ala	325	330	335
Gly	Pro	Val	Glu	Gln	Ala	Ser	Arg	Glu	Val	Glu	Lys	Glu	Asp	Ser	Val	340	345	350
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Met	Ile	Gly	Glu	Arg	Thr	Asn	Ser	Asn	Gly	Ser	Lys	Ala	Phe	Arg	Glu	370	375	380
Ala	Met	Leu	Ser	Gly	Asp	Trp	Glu	Lys	Cys	Val	Asp	Ile	Ala	Lys	Gln	385	390	395

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 Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala

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Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
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Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
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Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
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Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
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675 680 685

Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
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Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp
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Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu

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 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
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 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
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 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
 470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc
 1603
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
 490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg
 1651
 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
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cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag
 1699
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
 520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc
 1747
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
 535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca
 1795
 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
 550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag
 1843
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
 570 575 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg
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 35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
 50 55 60
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 65 70 75 80
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 100 105 110
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
 115 120 125
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
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 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
 355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro

370					375					380					
Ile	Thr	Gln	Glu	Leu	Pro	Gly	Arg	Ser	Arg	Gly	Ser	Phe	Asp	Thr	Arg
385					390					395					400
Val	Thr	Leu	Gln	Glu	Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr
				405					410					415	
Thr	Ile	Gly	Ser	Phe	Pro	Gln	Thr	Pro	Ser	Ile	Arg	Ser	Ala	Arg	Ala
			420					425					430		
Arg	Leu	Arg	Lys	Glu	Ser	Ile	Thr	Leu	Glu	Gln	Tyr	Glu	Glu	Ala	Met
		435					440					445			
Arg	Glu	Glu	Ile	Asp	Leu	Val	Ile	Ala	Lys	Gln	Glu	Glu	Leu	Gly	Leu
	450					455					460				
Asp	Val	Leu	Val	His	Gly	Glu	Pro	Glu	Arg	Asn	Asp	Met	Val	Gln	Tyr
465						470					475				480
Phe	Ser	Glu	Leu	Leu	Asp	Gly	Phe	Leu	Ser	Thr	Ala	Asn	Gly	Trp	Val
				485					490					495	
Gln	Ser	Tyr	Gly	Ser	Arg	Cys	Val	Arg	Pro	Pro	Val	Leu	Phe	Gly	Asn
			500					505					510		
Val	Ser	Arg	Pro	Ala	Pro	Met	Thr	Val	Lys	Trp	Phe	Gln	Tyr	Ala	Gln
		515					520					525			
Ser	Leu	Thr	Gln	Lys	His	Val	Lys	Gly	Met	Leu	Thr	Gly	Pro	Val	Thr
	530					535					540				
Ile	Leu	Ala	Trp	Ser	Phe	Val	Arg	Asp	Asp	Gln	Pro	Leu	Ala	Thr	Thr
545						550					555				560
Ala	Asp	Gln	Val	Ala	Leu	Ala	Leu	Arg	Asp	Glu	Ile	Asn	Asp	Leu	Ile
				565					570					575	
Glu	Ala	Gly	Ala	Lys	Ile	Ile	Gln	Val	Asp	Glu	Pro	Ala	Ile	Arg	Glu
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Leu	Leu	Pro	Ala	Thr	Arg	Arg	Arg								
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 <223> FRXA02086

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 Met Ser Leu Arg Phe
 1 5


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gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag 163
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
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tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac 211
Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
      25      30      35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc* aac gaa gtg atc 259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
      40      45      50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
      55      60      65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
      70      75      80      85

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct 403
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
      90      95      100

tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg 451
Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
      105      110      115

gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
      120      125      130

gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct 547
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
      135      140      145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600
Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
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aac 603

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<213> Corynebacterium glutamicum

<400> 718

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Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
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Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
      35      40      45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
      50      55      60

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Thr	Ile	Glu	Ala	Ala	Arg	Ser	Asp	Met	Gln	Val	Leu	Ala	Ala	Leu	Lys
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Ser	Ser	Gly	Phe	Glu	Leu	Gly	Val	Gly	Pro	Gly	Val	Trp	Asp	Ile	His
				85					90					95	
Ser	Pro	Arg	Val	Pro	Ser	Ala	Gln	Lys	Val	Asp	Gly	Leu	Leu	Glu	Ala
			100					105					110		
Ala	Leu	Gln	Ser	Val	Asp	Pro	Arg	Gln	Leu	Trp	Val	Asn	Pro	Asp	Cys
		115					120					125			
Gly	Leu	Lys	Thr	Arg	Gly	Trp	Pro	Glu	Val	Glu	Ala	Ser	Leu	Lys	Val
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 <223> RXN02648

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 Met Ser Gln Asn Arg
 1 5
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403

Leu	Gly	Gly	Leu	Thr	Met	Thr	Asp	Thr	Asp	Arg	Trp	Ala	Ser	Gln	Glu	
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gca	gtg	cgt	tcc	acc	cct	ggc	aac	atc	gag	ctg	acc	agc	ttc	tct	gat	451
Ala	Val	Arg	Ser	Thr	Pro	Gly	Asn	Ile	Glu	Leu	Thr	Ser	Phe	Ser	Asp	
			105					110					115			
cgt	cgc	gac	cgc	gca	ttg	ttc	agc	gaa	gca	tac	gag	gat	cca	gta	tct	499
Arg	Arg	Asp	Arg	Ala	Leu	Phe	Ser	Glu	Ala	Tyr	Glu	Asp	Pro	Val	Ser	
		120					125					130				
ggc	atc	ttc	acc	ggc	cgc	gct	tct	gtg	ggc	aac	cca	gag	ttc	acc	gga	547
Gly	Ile	Phe	Thr	Gly	Arg	Ala	Ser	Val	Gly	Asn	Pro	Glu	Phe	Thr	Gly	
	135					140					145					
cct	att	acc	tac	att	ggc	cag	gaa	gaa	act	cag	acg	gat	gtt	gat	ctg	595
Pro	Ile	Thr	Tyr	Ile	Gly	Gln	Glu	Glu	Thr	Gln	Thr	Asp	Val	Asp	Leu	
150					155					160					165	
ctg	aag	aag	ggc	atg	aac	gca	gcg	gga	gct	acc	gac	ggc	ttc	gtt	gca	643
Leu	Lys	Lys	Gly	Met	Asn	Ala	Ala	Gly	Ala	Thr	Asp	Gly	Phe	Val	Ala	
				170				175						180		
gca	cta	tcc	cca	gga	tct	gca	gct	cga	ttg	acc	aac	aag	ttc	tac	gac	691
Ala	Leu	Ser	Pro	Gly	Ser	Ala	Ala	Arg	Leu	Thr	Asn	Lys	Phe	Tyr	Asp	
			185					190					195			
act	gat	gaa	gaa	gtc	gtc	gca	gca	tgt	gct	gat	gcg	ctt	tcc	cag	gaa	739
Thr	Asp	Glu	Glu	Val	Val	Ala	Ala	Cys	Ala	Asp	Ala	Leu	Ser	Gln	Glu	
		200				205						210				
tac	aag	atc	atc	acc	gat	gca	ggc	ctg	acc	gtt	cag	ctc	gac	gca	ccg	787
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro	
	215					220					225					
gac	ttg	gca	gaa	gca	tgg	gat	cag	atc	aac	cca	gag	cca	agc	gtg	aag	835
Asp	Leu	Ala	Glu	Ala	Trp	Asp	Gln	Ile	Asn	Pro	Glu	Pro	Ser	Val	Lys	
230					235					240				245		
gat	tac	ttg	gac	tgg	atc	ggc	aca	cgc	atc	gat	gcc	atc	aac	agt	gca	883
Asp	Tyr	Leu	Asp	Trp	Ile	Gly	Thr	Arg	Ile	Asp	Ala	Ile	Asn	Ser	Ala	
				250				255						260		
gtg	aag	ggc	ctt	cca	aag	gaa	cag	acc	cgc	ctg	cac	atc	tgc	tgg	ggc	931
Val	Lys	Gly	Leu	Pro	Lys	Glu	Gln	Thr	Arg	Leu	His	Ile	Cys	Trp	Gly	
			265					270					275			
tct	tgg	cac	gga	cca	cac	gtc	act	gac	atc	cca	ttc	ggc	gac	atc	att	979
Ser	Trp	His	Gly	Pro	His	Val	Thr	Asp	Ile	Pro	Phe	Gly	Asp	Ile	Ile	
		280					285					290				
ggc	gag	atc	ctg	cgc	gca	gag	gtc	ggc	ggc	ttc	tcc	ttc	gaa	ggc	gca	
1027																
Gly	Glu	Ile	Leu	Arg	Ala	Glu	Val	Gly	Gly	Phe	Ser	Phe	Glu	Gly	Ala	
	295					300					305					
tct	cct	cgt	cac	gca	cac	gag	tgg	cgt	gta	tgg	gaa	gaa	aac	aag	ctt	
1075																
Ser	Pro	Arg	His	Ala	His	Glu	Trp	Arg	Val	Trp	Glu	Glu	Asn	Lys	Leu	
310					315					320					325	

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac
 1123
 Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
 330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc
 1171
 Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
 345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg
 1219
 Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
 360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta
 1267
 Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
 375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac
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 Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 390 395 400

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 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80
 Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95
 Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110
 Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg
 340 345 350
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
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 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
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 Phe

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<223> FRXA02648

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agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
           20           25           30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
           35           40           45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
           50           55           60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc 240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
  65           70           75           80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
           85           90           95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac 336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
           100           105           110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt 384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
           115           120           125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac 432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
           130           135           140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145           150           155           160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
           165           170           175

taagctagac aacgagggtt gct 548

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<400> 722

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  20           25           30

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Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95
 Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
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 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
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 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
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<212> DNA

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 Met Ser Gln Asn Arg
 1 5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85

 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
 90 95 100

 gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115

 cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130

 ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145

 cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165

 ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180

 gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195

 act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210

 tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
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<210> 724

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 724

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 Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30

 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn

65	70	75	80
Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg	85	90	95
Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu	100	105	110
Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr	115	120	125
Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn	130	135	140
Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln	145	150	155
Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr	165	170	175
Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr	180	185	190
Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp	195	200	205
Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val	210	215	220
Gln Leu Asp Ala	225		

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<211> 551

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(528)

<223> RXS02197

<400> 725

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ttg tgc atc gcg gat ttc att cgc cca cgc gag caa gct gtc aag gac	96
Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp	
20 25 30	
ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct	144
Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro	
35 40 45	
att gct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag	192
Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu	
50 55 60	
tac ttg gaa gtt cac ggc atc ggc gtg cag ctc acc gaa gca ttg gcc	240

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80
 gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt 288
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95
 gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110
 ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct 384
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125
 gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt 432
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
 130 135 140
 atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc 480
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
 145 150 155 160
 aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc 528
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
 165 170 175
 taacaccttt gagagggaaa act 551

<210> 726

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 726

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 Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
 20 25 30
 Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
 35 40 45
 Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
 50 55 60
 Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80
 Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95
 Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg

130		135		140
Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser				
145		150		155
Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val				
	165		170	175

<210> 727
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 <212> DNA
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<220>
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 <223> RXC00988

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ccgccggcga tgcgcgcacg ctgtttggaa aggaacctgc atg agc aag cgt gaa 115
 Met Ser Lys Arg Glu
 1 5

gaa tca att gag tac gga cca tta ggc aaa ggc cac gat cca tta aag 163
 Glu Ser Ile Glu Tyr Gly Pro Leu Gly Lys Gly His Asp Pro Leu Lys
 10 15 20

gat ccc atg aag ggt atc cga ggt gtc atg gcc ggc acc tta gtg atg 211
 Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala Gly Thr Leu Val Met
 25 30 35

gaa gca atc acc tta ggt ctt gtt ctc acc gtg att ctg cgc gtg gac 259
 Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val Ile Leu Arg Val Asp
 40 45 50

gac ggc atc tac tgg acc acc ttc aac tgg gtc tat gta tca gca gtc 307
 Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val Tyr Val Ser Ala Val
 55 60 65

gcg atc gca cac ttt gtt gct gca ttt ctg caa agg ttt agt tgg tcc 355
 Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln Arg Phe Ser Trp Ser
 70 75 80 85

atc ccg atg aac atc gtg ctg cag gtt ctt gca ctt gcc ggt ttc ttt 403
 Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala Leu Ala Gly Phe Phe
 90 95 100

gtt cac ccc gcg atg ggc ttc gcc gcc atc atc ttc atc atc gcg tgg 451
 Val His Pro Ala Met Gly Phe Ala Ala Ile Ile Phe Ile Ile Ala Trp
 105 110 115

gcg tac ctg ttc tac ctg cgc tct aat ctg att gat cgc atg aaa cgc 499
 Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile Asp Arg Met Lys Arg
 120 125 130

ggg ctg ctt acc acg cag cac agc taagctttaa ggccctccgg ggc 546
 Gly Leu Leu Thr Thr Gln His Ser
 135 140

<210> 728
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 <213> Corynebacterium glutamicum

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 His Asp Pro Leu Lys Asp Pro Met Lys Gly Ile Arg Gly Val Met Ala
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 Gly Thr Leu Val Met Glu Ala Ile Thr Leu Gly Leu Val Leu Thr Val
 35 40 45
 Ile Leu Arg Val Asp Asp Gly Ile Tyr Trp Thr Thr Phe Asn Trp Val
 50 55 60
 Tyr Val Ser Ala Val Ala Ile Ala His Phe Val Ala Ala Phe Leu Gln
 65 70 75 80
 Arg Phe Ser Trp Ser Ile Pro Met Asn Ile Val Leu Gln Val Leu Ala
 85 90 95
 Leu Ala Gly Phe Phe Val His Pro Ala Met Gly Phe Ala Ala Ile Ile
 100 105 110
 Phe Ile Ile Ala Trp Ala Tyr Leu Phe Tyr Leu Arg Ser Asn Leu Ile
 115 120 125
 Asp Arg Met Lys Arg Gly Leu Leu Thr Thr Gln His Ser
 130 135 140

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 <212> DNA
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 <223> RXC01518

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 Val Ala Phe Met Gln
 1 5
 aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163
 Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala
 10 15 20
 gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211

Val	Ser	Ala	Ile	Leu	Thr	Trp	Arg	Phe	Tyr	Gly	Ser	Met	Thr	Ser	Ile		
			25					30					35				
tcc	atc	acg	gta	tcc	atc	act	ttt	tgg	ttg	ttg	gcc	gtg	gtg	tgt	ggc	259	
Ser	Ile	Thr	Val	Ser	Ile	Thr	Phe	Trp	Leu	Leu	Ala	Val	Val	Cys	Gly		
		40					45					50					
ttc	gca	ggc	gtg	aag	gtc	caa	ggc	cgc	ctc	gat	gag	ggg	ctg	atc	ggc	307	
Phe	Ala	Gly	Val	Lys	Val	Gln	Gly	Arg	Leu	Asp	Glu	Gly	Leu	Ile	Gly		
	55					60					65						
cag	gac	aaa	tcc	caa	atg	aac	ccc	gtg	acc	att	gcc	tat	ctg	gcc	atg	355	
Gln	Asp	Lys	Ser	Gln	Met	Asn	Pro	Val	Thr	Ile	Ala	Tyr	Leu	Ala	Met		
	70				75					80					85		
ctg	ggc	cga	gcg	tgt	gcg	tgg	ggc	ggc	gca	att	ttc	ggc	ggc	gtt	tat	403	
Leu	Gly	Arg	Ala	Cys	Ala	Trp	Gly	Gly	Ala	Ile	Phe	Gly	Gly	Val	Tyr		
				90					95					100			
gtg	gga	att	ggc	agt	tat	gta	atc	cca	cgc	gcc	ggc	gag	ttg	tcc	gca	451	
Val	Gly	Ile	Gly	Ser	Tyr	Val	Ile	Pro	Arg	Ala	Gly	Glu	Leu	Ser	Ala		
			105					110					115				
gca	tcg	aat	gat	ctt	ccg	gga	gtt	att	gcc	tgt	gcg	ctg	ggc	gga	atc	499	
Ala	Ser	Asn	Asp	Leu	Pro	Gly	Val	Ile	Ala	Cys	Ala	Leu	Gly	Gly	Ile		
		120					125					130					
gca	ctc	tca	gct	gcc	gga	ctt	tat	tta	gag	cga	agc	tgt	gag	gct	ccg	547	
Ala	Leu	Ser	Ala	Ala	Gly	Leu	Tyr	Leu	Glu	Arg	Ser	Cys	Glu	Ala	Pro		
	135					140					145						
cct	ccc	caa	tct	ggc	gaa	gcg	atc	agc	tagattggaa	ttcatgaatc						594	
Pro	Pro	Gln	Ser	Gly	Glu	Ala	Ile	Ser									
	150				155												
aag																	597

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<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 730

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Gly	Phe	Leu	Ala	Ala	Val	Ser	Ala	Ile	Leu	Thr	Trp	Arg	Phe	Tyr	Gly		
			20					25					30				
Ser	Met	Thr	Ser	Ile	Ser	Ile	Thr	Val	Ser	Ile	Thr	Phe	Trp	Leu	Leu		
		35					40					45					
Ala	Val	Val	Cys	Gly	Phe	Ala	Gly	Val	Lys	Val	Gln	Gly	Arg	Leu	Asp		
	50					55					60						
Glu	Gly	Leu	Ile	Gly	Gln	Asp	Lys	Ser	Gln	Met	Asn	Pro	Val	Thr	Ile		
	65				70					75					80		
Ala	Tyr	Leu	Ala	Met	Leu	Gly	Arg	Ala	Cys	Ala	Trp	Gly	Gly	Ala	Ile		
				85					90					95			

Phe	Gly	Gly	Val	Tyr	Val	Gly	Ile	Gly	Ser	Tyr	Val	Ile	Pro	Arg	Ala	
			100					105					110			
Gly	Glu	Leu	Ser	Ala	Ala	Ser	Asn	Asp	Leu	Pro	Gly	Val	Ile	Ala	Cys	
		115					120					125				
Ala	Leu	Gly	Gly	Ile	Ala	Leu	Ser	Ala	Ala	Gly	Leu	Tyr	Leu	Glu	Arg	
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<223> RXC01942
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Met Leu Arg Ile Gly
1 5

cta aca gga ggg atc ggc agc ggt aaa tct acc gtt gcc gat ctt ttg 163
Leu Thr Gly Gly Ile Gly Ser Gly Lys Ser Thr Val Ala Asp Leu Leu
10 15 20

tca tct gaa gga ttt ctc atc gtc gac gcg gac caa gtt gcc cgc gat 211
Ser Ser Glu Gly Phe Leu Ile Val Asp Ala Asp Gln Val Ala Arg Asp
25 30 35

atc gtc gaa ccc gga caa ccg gca tta gca gag cta gct gaa gct ttt 259
Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu Leu Ala Glu Ala Phe
40 45 50

ggc caa gac atc tta aaa ccc gac ggc act cta gac cgc gcg gga tta 307
Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu Asp Arg Ala Gly Leu
55 60 65

gca gcc aaa gca ttt gtc agc gaa gaa caa aca gcg ctg ctc aat gcc 355
Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr Ala Leu Leu Asn Ala
70 75 80 85

att acc cac cct cgt atc gcc gaa gag tca gct cgt cga ttc aac gaa 403
Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala Arg Arg Phe Asn Glu
90 95 100

gcc gaa gat caa ggc gcc aaa gtt gcg gtt tat gac atg cct ttg ctt 451
Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr Asp Met Pro Leu Leu
105 110 115

gta gaa aaa ggc ctt gac cgc aag atg gac ctt gtc gtc gta gtt gat 499
Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu Val Val Val Val Asp

	120	125	130	
gtt gac gta gag gaa cgc gtc cgc aga ctt gtg gaa aaa cgt ggc ctc				547
Val Asp Val Glu Glu Arg Val Arg Arg Leu Val Glu Lys Arg Gly Leu				
135		140	145	
aca gag gac gac gtg cgg cgt cga atc gct tct caa gtg ccc gac gac				595
Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser Gln Val Pro Asp Asp				
150	155	160	165	
gtc aga ctt aaa gcc gct gac atc gtt gtg gac aat aac ggc acg cta				643
Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp Asn Asn Gly Thr Leu				
	170	175	180	
gag gac ctt cat gct gaa gca agc aag ctg att gct gag att ctt agt				691
Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile Ala Glu Ile Leu Ser				
	185	190	195	
cgc gtg aat tagcactaaa acatcgtcaa agt				723
Arg Val Asn				
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<210> 732

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 732

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	20														
Gln Val Ala Arg Asp Ile Val Glu Pro Gly Gln Pro Ala Leu Ala Glu							40						45		
	35														
Leu Ala Glu Ala Phe Gly Gln Asp Ile Leu Lys Pro Asp Gly Thr Leu							55						60		
	50														
Asp Arg Ala Gly Leu Ala Ala Lys Ala Phe Val Ser Glu Glu Gln Thr							70						75		80
	65														
Ala Leu Leu Asn Ala Ile Thr His Pro Arg Ile Ala Glu Glu Ser Ala															
			85						90					95	
Arg Arg Phe Asn Glu Ala Glu Asp Gln Gly Ala Lys Val Ala Val Tyr									105					110	
			100												
Asp Met Pro Leu Leu Val Glu Lys Gly Leu Asp Arg Lys Met Asp Leu							120						125		
			115												
Val Val Val Val Asp Val Asp Val Glu Glu Arg Val Arg Arg Leu Val							135						140		
	130														
Glu Lys Arg Gly Leu Thr Glu Asp Asp Val Arg Arg Arg Ile Ala Ser							150						155		160
	145														
Gln Val Pro Asp Asp Val Arg Leu Lys Ala Ala Asp Ile Val Val Asp															
			165						170					175	

Asn Asn Gly Thr Leu Glu Asp Leu His Ala Glu Ala Ser Lys Leu Ile
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Ala Glu Ile Leu Ser Arg Val Asn
 195 200

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<211> 1194

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1171)

<223> RXN02802

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agcaaacgcg cctcgacggc tccaccgatt gggtcggcct gtg aaa aac ctc gac 115
 Val Lys Asn Leu Asp
 1 5

atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa 163
 Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly Glu Ile Gly Gln Gln
 10 15 20

aaa caa caa tcg ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc 211
 Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser Val Ile Gly Ala Gly
 25 30 35

ggc ctc ggg tca ccc gcc ctg ctc tac ctt gct ggc gct ggc gtc ggc 259
 Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala Gly Ala Gly Val Gly
 40 45 50

cac atc cac atc att gac gat gac ctc gtc gac ctc tcc aac ctc cac 307
 His Ile His Ile Ile Asp Asp Asp Leu Val Asp Leu Ser Asn Leu His
 55 60 65

cgc cag gtc att cac acc acc gct ggc gtt gga aca ccc aag gcc gag 355
 Arg Gln Val Ile His Thr Thr Ala Gly Val Gly Thr Pro Lys Ala Glu
 70 75 80 85

tcc gcg cgc gaa gca atg ctg gca ctg aac cct tcc gtt aaa gtg acg 403
 Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro Ser Val Lys Val Thr
 90 95 100

gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca 451
 Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala
 105 110 115

gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499
 Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His
 120 125 130

ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc cac gtc tgg gca 547
 Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile Pro His Val Trp Ala
 135 140 145

tcc atc ctg ggt ttc gac gcc caa ctc tcc gtc ttc cac gcc ggc cac	595
Ser Ile Leu Gly Phe Asp Ala Gln Leu Ser Val Phe His Ala Gly His	
150 155 160 165	
ggc ccc atc tac gaa gac ctc ttc ccc acc ccg cca cca ccc gga tcc	643
Gly Pro Ile Tyr Glu Asp Leu Phe Pro Thr Pro Pro Pro Gly Ser	
170 175 180	
gtc cca tca tgt tcc caa gca ggc gtt ttg ggt cca gtt gtc ggc gta	691
Val Pro Ser Cys Ser Gln Ala Gly Val Leu Gly Pro Val Val Gly Val	
185 190 195	
atg ggc tcc gcg atg gcc atg gaa gcc ctc aaa atc atc acc ggc gtg	739
Met Gly Ser Ala Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val	
200 205 210	
ggc aca ccc ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc	787
Gly Thr Pro Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly	
215 220 225	
acc tgg gaa tac atc ccc gtc gtc ggt tcg ccg gag gtg ctg gaa cgg	835
Thr Trp Glu Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg	
230 235 240 245	
gtg ctt ggg tct gct ggt gtt tcg ggg att tct ggc ggt ttt ggt gag	883
Val Leu Gly Ser Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu	
250 255 260	
gtg ctc gat gtt cct cga gtt tcc gcg ctg gtt gac ggc gtt tcg ctc	931
Val Leu Asp Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu	
265 270 275	
atc gac gtc cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc	979
Ile Asp Val Arg Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly	
280 285 290	
gcg cac aac acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc	
1027	
Ala His Asn Thr Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro	
295 300 305	
tcc gtt tcc gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc	
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Ser Val Ser Ala Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val	
310 315 320 325	
cgc tcc gca caa gcc atc gca att tta gaa tcc gca ggc tac acc gga	
1123	
Arg Ser Ala Gln Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly	
330 335 340	
atg agc agc ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg	
1171	
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<211> 357

<212> PRT

<213> Corynebacterium glutamicum

<400> 734

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Val	Ile	Gly	Ala	Gly	Gly	Leu	Gly	Ser	Pro	Ala	Leu	Leu	Tyr	Leu	Ala
		35					40					45			
Gly	Ala	Gly	Val	Gly	His	Ile	His	Ile	Ile	Asp	Asp	Asp	Leu	Val	Asp
	50					55					60				
Leu	Ser	Asn	Leu	His	Arg	Gln	Val	Ile	His	Thr	Thr	Ala	Gly	Val	Gly
65					70					75					80
Thr	Pro	Lys	Ala	Glu	Ser	Ala	Arg	Glu	Ala	Met	Leu	Ala	Leu	Asn	Pro
				85					90					95	
Ser	Val	Lys	Val	Thr	Val	Ser	Val	Arg	Arg	Leu	Asp	Trp	Ser	Asn	Ala
			100					105					110		
Leu	Ser	Glu	Leu	Ala	Asp	Ser	Asp	Val	Ile	Leu	Asp	Gly	Ser	Asp	Asn
		115					120					125			
Phe	Asp	Thr	Arg	His	Leu	Ala	Ser	Trp	Ala	Ala	Ala	Lys	Leu	Gly	Ile
	130					135					140				
Pro	His	Val	Trp	Ala	Ser	Ile	Leu	Gly	Phe	Asp	Ala	Gln	Leu	Ser	Val
145					150					155					160
Phe	His	Ala	Gly	His	Gly	Pro	Ile	Tyr	Glu	Asp	Leu	Phe	Pro	Thr	Pro
				165					170					175	
Pro	Pro	Pro	Gly	Ser	Val	Pro	Ser	Cys	Ser	Gln	Ala	Gly	Val	Leu	Gly
			180					185					190		
Pro	Val	Val	Gly	Val	Met	Gly	Ser	Ala	Met	Ala	Met	Glu	Ala	Leu	Lys
		195					200					205			
Ile	Ile	Thr	Gly	Val	Gly	Thr	Pro	Leu	Ile	Gly	Lys	Leu	Gly	Tyr	Tyr
	210					215					220				
Ser	Ser	Leu	Asp	Gly	Thr	Trp	Glu	Tyr	Ile	Pro	Val	Val	Gly	Ser	Pro
225					230					235					240
Glu	Val	Leu	Glu	Arg	Val	Leu	Gly	Ser	Ala	Gly	Val	Ser	Gly	Ile	Ser
				245					250					255	
Gly	Gly	Phe	Gly	Glu	Val	Leu	Asp	Val	Pro	Arg	Val	Ser	Ala	Leu	Val
			260					265					270		
Asp	Gly	Val	Ser	Leu	Ile	Asp	Val	Arg	Glu	Pro	Ser	Glu	Phe	Ser	Ala
		275					280					285			
Tyr	Ser	Ile	Pro	Gly	Ala	His	Asn	Thr	Pro	Leu	Ser	Ala	Ile	Arg	Glu
	290					295					300				

Gly Ala Ile Pro Pro Ser Val Ser Ala Gly Lys Glu Val Ile Val Tyr
305 310 315 320

Cys Ala Ala Gly Val Arg Ser Ala Gln Ala Ile Ala Ile Leu Glu Ser
325 330 335

Ala Gly Tyr Thr Gly Met Ser Ser Leu Asp Gly Gly Ile Glu Gly Trp
340 345 350

Leu Asp Ser Leu Gly
355

<210> 735

<211> 497

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (7)..(474)

<223> FRXA02802

<400> 735

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Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val Gly Thr Pro
1 5 10 15

ttg atc gga aaa ctc ggc tac tac tcc tcc ctc gac ggc acc tgg gaa 99
Leu Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Glu
20 25 30

tac atc ccc gtc gtc ggt tcg ccg gag gtg ctg gaa cgg gtg ctt ggg 147
Tyr Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg Val Leu Gly
35 40 45

tct gct ggt gtt tcg ggg att tct ggc ggt ttt ggt gag gtg ctc gat 195
Ser Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu Val Leu Asp
50 55 60

gtt cct cga gtt tcc gcg ctg gtt gac ggc gtt tcg ctc atc gac gtc 243
Val Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val
65 70 75

cgc gaa ccc tcc gaa ttc tcc gcc tac tcc atc ccc ggc gcg cac aac 291
Arg Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn
80 85 90 95

acc cca ctg tcc gcc atc cgc gaa ggc gcc atc cca ccc tcc gtt tcc 339
Thr Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro Ser Val Ser
100 105 110

gca ggt aaa gag gtt atc gtc tac tgc gca gct ggt gtc cgc tcc gca 387
Ala Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala
115 120 125

caa gcc atc gca att tta gaa tcc gca ggc tac acc gga atg agc agc 435
Gln Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly Met Ser Ser
130 135 140

ctc gac ggc gga atc gaa ggc tgg cta gat tcc cta ggg taaaaccaag 484
 Leu Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly
 145 150 155

gcgttggtgcc acc 497

<210> 736

<211> 156

<212> PRT

<213> Corynebacterium glutamicum

<400> 736

Met Ala Met Glu Ala Leu Lys Ile Ile Thr Gly Val Gly Thr Pro Leu
 1 5 10 15

Ile Gly Lys Leu Gly Tyr Tyr Ser Ser Leu Asp Gly Thr Trp Glu Tyr
 20 25 30

Ile Pro Val Val Gly Ser Pro Glu Val Leu Glu Arg Val Leu Gly Ser
 35 40 45

Ala Gly Val Ser Gly Ile Ser Gly Gly Phe Gly Glu Val Leu Asp Val
 50 55 60

Pro Arg Val Ser Ala Leu Val Asp Gly Val Ser Leu Ile Asp Val Arg
 65 70 75 80

Glu Pro Ser Glu Phe Ser Ala Tyr Ser Ile Pro Gly Ala His Asn Thr
 85 90 95

Pro Leu Ser Ala Ile Arg Glu Gly Ala Ile Pro Pro Ser Val Ser Ala
 100 105 110

Gly Lys Glu Val Ile Val Tyr Cys Ala Ala Gly Val Arg Ser Ala Gln
 115 120 125

Ala Ile Ala Ile Leu Glu Ser Ala Gly Tyr Thr Gly Met Ser Ser Leu
 130 135 140

Asp Gly Gly Ile Glu Gly Trp Leu Asp Ser Leu Gly
 145 150 155

<210> 737

<211> 535

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA00438

<400> 737

ccttcgccgc ctgctccgac ctcgccgacg ccgtcaaagc ccaggtcccg atctggaaag 60

agcaaacgcg cctcgacggc tccaccgatt gggtcggcct gtg aaa aac ctc gac 115
 Val Lys Asn Leu Asp
 1 5

atc gcc cgc tac cgc cgc caa att atg ctc ggc gaa atc ggc cag caa 163
 Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly Glu Ile Gly Gln Gln
 10 15 20

aaa caa caa tcg ctt ttc gac gct aag gtc tcc gtc atc ggc gca ggc 211
 Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser Val Ile Gly Ala Gly
 25 30 35

ggc ctc ggg tca ccc gcc ctg ctc tac ctt gct ggc gct ggc gtc ggc 259
 Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala Gly Ala Gly Val Gly
 40 45 50

cac atc cac atc att gac gat gac ctc gtc gac ctc tcc aac ctc cac 307
 His Ile His Ile Ile Asp Asp Asp Leu Val Asp Leu Ser Asn Leu His
 55 60 65

cgc cag gtc att cac acc acc gct ggc gtt gga aca ccc aag gcc gag 355
 Arg Gln Val Ile His Thr Thr Ala Gly Val Gly Thr Pro Lys Ala Glu
 70 75 80 85

tcc gcg cgc gaa gca atg ctg gca ctg aac cct tcc gtt aaa gtg acg 403
 Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro Ser Val Lys Val Thr
 90 95 100

gtt tct gtc agg cga ctg gac tgg tca aat gca ctt tct gag ctg gca 451
 Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala Leu Ser Glu Leu Ala
 105 110 115

gat tcc gat gtg att ttg gat ggc tcc gat aac ttc gac acc cga cac 499
 Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn Phe Asp Thr Arg His
 120 125 130

ctc gca tcc tgg gcc gcc gca aaa ctt ggc atc ccc 535
 Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile Pro
 135 140 145

<210> 738

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 738

Val Lys Asn Leu Asp Ile Ala Arg Tyr Arg Arg Gln Ile Met Leu Gly
 1 5 10 15

Glu Ile Gly Gln Gln Lys Gln Gln Ser Leu Phe Asp Ala Lys Val Ser
 20 25 30

Val Ile Gly Ala Gly Gly Leu Gly Ser Pro Ala Leu Leu Tyr Leu Ala
 35 40 45

Gly Ala Gly Val Gly His Ile His Ile Ile Asp Asp Asp Leu Val Asp
 50 55 60

Leu Ser Asn Leu His Arg Gln Val Ile His Thr Thr Ala Gly Val Gly
 65 70 75 80

Thr Pro Lys Ala Glu Ser Ala Arg Glu Ala Met Leu Ala Leu Asn Pro
 85 90 95

Ser Val Lys Val Thr Val Ser Val Arg Arg Leu Asp Trp Ser Asn Ala
 100 105 110

Leu Ser Glu Leu Ala Asp Ser Asp Val Ile Leu Asp Gly Ser Asp Asn
 115 120 125

Phe Asp Thr Arg His Leu Ala Ser Trp Ala Ala Ala Lys Leu Gly Ile
 130 135 140

Pro
 145

<210> 739

<211> 579

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(556)

<223> RXN00437

<400> 739

ttcatcatgg cgctgcccgg ctccacgggt gcggcgcgcg atgccaccgc tgcctcgcac 60

ccactcattg atcacatcac tggaactctg caaggccacc atg aac act gac ccc 115
 Met Asn Thr Asp Pro
 1 5

gct tac gtc gcc gaa caa acc ggc aaa ctc atc gac gct ttc ctc acc 163
 Ala Tyr Val Ala Glu Gln Thr Gly Lys Leu Ile Asp Ala Phe Leu Thr
 10 15 20

acc gac ccc ctc gaa ccg ctg ctc gac gcc gcc aaa aac ggc gtc tgc 211
 Thr Asp Pro Leu Glu Pro Leu Leu Asp Ala Ala Lys Asn Gly Val Cys
 25 30 35

aca gag gcg atg ggc gcg ctg gtc acc ttc gaa ggc atc gtc cgc gac 259
 Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu Gly Ile Val Arg Asp
 40 45 50

cac gac ggc ggc gcc cgc gtg acc tcc ctg acc tac acc gcg cat ccc 307
 His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr Tyr Thr Ala His Pro
 55 60 65

acc gcg ccg cag gtc ctt tct gct gtc gcg gac tcc atc gtt gaa aaa 355
 Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp Ser Ile Val Glu Lys
 70 75 80 85

cac ccg cgc acc cgc ctc tgg acc gcg cac cgc acc ggc gcc ttg aaa 403
 His Pro Arg Thr Arg Leu Trp Thr Ala His Arg Thr Gly Ala Leu Lys
 90 95 100

atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc tcc gcc cac cgc gcc 451
 Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala Ser Ala His Arg Ala
 105 110 115

gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac gcc gtc aaa gcc cag 499
 Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp Ala Val Lys Ala Gln
 120 125 130

gtc ccg atc tgg aaa gag caa acg cgc ctc gac ggc tcc acc gat tgg 547
 Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp Gly Ser Thr Asp Trp
 135 140 145

gtc ggc ctg tgaaaaacct cgacatcgcc cgc 579
 Val Gly Leu
 150

<210> 740

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 740

Met Asn Thr Asp Pro Ala Tyr Val Ala Glu Gln Thr Gly Lys Leu Ile
 1 5 10 15

Asp Ala Phe Leu Thr Thr Asp Pro Leu Glu Pro Leu Leu Asp Ala Ala
 20 25 30

Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 35 40 45

Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
 50 55 60

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
 65 70 75 80

Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
 85 90 95

Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
 100 105 110

Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
 115 120 125

Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
 130 135 140

Gly Ser Thr Asp Trp Val Gly Leu
 145 150

<210> 741

<211> 383

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(360)

<223> FRXA00437

<400> 741

aaa aac ggc gtc tgc aca gag gcg atg ggc gcg ctg gtc acc ttc gaa 48
 Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
 1 5 10 15

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ggc atc gtc cgc gac cac gac ggc ggc gcc cgc gtg acc tcc ctg acc 96
Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
      20      25      30

tac acc gcg cat ccc acc gcg ccg cag gtc ctt tct gct gtc gcg gac 144
Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
      35      40      45

tcc atc gtt gaa aaa cac ccg cgc acc cgc ctc tgg acc gcg cac cgc 192
Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
      50      55      60

acc ggc gcc ttg aaa atc ggt gac gcc gcc ttc ctc gtc gtc gcc gcc 240
Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
      65      70      75      80

tcc gcc cac cgc gcc gac gcc ttc gcc gcc tgc tcc gac ctc gcc gac 288
Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
      85      90      95

gcc gtc aaa gcc cag gtc ccg atc tgg aaa gag caa acg cgc ctc gac 336
Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
      100      105      110

ggc tcc acc gat tgg gtc ggc ctg tgaaaaacct cgacatcgcc cgc 383
Gly Ser Thr Asp Trp Val Gly Leu
      115      120

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<210> 742

<211> 120

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 742

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Lys Asn Gly Val Cys Thr Glu Ala Met Gly Ala Leu Val Thr Phe Glu
  1      5      10      15

Gly Ile Val Arg Asp His Asp Gly Gly Ala Arg Val Thr Ser Leu Thr
      20      25      30

Tyr Thr Ala His Pro Thr Ala Pro Gln Val Leu Ser Ala Val Ala Asp
      35      40      45

Ser Ile Val Glu Lys His Pro Arg Thr Arg Leu Trp Thr Ala His Arg
      50      55      60

Thr Gly Ala Leu Lys Ile Gly Asp Ala Ala Phe Leu Val Val Ala Ala
      65      70      75      80

Ser Ala His Arg Ala Asp Ala Phe Ala Ala Cys Ser Asp Leu Ala Asp
      85      90      95

Ala Val Lys Ala Gln Val Pro Ile Trp Lys Glu Gln Thr Arg Leu Asp
      100      105      110

Gly Ser Thr Asp Trp Val Gly Leu
      115      120

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<210> 743
 <211> 591
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(568)
 <223> RXN00439

<400> 743

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tcgttaagat ttaccatttc aactaacagg agttaattta atg agc gag ctc acc 115
 Met Ser Glu Leu Thr
 1 5

cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa 163
 His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys
 10 15 20

aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg 211
 Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg
 25 30 35

ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggc gac 259
 Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp
 40 45 50

gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg 307
 Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr
 55 60 65

ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act 355
 Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr
 70 75 80 85

gtg gat ttt ttt gag ctt act gat ggt gtt cgg att gag gct tcg gtg 403
 Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg Ile Glu Ala Ser Val
 90 95 100

aaa acg cgt ggg gtt act ggt gtg gaa atg gag gcg ttg acg gcc gtg 451
 Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu Ala Leu Thr Ala Val
 105 110 115

agc act gcg gcg ctg acg gta tac gac atg atc aag gct gtg gat aag 499
 Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile Lys Ala Val Asp Lys
 120 125 130

atg gcc gtg att gat ggc att cgt gtg ctg tcg aaa act ggc ggt aaa 547
 Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser Lys Thr Gly Gly Lys
 135 140 145

tct ggg gat tgg tct gtt cag tgacagctct gggtatcggt gcg 591
 Ser Gly Asp Trp Ser Val Gln
 150 155

<210> 744
 <211> 156
 <212> PRT

<213> Corynebacterium glutamicum

<400> 744

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Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val
  1           5           10           15

Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly
          20           25           30

Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly
          35           40           45

Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met
          50           55           60

Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro
          65           70           75           80

Leu Gly Lys Ile Thr Val Asp Phe Phe Glu Leu Thr Asp Gly Val Arg
          85           90           95

Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr Gly Val Glu Met Glu
          100          105          110

Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr Val Tyr Asp Met Ile
          115          120          125

Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly Ile Arg Val Leu Ser
          130          135          140

Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val Gln
          145          150          155

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<210> 745

<211> 218

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(195)

<223> FRXA00439

<400> 745

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act gat ggt gtt cgg att gag gct tcg gtg aaa acg cgt ggg gtt act   48
Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr
  1           5           10           15

ggt gtg gaa atg gag gcg ttg acg gcc gtg agc act gcg gcg ctg acg   96
Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr
          20           25           30

gta tac gac atg atc aag gct gtg gat aag atg gcc gtg att gat ggc   144
Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly
          35           40           45

att cgt gtg ctg tcg aaa act ggc ggt aaa tct ggg gat tgg tct gtt   192
Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val
          50           55           60

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cag tgacagctct ggttatcggt gcg
Gln
65

218

<210> 746
<211> 65
<212> PRT
<213> Corynebacterium glutamicum

<400> 746
Thr Asp Gly Val Arg Ile Glu Ala Ser Val Lys Thr Arg Gly Val Thr
1 5 10 15
Gly Val Glu Met Glu Ala Leu Thr Ala Val Ser Thr Ala Ala Leu Thr
20 25 30
Val Tyr Asp Met Ile Lys Ala Val Asp Lys Met Ala Val Ile Asp Gly
35 40 45
Ile Arg Val Leu Ser Lys Thr Gly Gly Lys Ser Gly Asp Trp Ser Val
50 55 60

Gln
65

<210> 747
<211> 358
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(358)
<223> FRXA00442

<400> 747
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tcgttaagat ttaccattc aactaacagg agttaattta atg agc gag ctc acc 115
Met Ser Glu Leu Thr
1 5
cac gtt cga gca gac ggt tcc gca cat atg gtg gat gtg acg ggc aaa 163
His Val Arg Ala Asp Gly Ser Ala His Met Val Asp Val Thr Gly Lys
10 15 20
aat gaa aca tcg aga act gct gtt gcc gaa ggg ttt gtg aag atg agg 211
Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly Phe Val Lys Met Arg
25 30 35
ggg gac gtc gta aag cag ctt ttt agt gct ggt ctg cct aaa ggg gac 259
Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly Leu Pro Lys Gly Asp
40 45 50
gcg cta cct gtg gcg cgg att gcg ggt atc atg ggt gcg aag aag acg 307
Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met Gly Ala Lys Lys Thr
55 60 65
ccg gac att atc cct tta tgc cac ccg ttg ccg ctg ggc aaa att act 355

Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro Leu Gly Lys Ile Thr
70 75 80 85

gtg
Val

358

<210> 748
<211> 86
<212> PRT
<213> Corynebacterium glutamicum

<400> 748
Met Ser Glu Leu Thr His Val Arg Ala Asp Gly Ser Ala His Met Val
1 5 10 15
Asp Val Thr Gly Lys Asn Glu Thr Ser Arg Thr Ala Val Ala Glu Gly
20 25 30
Phe Val Lys Met Arg Gly Asp Val Val Lys Gln Leu Phe Ser Ala Gly
35 40 45
Leu Pro Lys Gly Asp Ala Leu Pro Val Ala Arg Ile Ala Gly Ile Met
50 55 60
Gly Ala Lys Lys Thr Pro Asp Ile Ile Pro Leu Cys His Pro Leu Pro
65 70 75 80
Leu Gly Lys Ile Thr Val
85

<210> 749
<211> 582
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(559)
<223> RXA00440

<400> 749
cggatatacga catgatcaag gctgtggata agatggccgt gattgatggc attcgtgtgc 60
tgatcgaaaac tggcggtaaa tctggggatt ggtctgttca gtg aca gct ctg gtt 115
Val Thr Ala Leu Val
1 5
atc gtt gcg tcc act cgc gcc gct gcc ggg gtg tat gag gat cgc tct 163
Ile Val Ala Ser Thr Arg Ala Ala Ala Gly Val Tyr Glu Asp Arg Ser
10 15 20
ggc cca att ttg gtg tcg tgg ctg cgt gca aaa ggt ttt gac aca ccc 211
Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys Gly Phe Asp Thr Pro
25 30 35
gcc ccc gtg atc gtg gcg gac gcc aac ctg ccc gca ttc ctg gac gag 259
Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro Ala Phe Leu Asp Glu
40 45 50

ctg gaa ttt ccg cag gta gta ctt att tca ggc ggc acc gga ctc acg 307
 Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly Gly Thr Gly Leu Thr
 55 60 65
 cct gat gac atc acc gtg gac act tta atc ccg cgc ctc gac aaa gaa 355
 Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro Arg Leu Asp Lys Glu
 70 75 80 85
 atc ccc ggc atc gcc cac gct ttt tgg aat tac agc atg gac gcc gtc 403
 Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr Ser Met Asp Ala Val
 90 95 100
 ccg acc gca gta ttg tgc cgc acc gtc gcg ggc acc atc ggc ggc agt 451
 Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly Thr Ile Gly Gly Ser
 105 110 115
 ttc atc atg gcg ctg ccc ggc tcc acg ggt gcg gcg cgc gat gcc acc 499
 Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala Ala Arg Asp Ala Thr
 120 125 130
 gct gtc ctc gac cca ctc att gat cac atc act gga act ctg caa ggc 547
 Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr Gly Thr Leu Gln Gly
 135 140 145
 cac cat gaa cac tgaccccgct tacgtcgccg aac 582
 His His Glu His
 150

<210> 750
 <211> 153
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 750
 Val Thr Ala Leu Val Ile Val Ala Ser Thr Arg Ala Ala Ala Gly Val
 1 5 10 15
 Tyr Glu Asp Arg Ser Gly Pro Ile Leu Val Ser Trp Leu Arg Ala Lys
 20 25 30
 Gly Phe Asp Thr Pro Ala Pro Val Ile Val Ala Asp Ala Asn Leu Pro
 35 40 45
 Ala Phe Leu Asp Glu Leu Glu Phe Pro Gln Val Val Leu Ile Ser Gly
 50 55 60
 Gly Thr Gly Leu Thr Pro Asp Asp Ile Thr Val Asp Thr Leu Ile Pro
 65 70 75 80
 Arg Leu Asp Lys Glu Ile Pro Gly Ile Ala His Ala Phe Trp Asn Tyr
 85 90 95
 Ser Met Asp Ala Val Pro Thr Ala Val Leu Ser Arg Thr Val Ala Gly
 100 105 110
 Thr Ile Gly Gly Ser Phe Ile Met Ala Leu Pro Gly Ser Thr Gly Ala
 115 120 125
 Ala Arg Asp Ala Thr Ala Val Leu Asp Pro Leu Ile Asp His Ile Thr

130	135	140
Gly Thr Leu Gln Gly His His Glu His		
145	150	
<p><210> 751</p> <p><211> 1287</p> <p><212> DNA</p> <p><213> Corynebacterium glutamicum</p> <p><220></p> <p><221> CDS</p> <p><222> (101)..(1264)</p> <p><223> RXN00441</p> <p><400> 751</p>		
<p>agccttgaggga gcggtgatta tgctttttggc tgtctatgtc ctcattcattg gagccatcgg 60</p> <p>agcgttacga ttgtttttcca aggtgagaaa ggttttaattg atg tct cgt tcg ccg 115</p> <p>Met Ser Arg Ser Pro 5</p> <p>1</p> <p>gag caa cat ttg gca gaa att tca gcg ctg ctt ccc cca caa aag tcc 163</p> <p>Glu Gln His Leu Ala Glu Ile Ser Ala Leu Leu Pro Pro Gln Lys Ser 20</p> <p>10 15</p> <p>acg ttc gtg aat ctg cgc gaa gcg ttg gga cgc cgc acg ttt tca gcg 211</p> <p>Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg Arg Thr Phe Ser Ala 35</p> <p>25 30</p> <p>gtc act gcg cag tgg gat tcg cca cgt ttt gat aat tcc caa atg gat 259</p> <p>Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp Asn Ser Gln Met Asp 50</p> <p>40 45</p> <p>ggc ttc gcg ctt ggc ccc tca cat ctt aac ggt ggc acc ttc gca gtc 307</p> <p>Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly Gly Thr Phe Ala Val 65</p> <p>55 60</p> <p>ggt cca acc att ccc gct ggt cat gat cct gat cag tgg tac cca cga 355</p> <p>Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp Gln Trp Tyr Pro Arg 85</p> <p>70 75 80</p> <p>ggc atc gaa aaa gac atc gcg ccg att atg acg ggt gcg cgc ctt cct 403</p> <p>Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr Gly Ala Arg Leu Pro 100</p> <p>90 95</p> <p>aaa aac acc gcc gcg atc att cct gtg gag aaa acc aca ccg gga aat 451</p> <p>Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys Thr Thr Pro Gly Asn 115</p> <p>105 110</p> <p>ttc gac gcc cca cag gta gaa atc ccc gcc acc ccg caa ggt cag ttc 499</p> <p>Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr Pro Gln Gly Gln Phe 130</p> <p>120 125</p> <p>ata cgg ttg cag ggt tcg gat att act gcc ggc gac gag atc att cca 547</p> <p>Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly Asp Glu Ile Ile Pro 145</p> <p>135 140</p> <p>gca ggt acg gag ctt aac tcg gtg cac atc ggg gtg ttg gct agt cag 595</p> <p>Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly Val Leu Ala Ser Gln</p>		

150	155	160	165	
tcg atc aag agc att gaa gtc gca gca aag cca cgt gtc ctc atc atc				643
Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro Arg Val Leu Ile Ile	170	175	180	
acc ggc ggg tct gaa att tca gaa cag cac gga ccc gcc acg atc cct				691
Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly Pro Ala Thr Ile Pro	185	190	195	
gat gcc aac ggc cct ctg ctt cgt tcc ctg tgc gcc cgc aac aat atc				739
Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys Ala Arg Asn Asn Ile	200	205	210	
gag gtc atc gcg gga ctg cac acc aac gac gat cct gaa cga ctc cgc				787
Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp Pro Glu Arg Leu Arg	215	220	225	
ttt gaa ctg gaa aac gcc att gac cag tat caa ccg gat gtc atc atc				835
Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln Pro Asp Val Ile Ile	230	235	240	245
acc tct ggc ggt atc agc cac ggt aaa ttt gag gtg ttt agg cag atc				883
Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu Val Phe Arg Gln Ile	250	255	260	
ctc gaa ggc acc ccg aac tcc tgg ttt gga cat gtc gat cag cag cct				931
Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His Val Asp Gln Gln Pro	265	270	275	
ggc ggt cct caa ggc atc tcc act ttt gct gaa act cct gtc att tca				979
Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu Thr Pro Val Ile Ser	280	285	290	
ctt ccc gga aat ccg att tcc acc ttg gtg agt ttc aca ctt ttg gtc				
1027 Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser Phe Thr Leu Leu Val	295	300	305	
gcg cca gcg ctc aac cgc cag ccg ctc cgc cac ctc gat gcc cgc atc				
1075 Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His Leu Asp Ala Arg Ile	310	315	320	325
acc gct ccg gtc cag ggc ttg caa gac aat cgc gag caa ttc ctt cgc				
1123 Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg Glu Gln Phe Leu Arg	330	335	340	
ggc acc atc agt tac cgc aac ggg cca cgt cct cgc cac gcc tct cct				
1171 Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro Arg His Ala Ser Pro	345	350	355	
ggg cac cag ttc cca cct gct ggt tca agc tgc cac cgc aga ctg tct				
1219 Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys His Arg Arg Leu Ser	360	365	370	
gat cag gat ccc ggc gcg gac tac ggt gga gga aaa cga cat cgt				
1264				

Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly Lys Arg His Arg
 375 380 385

taagatttac ccattcaact aac
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<210> 752

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 752

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Pro Pro Gln Lys Ser Thr Phe Val Asn Leu Arg Glu Ala Leu Gly Arg
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Arg Thr Phe Ser Ala Val Thr Ala Gln Trp Asp Ser Pro Arg Phe Asp
 35 40 45

Asn Ser Gln Met Asp Gly Phe Ala Leu Gly Pro Ser His Leu Asn Gly
 50 55 60

Gly Thr Phe Ala Val Gly Pro Thr Ile Pro Ala Gly His Asp Pro Asp
 65 70 75 80

Gln Trp Tyr Pro Arg Gly Ile Glu Lys Asp Ile Ala Pro Ile Met Thr
 85 90 95

Gly Ala Arg Leu Pro Lys Asn Thr Ala Ala Ile Ile Pro Val Glu Lys
 100 105 110

Thr Thr Pro Gly Asn Phe Asp Ala Pro Gln Val Glu Ile Pro Ala Thr
 115 120 125

Pro Gln Gly Gln Phe Ile Arg Leu Gln Gly Ser Asp Ile Thr Ala Gly
 130 135 140

Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser Val His Ile Gly
 145 150 155 160

Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val Ala Ala Lys Pro
 165 170 175

Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser Glu Gln His Gly
 180 185 190

Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu Arg Ser Leu Cys
 195 200 205

Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His Thr Asn Asp Asp
 210 215 220

Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile Asp Gln Tyr Gln
 225 230 235 240

Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His Gly Lys Phe Glu
 245 250 255

Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser Trp Phe Gly His
 260 265 270
 Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser Thr Phe Ala Glu
 275 280 285
 Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser Thr Leu Val Ser
 290 295 300
 Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln Pro Leu Arg His
 305 310 315 320
 Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu Gln Asp Asn Arg
 325 330 335
 Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn Gly Pro Arg Pro
 340 345 350
 Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala Gly Ser Ser Cys
 355 360 365
 His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp Tyr Gly Gly Gly
 370 375 380
 Lys Arg His Arg
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 <211> 815
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(792)
 <223> FRXA00441

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 att act gcc ggc gac gag atc att cca gca ggt acg gag ctt aac tcg 96
 Ile Thr Ala Gly Asp Glu Ile Ile Pro Ala Gly Thr Glu Leu Asn Ser
 20 25 30
 gtg cac atc ggg gtg ttg gct agt cag tcg atc aag agc att gaa gtc 144
 Val His Ile Gly Val Leu Ala Ser Gln Ser Ile Lys Ser Ile Glu Val
 35 40 45
 gca gca aag cca cgt gtc ctc atc atc acc ggc ggg tct gaa att tca 192
 Ala Ala Lys Pro Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser
 50 55 60
 gaa cag cac gga ccc gcc acg atc cct gat gcc aac ggc cct ctg ctt 240
 Glu Gln His Gly Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu
 65 70 75 80
 cgt tcc ctg tgc gcc cgc aac aat atc gag gtc atc gcg gga ctg cac 288
 Arg Ser Leu Cys Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His

85								90				95				
acc	aac	gac	gat	cct	gaa	cga	ctc	cgc	ttt	gaa	ctg	gaa	aac	gcc	att	336
Thr	Asn	Asp	Asp	Pro	Glu	Arg	Leu	Arg	Phe	Glu	Leu	Glu	Asn	Ala	Ile	
			100					105					110			
gac	cag	tat	caa	ccg	gat	gtc	atc	atc	acc	tct	ggc	ggg	atc	agc	cac	384
Asp	Gln	Tyr	Gln	Pro	Asp	Val	Ile	Ile	Thr	Ser	Gly	Gly	Ile	Ser	His	
		115					120					125				
ggg	aaa	ttt	gag	gtg	ttt	agg	cag	atc	ctc	gaa	ggc	acc	ccg	aac	tcc	432
Gly	Lys	Phe	Glu	Val	Phe	Arg	Gln	Ile	Leu	Glu	Gly	Thr	Pro	Asn	Ser	
	130					135					140					
tgg	ttt	gga	cat	gtc	gat	cag	cag	cct	ggc	ggg	cct	caa	ggc	atc	tcc	480
Trp	Phe	Gly	His	Val	Asp	Gln	Gln	Pro	Gly	Gly	Pro	Gln	Gly	Ile	Ser	
145					150					155					160	
act	ttt	gct	gaa	act	cct	gtc	att	tca	ctt	ccc	gga	aac	ccg	att	tcc	528
Thr	Phe	Ala	Glu	Thr	Pro	Val	Ile	Ser	Leu	Pro	Gly	Asn	Pro	Ile	Ser	
				165					170					175		
acc	ttg	gtg	agt	ttc	aca	ctt	ttg	gtc	gcg	cca	gcg	ctc	aac	cgc	cag	576
Thr	Leu	Val	Ser	Phe	Thr	Leu	Leu	Val	Ala	Pro	Ala	Leu	Asn	Arg	Gln	
			180					185					190			
ccg	ctc	cgc	cac	ctc	gat	gcc	cgc	atc	acc	gct	ccg	gtc	cag	ggc	ttg	624
Pro	Leu	Arg	His	Leu	Asp	Ala	Arg	Ile	Thr	Ala	Pro	Val	Gln	Gly	Leu	
		195					200					205				
caa	gac	aac	cgc	gag	caa	ttc	ctt	cgc	ggc	acc	atc	agt	tac	cgc	aac	672
Gln	Asp	Asn	Arg	Glu	Gln	Phe	Leu	Arg	Gly	Thr	Ile	Ser	Tyr	Arg	Asn	
	210					215					220					
ggg	cca	cgt	cct	cgc	cac	gcc	tct	cct	ggg	cac	cag	ttc	cca	cct	gct	720
Gly	Pro	Arg	Pro	Arg	His	Ala	Ser	Pro	Gly	His	Gln	Phe	Pro	Pro	Ala	
225					230					235					240	
ggg	tca	agc	tgc	cac	cgc	aga	ctg	tct	gat	cag	gat	ccc	ggc	gcg	gac	768
Gly	Ser	Ser	Cys	His	Arg	Arg	Leu	Ser	Asp	Gln	Asp	Pro	Gly	Ala	Asp	
				245				250					255			
tac	ggg	gga	gga	aaa	cga	cat	cgt	taagatttac	ccattcaact	aac						815
Tyr	Gly	Gly	Gly	Lys	Arg	His	Arg									
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<210> 754

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 754

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Val	His	Ile	Gly	Val	Leu	Ala	Ser	Gln	Ser	Ile	Lys	Ser	Ile	Glu	Val
		35					40					45			

Ala Ala Lys Pro Arg Val Leu Ile Ile Thr Gly Gly Ser Glu Ile Ser
 50 55 60
 Glu Gln His Gly Pro Ala Thr Ile Pro Asp Ala Asn Gly Pro Leu Leu
 65 70 75 80
 Arg Ser Leu Cys Ala Arg Asn Asn Ile Glu Val Ile Ala Gly Leu His
 85 90 95
 Thr Asn Asp Asp Pro Glu Arg Leu Arg Phe Glu Leu Glu Asn Ala Ile
 100 105 110
 Asp Gln Tyr Gln Pro Asp Val Ile Ile Thr Ser Gly Gly Ile Ser His
 115 120 125
 Gly Lys Phe Glu Val Phe Arg Gln Ile Leu Glu Gly Thr Pro Asn Ser
 130 135 140
 Trp Phe Gly His Val Asp Gln Gln Pro Gly Gly Pro Gln Gly Ile Ser
 145 150 155 160
 Thr Phe Ala Glu Thr Pro Val Ile Ser Leu Pro Gly Asn Pro Ile Ser
 165 170 175
 Thr Leu Val Ser Phe Thr Leu Leu Val Ala Pro Ala Leu Asn Arg Gln
 180 185 190
 Pro Leu Arg His Leu Asp Ala Arg Ile Thr Ala Pro Val Gln Gly Leu
 195 200 205
 Gln Asp Asn Arg Glu Gln Phe Leu Arg Gly Thr Ile Ser Tyr Arg Asn
 210 215 220
 Gly Pro Arg Pro Arg His Ala Ser Pro Gly His Gln Phe Pro Pro Ala
 225 230 235 240
 Gly Ser Ser Cys His Arg Arg Leu Ser Asp Gln Asp Pro Gly Ala Asp
 245 250 255
 Tyr Gly Gly Gly Lys Arg His Arg
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<210> 755
 <211> 2358
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2335)
 <223> RXN02085

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 Met Thr Ser Asn Phe
 1 5

tct	tcc	act	gtc	gct	ggc	ctt	cct	cgc	atc	gga	gcg	aag	cgt	gaa	ctg	163
Ser	Ser	Thr	Val	Ala	Gly	Leu	Pro	Arg	Ile	Gly	Ala	Lys	Arg	Glu	Leu	
			10						15					20		
aag	ttc	gcg	ctc	gaa	ggc	tac	tgg	aat	gga	tca	att	gaa	ggc	cgc	gaa	211
Lys	Phe	Ala	Leu	Glu	Gly	Tyr	Trp	Asn	Gly	Ser	Ile	Glu	Gly	Arg	Glu	
			25					30					35			
ctt	gcg	cag	acc	gcc	cgc	caa	ttg	gtc	aac	act	gca	tcg	gat	tct	ttg	259
Leu	Ala	Gln	Thr	Ala	Arg	Gln	Leu	Val	Asn	Thr	Ala	Ser	Asp	Ser	Leu	
			40				45					50				
tct	gga	ttg	gat	tcc	gtt	ccg	ttt	gca	gga	cgt	tcc	tac	tac	gac	gca	307
Ser	Gly	Leu	Asp	Ser	Val	Pro	Phe	Ala	Gly	Arg	Ser	Tyr	Tyr	Asp	Ala	
	55					60					65					
atg	ctc	gat	acc	gcc	gct	att	ttg	ggc	gtg	ctg	ccg	gag	cgt	ttt	gat	355
Met	Leu	Asp	Thr	Ala	Ala	Ile	Leu	Gly	Val	Leu	Pro	Glu	Arg	Phe	Asp	
	70				75					80					85	
gac	atc	gct	gat	cat	gaa	aac	gat	ggc	ctc	cca	ctg	tgg	att	gac	cgc	403
Asp	Ile	Ala	Asp	His	Glu	Asn	Asp	Gly	Leu	Pro	Leu	Trp	Ile	Asp	Arg	
				90					95					100		
tac	ttt	ggc	gct	gct	cgc	ggc	act	gag	acc	ctg	cct	gca	cag	gca	atg	451
Tyr	Phe	Gly	Ala	Ala	Arg	Gly	Thr	Glu	Thr	Leu	Pro	Ala	Gln	Ala	Met	
			105					110					115			
acc	aag	tgg	ttt	gat	acc	aac	tac	cac	tac	ctc	gtg	ccg	gag	ttg	tct	499
Thr	Lys	Trp	Phe	Asp	Thr	Asn	Tyr	His	Tyr	Leu	Val	Pro	Glu	Leu	Ser	
		120					125					130				
gcg	gat	aca	cgt	ttc	gtt	ttg	gat	gcg	tcc	gcg	ctg	att	gag	gat	ctc	547
Ala	Asp	Thr	Arg	Phe	Val	Leu	Asp	Ala	Ser	Ala	Leu	Ile	Glu	Asp	Leu	
	135					140					145					
cgt	tgc	cag	cag	gtt	cgt	ggc	gtt	aat	gcc	cgc	cct	gtt	ctg	gtt	ggc	595
Arg	Cys	Gln	Gln	Val	Arg	Gly	Val	Asn	Ala	Arg	Pro	Val	Leu	Val	Gly	
	150				155					160					165	
cca	ctg	act	ttc	ctt	tcc	ctt	gct	cgc	acc	act	gat	ggc	tcc	aat	cct	643
Pro	Leu	Thr	Phe	Leu	Ser	Leu	Ala	Arg	Thr	Thr	Asp	Gly	Ser	Asn	Pro	
				170					175					180		
ttg	gat	cac	ctg	cct	gca	ctg	ttt	gag	gtc	tac	gag	cgc	ctc	atc	aag	691
Leu	Asp	His	Leu	Pro	Ala	Leu	Phe	Glu	Val	Tyr	Glu	Arg	Leu	Ile	Lys	
			185					190					195			
tct	ttc	gat	act	gag	tgg	gtt	cag	atc	gat	gag	cct	gcg	ttg	gtc	acc	739
Ser	Phe	Asp	Thr	Glu	Trp	Val	Gln	Ile	Asp	Glu	Pro	Ala	Leu	Val	Thr	
		200					205					210				
gat	gtt	gct	cct	gag	gtt	ttg	gag	cag	gtc	cgc	gct	ggc	tac	acc	act	787
Asp	Val	Ala	Pro	Glu	Val	Leu	Glu	Gln	Val	Arg	Ala	Gly	Tyr	Thr	Thr	
	215					220					225					
ttg	gct	aag	cgc	gat	ggc	gtg	ttt	gtc	aat	act	tac	ttc	ggc	tct	ggc	835
Leu	Ala	Lys	Arg	Asp	Gly	Val	Phe	Val	Asn	Thr	Tyr	Phe	Gly	Ser	Gly	
	230				235					240					245	
gat	cag	gcg	ctg	aac	act	ctt	gcg	ggc	atc	ggc	ctt	ggc	gcg	att	ggc	883

Asp	Gln	Ala	Leu	Asn	Thr	Leu	Ala	Gly	Ile	Gly	Leu	Gly	Ala	Ile	Gly		
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Val	Asp	Leu	Val	Thr	His	Gly	Val	Thr	Glu	Leu	Ala	Ala	Trp	Lys	Gly		
			265					270					275				
gag	gag	ctg	ctg	gtt	gcg	ggc	atc	gtt	gat	ggt	cgt	aac	att	tgg	cgc	979	
Glu	Glu	Leu	Leu	Val	Ala	Gly	Ile	Val	Asp	Gly	Arg	Asn	Ile	Trp	Arg		
		280					285					290					
acc	gac	ctg	tgt	gct	gct	ctt	gct	tcc	ctg	aag	cgc	ctg	gca	gct	cgc		
1027																	
Thr	Asp	Leu	Cys	Ala	Ala	Leu	Ala	Ser	Leu	Lys	Arg	Leu	Ala	Ala	Arg		
	295					300					305						
ggc	cca	atc	gca	gtg	tct	acc	tct	tgt	tca	ctg	ctg	cac	gtt	cct	tac		
1075																	
Gly	Pro	Ile	Ala	Val	Ser	Thr	Ser	Cys	Ser	Leu	Leu	His	Val	Pro	Tyr		
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1123																	
Thr	Leu	Glu	Ala	Glu	Asn	Ile	Glu	Pro	Glu	Val	Arg	Asp	Trp	Leu	Ala		
				330				335						340			
ttc	ggc	tcg	gag	aag	atc	acc	gag	gtc	aag	ctg	ctt	gcc	gac	gcc	cta		
1171																	
Phe	Gly	Ser	Glu	Lys	Ile	Thr	Glu	Val	Lys	Leu	Leu	Ala	Asp	Ala	Leu		
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gcc	ggc	aac	atc	gac	gcg	gct	gcg	ttc	gat	gcg	gcg	tcc	gca	gca	att		
1219																	
Ala	Gly	Asn	Ile	Asp	Ala	Ala	Ala	Phe	Asp	Ala	Ala	Ser	Ala	Ala	Ile		
		360					365					370					
gct	tct	cga	cgc	acc	tcc	cca	cgc	acc	gca	cca	atc	acg	cag	gaa	ctc		
1267																	
Ala	Ser	Arg	Arg	Thr	Ser	Pro	Arg	Thr	Ala	Pro	Ile	Thr	Gln	Glu	Leu		
	375					380					385						
cct	ggc	cgt	agc	cgt	gga	tcc	ttc	gac	act	cgt	gtt	acg	ctg	cag	gag		
1315																	
Pro	Gly	Arg	Ser	Arg	Gly	Ser	Phe	Asp	Thr	Arg	Val	Thr	Leu	Gln	Glu		
390					395					400					405		
aag	tca	ctg	gag	ctt	cca	gct	ctg	cca	acc	acc	acc	att	ggt	tct	ttc		
1363																	
Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe		
				410					415					420			
cca	cag	acc	cca	tcc	att	cgt	tct	gct	cgc	gct	cgt	ctg	cgc	aag	gaa		
1411																	
Pro	Gln	Thr	Pro	Ser	Ile	Arg	Ser	Ala	Arg	Ala	Arg	Leu	Arg	Lys	Glu		
			425					430					435				
tcc	atc	act	ttg	gag	cag	tac	gaa	gag	gca	atg	cgc	gaa	gaa	atc	gat		
1459																	
Ser	Ile	Thr	Leu	Glu	Gln	Tyr	Glu	Glu	Ala	Met	Arg	Glu	Glu	Ile	Asp		
			440				445					450					

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc	883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
250 255 260	
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt	931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
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Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu	
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 Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu
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 Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly
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 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
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 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu

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 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
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 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
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 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
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 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
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 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
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 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
 580 585 590
 Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser
 595 600 605
 Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
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 Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
 625 630 635 640
 Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
 645 650 655
 Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
 660 665 670
 Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala
 675 680 685
 Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
 690 695 700
 Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp
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 Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln
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											1								
tct	tcc	act	gtc	gct	ggg	ctt	cct	cgc	atc	gga	gcg	aag	cgt	gaa	ctg	163			
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Lys	Phe	Ala	Leu	Glu	Gly	Tyr	Trp	Asn	Gly	Ser	Ile	Glu	Gly	Arg	Glu				
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Ser	Gly	Leu	Asp	Ser	Val	Pro	Phe	Ala	Gly	Arg	Ser	Tyr	Tyr	Asp	Ala				
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Tyr	Phe	Gly	Ala	Ala	Arg	Gly	Thr	Glu	Thr	Leu	Pro	Ala	Gln	Ala	Met				
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acc	aag	tgg	ttt	gat	acc	aac	tac	cac	tac	ctc	gtg	ccg	gag	ttg	tct	499			
Thr	Lys	Trp	Phe	Asp	Thr	Asn	Tyr	His	Tyr	Leu	Val	Pro	Glu	Leu	Ser				
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gcg	gat	aca	cgt	ttc	gtt	ttg	gat	gcg	tcc	gcg	ctg	att	gag	gat	ctc	547			
Ala	Asp	Thr	Arg	Phe	Val	Leu	Asp	Ala	Ser	Ala	Leu	Ile	Glu	Asp	Leu				
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cgt	tgc	cag	cag	gtt	cgt	ggc	gtt	aat	gcc	cgc	cct	gtt	ctg	gtt	ggg	595			
Arg	Cys	Gln	Gln	Val	Arg	Gly	Val	Asn	Ala	Arg	Pro	Val	Leu	Val	Gly				
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Pro	Leu	Thr	Phe	Leu	Ser	Leu	Ala	Arg	Thr	Thr	Asp	Gly	Ser	Asn	Pro				
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Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
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Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
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gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
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Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
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Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
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Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
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Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
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1267	
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1315	

Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
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 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
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 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
 425 430 435
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 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
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 ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac
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 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
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 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
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 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
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 1699
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
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 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
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 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
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 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
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 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr

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590

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1923

Arg Arg Arg

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Ile	Glu	Gly	Arg	Glu	Leu	Ala	Gln	Thr	Ala	Arg	Gln	Leu	Val	Asn	Thr
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Ala	Ser	Asp	Ser	Leu	Ser	Gly	Leu	Asp	Ser	Val	Pro	Phe	Ala	Gly	Arg
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Ser	Tyr	Tyr	Asp	Ala	Met	Leu	Asp	Thr	Ala	Ala	Ile	Leu	Gly	Val	Leu
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Pro	Glu	Arg	Phe	Asp	Asp	Ile	Ala	Asp	His	Glu	Asn	Asp	Gly	Leu	Pro
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Leu	Trp	Ile	Asp	Arg	Tyr	Phe	Gly	Ala	Ala	Arg	Gly	Thr	Glu	Thr	Leu
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Ala	Gly	Tyr	Thr	Thr	Leu	Ala	Lys	Arg	Asp	Gly	Val	Phe	Val	Asn	Thr
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 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
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 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
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 Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
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 Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
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 Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
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gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt 499
 Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
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Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
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Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
 65 70 75 80

Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
 85 90 95

Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
 100 105 110

Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
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Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
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<210> 761

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1303)

<223> RXN02648

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Leu	Gly	Gly	Leu	Thr	Met	Thr	Asp	Thr	Asp	Arg	Trp	Ala	Ser	Gln	Glu																
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act	gat	gaa	gaa	gtc	gtc	gca	gca	tgt	gct	gat	gcg	ctt	tcc	cag	gaa	739															
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tac	aag	atc	atc	acc	gat	gca	ggt	ctg	acc	gtt	cag	ctc	gac	gca	ccg	787															
Tyr	Lys	Ile	Ile	Thr	Asp	Ala	Gly	Leu	Thr	Val	Gln	Leu	Asp	Ala	Pro																
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gac	ttg	gca	gaa	gca	tgg	gat	cag	atc	aac	cca	gag	cca	agc	gtg	aag	835															
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										240						245															

gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca 883
 Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala
 250 255 260

gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc 931
 Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly
 265 270 275

tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att 979
 Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile
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ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca
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 Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala
 295 300 305

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 1075
 Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu
 310 315 320 325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac
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 Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
 330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc
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 Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
 345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg
 1219
 Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
 360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta
 1267
 Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
 375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac
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<210> 762

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 762

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Gly	Glu	Glu	Glu	Phe	Phe	Gln	Ile	Leu	Gln	Ser	Ser	Val	Asp	Asp	Val			
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Ile	Lys	Arg	Gln	Val	Asp	Leu	Gly	Ile	Asp	Ile	Leu	Asn	Glu	Gly	Glu			
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Tyr	Gly	His	Val	Thr	Ser	Gly	Ala	Val	Asp	Phe	Gly	Ala	Trp	Trp	Asn			
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Tyr	Ser	Phe	Thr	Arg	Leu	Gly	Gly	Leu	Thr	Met	Thr	Asp	Thr	Asp	Arg			
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Trp	Ala	Ser	Gln	Glu	Ala	Val	Arg	Ser	Thr	Pro	Gly	Asn	Ile	Glu	Leu			
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Thr	Ser	Phe	Ser	Asp	Arg	Arg	Asp	Arg	Ala	Leu	Phe	Ser	Glu	Ala	Tyr			
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Glu	Asp	Pro	Val	Ser	Gly	Ile	Phe	Thr	Gly	Arg	Ala	Ser	Val	Gly	Asn			
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Pro	Glu	Phe	Thr	Gly	Pro	Ile	Thr	Tyr	Ile	Gly	Gln	Glu	Glu	Thr	Gln			
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Glu	Pro	Ser	Val	Lys	Asp	Tyr	Leu	Asp	Trp	Ile	Gly	Thr	Arg	Ile	Asp			
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His	Ile	Cys	Trp	Gly	Ser	Trp	His	Gly	Pro	His	Val	Thr	Asp	Ile	Pro			
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Phe	Gly	Asp	Ile	Ile	Gly	Glu	Ile	Leu	Arg	Ala	Glu	Val	Gly	Gly	Phe			
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Glu	Glu	Asn	Lys	Leu	Pro	Glu	Gly	Ser	Val	Ile	Tyr	Pro	Gly	Val	Val			
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Ser	His	Ser	Ile	Asn	Ala	Val	Glu	His	Pro	Arg	Leu	Val	Ala	Asp	Arg			

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Thr Asp Cys Gly Leu Gly Gly	Arg Leu His Ser Gln Ile	Ala Trp Ala
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Lys Leu Glu Ser Leu Val Glu Gly	Ala Arg Ile Ala Ser Lys	Glu Leu
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Phe

<210> 763

<211> 548

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(525)

<223> FRXA02648

<400> 763

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agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc	96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile	
20 25 30	
aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc	144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile	
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tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt	192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly	
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Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe	
65 70 75 80	
gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa	288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu	
85 90 95	
aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac	336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His	
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Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val	
115 120 125	
cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac	432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp	
130 135 140	

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg 480
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc 525
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<210> 764

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 764

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Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
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Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
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<211> 784

<212> DNA

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<222> (101)..(784)

<223> FRXA02658

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 Met Ser Gln Asn Arg
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atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
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gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
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tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
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ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
 90 95 100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165

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 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
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 200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784

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<210> 766

<211> 228

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<213> Corynebacterium glutamicum

<400> 766

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 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
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Gln Leu Asp Ala
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<223> RXA01516

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 Met Ala Asp Arg Ile
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gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt 163
 Glu Leu Lys Gly Leu Glu Cys Phe Gly His His Gly Val Phe Asp Phe
 10 15 20

gaa aaa gag caa ggc cag ccc ttc att gtg gat gtc acc tgc tgg atg 211
 Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met
 25 30 35

gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat 259
 Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp
 40 45 50

tac ggc gcg ttg gca ttg ttg gtt gct gaa atc gtg gaa ggc cca tcc 307
 Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile Val Glu Gly Pro Ser
 55 60 65

agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg 355
 Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser Ala Asp Ala Val Met
 70 75 80 85

gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc 403
 Ala Lys Phe Asp Ala Leu His Ala Val Glu Val Thr Ile His Lys Pro
 90 95 100

aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gtt gcc cga 451
 Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg
 105 110 115

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<210> 768

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<212> PRT

<213> Corynebacterium glutamicum

<400> 768

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 35 40 45

Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile
 50 55 60

Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser
 65 70 75 80

Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val
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Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val
 100 105 110

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Asn Ala
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 Met Asn Val Ser Ser
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 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr
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 25 30 35

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 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp
 40 45 50

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 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser
 55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala
 70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala
 90 95 100

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Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val
120 125 130

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Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln
135 140 145

gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595
Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp
150 155 160 165

gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643
Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile
170 175 180

gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691
Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp
185 190 195

cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739
Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile
200 205 210

ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787
Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp
215 220 225

cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835
Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala
230 235 240 245

gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883
Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His
250 255 260

gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931
Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg
265 270 275

agt gga gga act cac cat ggc tgatcgtatt gaacttaaag gcc 975
Ser Gly Gly Thr His His Gly
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<210> 770

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 770

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Met Asn Val Ser Ser Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly
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20 25 30

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Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly
 35 40 45
 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val
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 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys
 65 70 75 80
 Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala
 85 90 95
 Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp
 100 105 110
 Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu
 115 120 125
 Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly
 130 135 140
 Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val
 145 150 155 160
 His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val
 165 170 175
 Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser
 180 185 190
 Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser
 195 200 205
 Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala
 210 215 220
 Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp
 225 230 235 240
 Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp
 245 250 255
 Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val
 260 265 270
 Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly
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<211> 859

<212> DNA

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<220>

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<222> (101)..(859)

<223> RXA02024

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	Met Ser Ser Leu Pro	
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gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag	163	
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys		
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ggg gcg aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc	211	
Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val		
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att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc	259	
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly		
	40 45 50	
ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca	307	
Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro		
	55 60 65	
atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt	355	
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val		
	70 75 80 85	
gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca	403	
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala		
	90 95 100	
acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag	451	
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln		
	105 110 115	
gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg	499	
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly		
	120 125 130	
gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg	547	
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val		
	135 140 145	
gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt	595	
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg		
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gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc	643	
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe		
	170 175 180	
ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag	691	
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu		
	185 190 195	
gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat	739	
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp		
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ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc	787	
Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly		
	215 220 225	

acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt 835
 Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe
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cgc gtg cat gaa gtt gcg gaa acc 859
 Arg Val His Glu Val Ala Glu Thr
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<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 772

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 20 25 30

Arg Ala Ala Glu Val Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly
 35 40 45

Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile
 50 55 60

Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp
 65 70 75 80

Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala
 85 90 95

Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp
 100 105 110

His Glu Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys
 115 120 125

Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His
 130 135 140

Phe Asp Asp Ile Val Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala
 145 150 155 160

Glu Gln Ala Val Arg Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp
 165 170 175

Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu
 180 185 190

Arg Arg Ile Asp Glu Val Val Ala Thr Gly Trp Pro Val Leu Met Ala
 195 200 205

Leu Ser Asn Lys Asp Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp
 210 215 220

Lys Arg Val Ala Gly Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg
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Gly Val Ala Ala Phe Arg Val His Glu Val Ala Glu Thr

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250

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXA01719

<400> 773

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                                   Met Asn Ile Ile Ile
                                   1 5

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Leu Ala Gly Gly Glu Gly Lys Arg Met Gly Gly Val Asp Lys Ala Ala
                                   10 15 20

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Val Ala Val Asp Gly Arg Thr Leu Leu Asp Ile Leu Leu Ser Gln Leu
                                   25 30 35

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Asp Pro Glu Asp Asp Val Val Val Val Ser Pro Ala Ile Ile Asp Gly
                                   40 45 50

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Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly Gly Pro Val Ala Gly
                                   55 60 65

atc gag gca ggg ctg aat tct ttt gag cac gcc cat gaa ttc act gcg 355
Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala His Glu Phe Thr Ala
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Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala Met Leu Pro Leu Leu
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cag gca cag att ggc aaa gcc gat gtg gcc gta acc ctt gct gcc gat 451
Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val Thr Leu Ala Ala Asp
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gcg gtg att cac agc ctg ggc gag act aga aat cga ccg gca aaa gcg 547
Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn Arg Pro Ala Lys Ala
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tta ctg aag caa gcg gga cac att gtg gaa gtg ggt ggc gat ggc act 595
Leu Leu Lys Gln Ala Gly His Ile Val Glu Val Gly Gly Asp Gly Thr
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gaa aaa gac tac gat acg gtg gct gaa ctg gag gta ttg ggc aac gta 643

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Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu Val Leu Gly Asn Val
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<400> 774
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 35 40 45

Ala Ile Ile Asp Gly Ile Thr Thr Val Cys Glu Glu Pro Pro Leu Gly
 50 55 60

Gly Pro Val Ala Gly Ile Glu Ala Gly Leu Asn Ser Phe Glu His Ala
 65 70 75 80

His Glu Phe Thr Ala Ile Leu Ala Val Asp Ala Pro Tyr Ser Ala Ala
 85 90 95

Met Leu Pro Leu Leu Gln Ala Gln Ile Gly Lys Ala Asp Val Ala Val
 100 105 110

Thr Leu Ala Ala Asp Gly Trp Val Gln Pro Leu Cys Ala Leu Trp Arg
 115 120 125

Ser Gly Ser Leu Glu Ala Val Ile His Ser Leu Gly Glu Thr Arg Asn
 130 135 140

Arg Pro Ala Lys Ala Leu Leu Lys Gln Ala Gly His Ile Val Glu Val
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Gly Gly Asp Gly Thr Glu Lys Asp Tyr Asp Thr Val Ala Glu Leu Glu
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Val Leu Gly Asn Val Thr Leu Pro Lys Ala His
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 <223> RXA01720

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 Val Ala Gln Gln Arg
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agc gtc gat gac tat ctt tcc att ttg ata gac agc gtc gca ccg ctt 163
 Ser Val Asp Asp Tyr Leu Ser Ile Leu Ile Asp Ser Val Ala Pro Leu
 10 15 20

ccg cca gta aaa acc cct atc ctc ggc gcg cat ccg tta agt cac ctt 211
 Pro Pro Val Lys Thr Pro Ile Leu Gly Ala His Pro Leu Ser His Leu
 25 30 35

gca gag gat gtt gtc gcg aca att cct atc ccg aaa ttt act aat tct 259
 Ala Glu Asp Val Val Ala Thr Ile Pro Ile Pro Lys Phe Thr Asn Ser
 40 45 50

gct gtt gat ggt tac gcc att ttg aaa gaa gac atc cat ggc agc ggg 307
 Ala Val Asp Gly Tyr Ala Ile Leu Lys Glu Asp Ile His Gly Ser Gly
 55 60 65

ccg tgg aca ttt ctt gtg ggc ggt gat act ccg gcg ggt tct gcg ccg 355
 Pro Trp Thr Phe Leu Val Gly Gly Asp Thr Pro Ala Gly Ser Ala Pro
 70 75 80 85

gcg agc att aat aat gga aaa gcc atc cgt gtg atg aca ggt gga ccc 403
 Ala Ser Ile Asn Asn Gly Lys Ala Ile Arg Val Met Thr Gly Gly Pro
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gtc cca tcc acc aac aag gac atg atc gtg gtt cca gtg gag ctc acc 451
 Val Pro Ser Thr Asn Lys Asp Met Ile Val Val Pro Val Glu Leu Thr
 105 110 115

aat gct ccg gtg gat cac tcg ctt cct aca gaa atc acg atc aat gag 499
 Asn Ala Pro Val Asp His Ser Leu Pro Thr Glu Ile Thr Ile Asn Glu
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cta cca ggt gag agg aat aat att cgc cat gct ggt gag cat ctt aaa 547
 Leu Pro Gly Glu Arg Asn Asn Ile Arg His Ala Gly Glu His Leu Lys
 135 140 145

gaa ggc gaa att gcg gtt gct gcg ggg acg gca ttt gat gcg ggt act 595
 Glu Gly Glu Ile Ala Val Ala Ala Gly Thr Ala Phe Asp Ala Gly Thr
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 Val Ser Thr Val Ile Ser Val Gly His Asp Thr Val Lys Ala His Pro
 170 175 180

tgc cct cgg gtt gcg gtg atc act acc ggt gat gag cta aac cag gga 691
 Cys Pro Arg Val Ala Val Ile Thr Thr Gly Asp Glu Leu Asn Gln Gly
 185 190 195

aat ccc tgg ggt atc cct aat tcc aat ggg ccg atg ctg gtt gcg gag 739
 Asn Pro Trp Gly Ile Pro Asn Ser Asn Gly Pro Met Leu Val Ala Glu
 200 205 210

cta aaa cgc gtg ggg att aag gat ccg cag cat ttc cat tcc gat gat 787
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<212> PRT

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<400> 776

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			20					25					30		
Pro	Leu	Ser	His	Leu	Ala	Glu	Asp	Val	Val	Ala	Thr	Ile	Pro	Ile	Pro
		35					40					45			
Lys	Phe	Thr	Asn	Ser	Ala	Val	Asp	Gly	Tyr	Ala	Ile	Leu	Lys	Glu	Asp
	50					55					60				
Ile	His	Gly	Ser	Gly	Pro	Trp	Thr	Phe	Leu	Val	Gly	Gly	Asp	Thr	Pro
65					70					75					80
Ala	Gly	Ser	Ala	Pro	Ala	Ser	Ile	Asn	Asn	Gly	Lys	Ala	Ile	Arg	Val
				85					90					95	
Met	Thr	Gly	Gly	Pro	Val	Pro	Ser	Thr	Asn	Lys	Asp	Met	Ile	Val	Val
			100					105					110		
Pro	Val	Glu	Leu	Thr	Asn	Ala	Pro	Val	Asp	His	Ser	Leu	Pro	Thr	Glu
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	130					135					140				
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145					150					155					160
Phe	Asp	Ala	Gly	Thr	Val	Ser	Thr	Val	Ile	Ser	Val	Gly	His	Asp	Thr
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Val	Lys	Ala	His	Pro	Cys	Pro	Arg	Val	Ala	Val	Ile	Thr	Thr	Gly	Asp
			180					185					190		
Glu	Leu	Asn	Gln	Gly	Asn	Pro	Trp	Gly	Ile	Pro	Asn	Ser	Asn	Gly	Pro
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225					230					235					240
Pro	Ala	Glu	Val	Ala	Asp	Val	Ile	Ile	Thr	Val	Gly	Gly	Ile	Ser	Ala
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Gly	Ala	Phe	Asp	Val	Val	Lys	Ala	Val	Gly	Thr	Lys	Thr	Gly	Gly	Phe
			260					265					270		
Glu	Phe	Phe	Pro	Ile	Ala	Met	Lys	Pro	Gly	Lys	Pro	Gln	Gly	His	Gly
		275					280					285			
Gln	Trp	Gly	Asp	Ala	Lys	Val	Val	Cys	Leu	Pro	Gly	Asn	Pro	Val	Ala
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Gly Gly Gly Lys Arg Leu Ala Ser Ile Ser Glu Leu Pro Val Val Ala
 325 330 335

Leu Arg Ser Asn Arg Ala Leu Lys Ala Arg Glu Gly Pro Val Leu Ala
 340 345 350

Ile Pro Val Ala Ile Asp Trp Glu Lys Arg Met Ala Asn Ser Gln Ala
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His Arg Ser His Met Val Gly Ala Leu Ala Gly Ser Gly Gly Ile Ala
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Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys	
35 40 45	
tcg ttt agc cag caa ctg ccg gtt gct cct ccg gaa aaa tcc ctg ccc	193
Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro	
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65 70 75 80	
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Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu	
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Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg	
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Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu	

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 Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val
 370 375 380

aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa
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 Gly Arg

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Ala Glu Glu Val Gln Ala Ser Arg Ala Leu Pro Gly Phe Ala Gln Ala
 20 25 30

Ala Ile Asp Gly Tyr Ala Val Arg Ala Val Asp Val Gly Gly Glu Lys
 35 40 45

Ser Phe Ser Gln Gln Leu Pro Val Ala Pro Pro Glu Lys Ser Leu Pro
 50 55 60

Val Val Gly Glu Val Ala Ala Gly Ser Gln Gln Pro Leu Arg Leu Gln
 65 70 75 80

Pro Lys Gln Ala Val Met Val His Thr Gly Ala Pro Leu Pro Met Leu
 85 90 95

Ala Asp Ala Val Leu Pro Met Ala Trp Ser Asp Arg Gly Arg Lys Arg
 100 105 110

Val Thr Ala Gln Arg Pro Val Arg Ser Gly Glu Phe Val Arg Lys Glu
 115 120 125

Gly Asp Asp Ile Gln Pro Gly Asp Ile Ala Val Ser Ala Gly Ala Val
 130 135 140

Leu Gly Pro Ala Gln Ile Gly Leu Leu Ala Ala Val Gly Arg Ser Lys
 145 150 155 160

Val Leu Val Tyr Pro Arg Pro Arg Met Ser Val Ile Ser Val Gly Ala
 165 170 175

Glu Leu Val Asp Ile Asp Arg Gln Pro Gly Leu Gly Gln Val Tyr Asp

180						185						190					
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp		
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Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu		
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Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly		
225					230					235					240		
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu		
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Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val		
			260					265					270				
Gln	Gly	Phe	Gly	Leu	Leu	Gly	Glu	Asn	Lys	Ile	Pro	Cys	Phe	Leu	Leu		
		275					280						285				
Pro	Ser	Asn	Pro	Val	Ala	Ser	Leu	Val	Ile	Phe	Glu	Thr	Phe	Val	Arg		
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Pro	Val	Val	Arg	Met	Ser	Leu	Gly	Lys	Ser	Asn	Ala	Ala	Arg	Arg	Val		
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Val	Arg	Ala	Arg	Ala	Leu	Asn	His	Val	Val	Ser	Val	Ala	Gly	Arg	Lys		
				325					330					335			
Gly	Phe	Ile	Arg	Ser	Arg	Leu	Met	Arg	Asp	Ala	Glu	Thr	Gln	Asp	Tyr		
			340					345					350				
Leu	Val	Glu	Ala	Leu	Gly	Gly	Ala	Thr	Gly	Ala	Pro	Ser	His	Leu	Leu		
		355					360						365				
Ala	Gly	Leu	Ser	Glu	Ala	Asn	Gly	Met	Ile	Arg	Ile	Pro	Glu	Asp	Val		
	370					375					380						
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 <211> 1229
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (1)..(1206)
 <223> FRXA01970

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 gcg gaa gag gtt caa gct agt cgt gct ttg ccg ggt ttc gcg caa gca 96

Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala		
			20					25					30				
gcg	att	gat	ggt	tat	gcg	gtt	cga	gca	gtc	gat	gtc	ggc	ggc	gag	aag	144	
Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys		
		35					40					45					
tcg	ttt	agc	cag	caa	ctg	ccg	gtt	gct	cct	ccg	gaa	aaa	tcc	ctg	ccc	192	
Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro		
	50					55					60						
gtg	gtg	ggt	gaa	gta	gct	gcg	ggt	tct	cag	cag	ccg	ttg	cgc	ctg	cag	240	
Val	Val	Gly	Glu	Val	Ala	Ala	Gly	Ser	Gln	Gln	Pro	Leu	Arg	Leu	Gln		
	65				70				75						80		
cct	aaa	caa	gca	gtc	atg	gtc	cac	acc	ggc	gcg	cca	ctg	ccg	atg	ctt	288	
Pro	Lys	Gln	Ala	Val	Met	Val	His	Thr	Gly	Ala	Pro	Leu	Pro	Met	Leu		
				85				90						95			
gcg	gat	gcg	gtg	ctg	ccc	atg	gcg	tgg	tca	gat	cgt	ggc	cgc	aaa	cga	336	
Ala	Asp	Ala	Val	Leu	Pro	Met	Ala	Trp	Ser	Asp	Arg	Gly	Arg	Lys	Arg		
			100					105					110				
gta	acc	gcg	cag	cga	cct	gtg	cgc	tct	ggc	gag	ttt	gtg	cgc	aaa	gaa	384	
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu		
		115					120					125					
ggc	gat	gac	atc	caa	ccg	gga	gac	atc	gca	gtc	agc	gcc	ggc	gcg	gtc	432	
Gly	Asp	Asp	Ile	Gln	Pro	Gly	Asp	Ile	Ala	Val	Ser	Ala	Gly	Ala	Val		
	130					135					140						
tta	ggc	cct	gcc	caa	att	ggt	ttg	ctc	gca	gct	gtt	ggt	cgc	tcc	aaa	480	
Leu	Gly	Pro	Ala	Gln	Ile	Gly	Leu	Leu	Ala	Ala	Val	Gly	Arg	Ser	Lys		
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gtg	ttg	gtg	tac	cca	cgc	cca	cgc	atg	tcg	gtt	atc	tcc	gta	ggc	gct	528	
Val	Leu	Val	Tyr	Pro	Arg	Pro	Arg	Met	Ser	Val	Ile	Ser	Val	Gly	Ala		
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gaa	ctt	gtt	gat	att	gat	cgc	cag	cca	ggc	ctc	ggc	cag	gtt	tat	gat	576	
Glu	Leu	Val	Asp	Ile	Asp	Arg	Gln	Pro	Gly	Leu	Gly	Gln	Val	Tyr	Asp		
			180				185					190					
gtc	aat	tcc	tat	tct	ctg	gct	gcc	gcc	ggc	agg	gaa	gcg	ggc	gca	gat	624	
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp		
		195					200					205					
gtg	tac	cgc	tac	ggc	att	gct	gcc	ggc	gaa	cct	cgt	cgc	atc	aaa	gag	672	
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu		
	210				215						220						
atc	att	gaa	tcc	cag	atg	ctg	cgc	tcg	gaa	atc	atc	gtc	atc	acc	gga	720	
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly		
	225				230				235						240		
gct	gtt	ggc	ggt	gct	ggc	tca	gct	ggc	gtg	cgc	cag	gtt	ctc	aac	gag	768	
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu		
				245					250					255			
cta	ggc	gat	atc	gac	acc	gaa	cgc	gtc	gca	atg	cac	ccc	ggc	tct	gtc	816	
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val		

260	265	270	
caa gga ttc ggt ctg ctc ggc gag aac aag att cca tgc ttc ctt ctg			864
Gln Gly Phe Gly Leu Leu Gly Glu Asn Lys Ile Pro Cys Phe Leu Leu			
275	280	285	
cct tcc aat ccg gtg gcg tcg tta gtt att ttt gaa acc ttc gtc cgc			912
Pro Ser Asn Pro Val Ala Ser Leu Val Ile Phe Glu Thr Phe Val Arg			
290	295	300	
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Pro Val Val Arg Met Ser Leu Gly Lys Ser Asn Ala Ala Arg Arg Val			
305	310	315	320
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1008			
Val Arg Ala Arg Ala Leu Asn His Val Val Ser Val Ala Gly Arg Lys			
325	330	335	
ggt ttc atc agg tcc agg ctc atg cgc gat gca gaa acc cag gac tac			
1056			
Gly Phe Ile Arg Ser Arg Leu Met Arg Asp Ala Glu Thr Gln Asp Tyr			
340	345	350	
ctc gtg gag gct ttg ggt ggt gca acg ggc gca cca tcg cac cta ttg			
1104			
Leu Val Glu Ala Leu Gly Gly Ala Thr Gly Ala Pro Ser His Leu Leu			
355	360	365	
gca gga ttg tcc gaa gca aac ggt atg atc cgc att cca gaa gat gtc			
1152			
Ala Gly Leu Ser Glu Ala Asn Gly Met Ile Arg Ile Pro Glu Asp Val			
370	375	380	
aca gaa atc cga ccg gga gat gtc gtg gac gtg atc ttc ctt gcc caa			
1200			
Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln			
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1229			
Gly Arg			

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<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 780

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Ala	Glu	Glu	Val	Gln	Ala	Ser	Arg	Ala	Leu	Pro	Gly	Phe	Ala	Gln	Ala
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Ala	Ile	Asp	Gly	Tyr	Ala	Val	Arg	Ala	Val	Asp	Val	Gly	Gly	Glu	Lys
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Ser	Phe	Ser	Gln	Gln	Leu	Pro	Val	Ala	Pro	Pro	Glu	Lys	Ser	Leu	Pro
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50					55					60					
Val	Val	Gly	Glu	Val	Ala	Ala	Gly	Ser	Gln	Gln	Pro	Leu	Arg	Leu	Gln
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Pro	Lys	Gln	Ala	Val	Met	Val	His	Thr	Gly	Ala	Pro	Leu	Pro	Met	Leu
				85					90					95	
Ala	Asp	Ala	Val	Leu	Pro	Met	Ala	Trp	Ser	Asp	Arg	Gly	Arg	Lys	Arg
			100					105					110		
Val	Thr	Ala	Gln	Arg	Pro	Val	Arg	Ser	Gly	Glu	Phe	Val	Arg	Lys	Glu
		115					120					125			
Gly	Asp	Asp	Ile	Gln	Pro	Gly	Asp	Ile	Ala	Val	Ser	Ala	Gly	Ala	Val
	130					135					140				
Leu	Gly	Pro	Ala	Gln	Ile	Gly	Leu	Leu	Ala	Ala	Val	Gly	Arg	Ser	Lys
145						150					155				160
Val	Leu	Val	Tyr	Pro	Arg	Pro	Arg	Met	Ser	Val	Ile	Ser	Val	Gly	Ala
				165					170					175	
Glu	Leu	Val	Asp	Ile	Asp	Arg	Gln	Pro	Gly	Leu	Gly	Gln	Val	Tyr	Asp
			180					185					190		
Val	Asn	Ser	Tyr	Ser	Leu	Ala	Ala	Ala	Gly	Arg	Glu	Ala	Gly	Ala	Asp
		195					200					205			
Val	Tyr	Arg	Tyr	Gly	Ile	Ala	Ala	Gly	Glu	Pro	Arg	Arg	Ile	Lys	Glu
	210					215					220				
Ile	Ile	Glu	Ser	Gln	Met	Leu	Arg	Ser	Glu	Ile	Ile	Val	Ile	Thr	Gly
225						230					235				240
Ala	Val	Gly	Gly	Ala	Gly	Ser	Ala	Gly	Val	Arg	Gln	Val	Leu	Asn	Glu
				245					250					255	
Leu	Gly	Asp	Ile	Asp	Thr	Glu	Arg	Val	Ala	Met	His	Pro	Gly	Ser	Val
			260					265					270		
Gln	Gly	Phe	Gly	Leu	Leu	Gly	Glu	Asn	Lys	Ile	Pro	Cys	Phe	Leu	Leu
		275					280					285			
Pro	Ser	Asn	Pro	Val	Ala	Ser	Leu	Val	Ile	Phe	Glu	Thr	Phe	Val	Arg
		290				295					300				
Pro	Val	Val	Arg	Met	Ser	Leu	Gly	Lys	Ser	Asn	Ala	Ala	Arg	Arg	Val
305						310					315				320
Val	Arg	Ala	Arg	Ala	Leu	Asn	His	Val	Val	Ser	Val	Ala	Gly	Arg	Lys
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Gly	Phe	Ile	Arg	Ser	Arg	Leu	Met	Arg	Asp	Ala	Glu	Thr	Gln	Asp	Tyr
			340					345					350		
Leu	Val	Glu	Ala	Leu	Gly	Gly	Ala	Thr	Gly	Ala	Pro	Ser	His	Leu	Leu
		355					360					365			
Ala	Gly	Leu	Ser	Glu	Ala	Asn	Gly	Met	Ile	Arg	Ile	Pro	Glu	Asp	Val
	370					375					380				

Thr Glu Ile Arg Pro Gly Asp Val Val Asp Val Ile Phe Leu Ala Gln
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Gly Arg

<210> 781

<211> 708

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(685)

<223> RXA02629

<400> 781

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 Met Ser Lys Asp Pro
 1 5

ttg gga agt ctt acc gat gtt gta gac aca cga gtt ccg ctt ccg gat 163
 Leu Gly Ser Leu Thr Asp Val Val Asp Thr Arg Val Pro Leu Pro Asp
 10 15 20

gtt gaa ccg gat ccg gag ttc ctg aag gct acg gaa aaa gaa ttc cac 211
 Val Glu Pro Asp Pro Glu Phe Leu Lys Ala Thr Glu Lys Glu Phe His
 25 30 35

atg gca tcc cag aag cgc gct ctt gtt gtc ctg gtg ggc gat cat gtc 259
 Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu Val Gly Asp His Val
 40 45 50

gct gag gca gat ggg act ggc cgt ttg gtt acg gag ctg ctc tta gag 307
 Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr Glu Leu Leu Leu Glu
 55 60 65

tct ggc ttc aac gtg gac gct gtg gtc agc gtg aag tct aag aag tct 355
 Ser Gly Phe Asn Val Asp Ala Val Val Ser Val Lys Ser Lys Lys Ser
 70 75 80 85

cag att agg caa gct att gaa acc gca gtt gtt ggc ggc gct gac ctt 403
 Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val Gly Gly Ala Asp Leu
 90 95 100

gtg ctg acc atc ggc gga gtg ggc gtt ggt cct cgg gat aaa act cct 451
 Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro Arg Asp Lys Thr Pro
 105 110 115

gag gca acc agc gct gtg ttg gac cag gac gtc cca gga atc gcg cag 499
 Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val Pro Gly Ile Ala Gln
 120 125 130

gcg ctt cgt tcc tcc ggt ttg gcc tgt ggc gcg gtg gat gca agt gtt 547
 Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala Val Asp Ala Ser Val
 135 140 145

tcc cga ggc gta gcg ggc gta tcc ggc tca acc gtg gtg gtc aac ctc 595
 Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr Val Val Val Asn Leu
 150 155 160 165

gct gag tct cgt tcg gca att cgt gat ggc atg gca act ctg aca ccg 643
 Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met Ala Thr Leu Thr Pro
 170 175 180

ttg gtt gat ttt gtt gta gat cag ctt cgc act tcc gtg gtt 685
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tgagttggtc ggggtgtgagt aga 708

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<211> 195

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<213> Corynebacterium glutamicum

<400> 782

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 20 25 30

Glu Lys Glu Phe His Met Ala Ser Gln Lys Arg Ala Leu Val Val Leu
 35 40 45

Val Gly Asp His Val Ala Glu Ala Asp Gly Thr Gly Arg Leu Val Thr
 50 55 60

Glu Leu Leu Leu Glu Ser Gly Phe Asn Val Asp Ala Val Val Ser Val
 65 70 75 80

Lys Ser Lys Lys Ser Gln Ile Arg Gln Ala Ile Glu Thr Ala Val Val
 85 90 95

Gly Gly Ala Asp Leu Val Leu Thr Ile Gly Gly Val Gly Val Gly Pro
 100 105 110

Arg Asp Lys Thr Pro Glu Ala Thr Ser Ala Val Leu Asp Gln Asp Val
 115 120 125

Pro Gly Ile Ala Gln Ala Leu Arg Ser Ser Gly Leu Ala Cys Gly Ala
 130 135 140

Val Asp Ala Ser Val Ser Arg Gly Val Ala Gly Val Ser Gly Ser Thr
 145 150 155 160

Val Val Val Asn Leu Ala Glu Ser Arg Ser Ala Ile Arg Asp Gly Met
 165 170 175

Ala Thr Leu Thr Pro Leu Val Asp Phe Val Val Asp Gln Leu Arg Thr
 180 185 190

Ser Val Val
 195

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<223> RXA02318
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1088

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		Met His Ala Val Leu	
		1 5	
tcc atc ggt tcc aac atg gat gat cgc tac gcg ctg ctc aac aca gtg	163		
Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala Leu Leu Asn Thr Val			
	10	15	20
atc gag gaa ttc aaa gat gag atc gtg gcg cag tct gcg atc tac tca	211		
Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser			
	25	30	35
acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg	259		
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val			
	40	45	50
ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc	307		
Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly			
	55	60	65
caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg	355		
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly			
	70	75	85
cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa	403		
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu			
	90	95	100
gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct	451		
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala			
	105	110	115
tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat	499		
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp			
	120	125	130
gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat	547		
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp			
	135	140	145
ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggctttcat	597		
Pro Thr Asp Ile Glu Gly Val Thr Lys Ile			

150

155

gca

600

<210> 786

<211> 159

<212> PRT

<213> Corynebacterium glutamicum

<400> 786

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 20 25 30

Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu
 35 40 45

Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu
 50 55 60

Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg
 65 70 75 80

Val Arg Lys Trp Gly Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile
 85 90 95

Ile Lys Asp Gly Glu Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu
 100 105 110

Pro His Pro Trp Ala Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu
 115 120 125

Glu Ala Glu Pro Asp Ala Val Leu His Gly Thr Thr Ile Ala Glu His
 130 135 140

Val Asp Asn Leu Asp Pro Thr Asp Ile Glu Gly Val Thr Lys Ile
 145 150 155

<210> 787

<211> 609

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXN01304

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 Met Pro Ala Gln Asn
 1 5

aaa aac ctc cca gga tcc gtc atc gtt gtg tct gat cgg att aaa tcg 163
 Lys Asn Leu Pro Gly Ser Val Ile Val Val Ser Asp Arg Ile Lys Ser

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gga gaa aga att gat aaa gca gga ccc gta gca gta gac ctt ctt cag	25	30	35	211
Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala Val Asp Leu Leu Gln				
gaa tca ggc gtg gag att tcc aca ttc acc gtc gtg gag gag ggc ttt	40	45	50	259
Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val Val Glu Glu Gly Phe				
gaa cct gtc cat caa gaa ttg gtt aag gcg ttg gcg cgc cgg gat cgc	55	60	65	307
Glu Pro Val His Gln Glu Leu Val Lys Ala Leu Ala Arg Arg Asp Arg				
gtc atc atc acc atc ggc gga acg ggc gtg ggg cct aga aat cgg acg	70	75	80	355
Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly Pro Arg Asn Arg Thr				
ccg gag gcc aca gaa ccg cac atc gat acg cta ctg ccg ggt ctg atg	90	95	100	403
Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu Leu Pro Gly Leu Met				
acg cag att ttg ttc tct gga ctg tcc aat acc gcg cag gcg ggg tta	105	110	115	451
Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr Ala Gln Ala Gly Leu				
tct cgg ggg ctg gtg ggc ttg agt gct cgc gat tcc acg gcc gcg ctc	120	125	130	499
Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp Ser Thr Ala Ala Leu				
atc gtc aac gcg ccg agt tct tcc ggg ggc gtg cgc gac gcg ctc ggg	135	140	145	547
Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val Arg Asp Ala Leu Gly				
gtg gtc tgc ccg ctt ttc ggt tcc att ttt gag cgt ctt taaaagattt	150	155	160	596
Val Val Cys Pro Leu Phe Gly Ser Ile Phe Glu Arg Leu				
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Asp Arg Ile Lys Ser Gly Glu Arg Ile Asp Lys Ala Gly Pro Val Ala	20	25	30	
Val Asp Leu Leu Gln Glu Ser Gly Val Glu Ile Ser Thr Phe Thr Val	35	40	45	
Val Glu Glu Gly Phe Glu Pro Val His Gln Glu Leu Val Lys Ala Leu	50	55	60	
Ala Arg Arg Asp Arg Val Ile Ile Thr Ile Gly Gly Thr Gly Val Gly	65	70	75	80

Pro Arg Asn Arg Thr Pro Glu Ala Thr Glu Pro His Ile Asp Thr Leu
85 90 95

Leu Pro Gly Leu Met Thr Gln Ile Leu Phe Ser Gly Leu Ser Asn Thr
100 105 110

Ala Gln Ala Gly Leu Ser Arg Gly Leu Val Gly Leu Ser Ala Arg Asp
115 120 125

Ser Thr Ala Ala Leu Ile Val Asn Ala Pro Ser Ser Ser Gly Gly Val
130 135 140

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<210> 789

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<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) .. (1258)

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<400> 789

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Leu Ile Val Ser Thr
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cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163
Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val
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atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211
Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr
25 30 35

ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259
Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala
40 45 50

aac acc ttc aac cgt ggc aat cag aag caa ggc gat cag cag aag gcg 307
Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala
55 60 65

ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355
Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp
70 75 80 85

gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg 403
Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val
90 95 100

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg	451
Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu	
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ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct	499
Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro	
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gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg	547
Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu	
135 140 145	
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Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly	
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Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala	
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acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca	691
Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro	
185 190 195	
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Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln	
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ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att	787
Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile	
215 220 225	
gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta	835
Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val	
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tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt	883
Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val	
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ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc	931
Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly	
265 270 275	
tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac	979
Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp	
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gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg	
1027 Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val	
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gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa	
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1123 Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile	

330	335	340
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Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys 345 350 355		
aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta 1219		
Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val 360 365 370		
aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca 1268		
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Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly 50 55 60		
Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met 65 70 75 80		
Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile 85 90 95		
Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile 100 105 110		
Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu 115 120 125		
Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile 130 135 140		
Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn 145 150 155 160		
Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys 165 170 175		
Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu		

180								185				190			
Val	Ala	Pro	Glu	Pro	Gly	Gln	Tyr	Thr	Ser	Ile	Gly	Val	Val	Leu	Asp
195								200				205			
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Thr	Glu	Tyr	Arg	Ile	Ala	Val	Glu	Asp	Asn	Gly	Glu	Val	Ser	Gly	Phe
225								230				235			
Leu	Arg	Asp	Arg	Val	Ser	Val	Gly	Asp	Lys	Ile	Glu	Ala	Thr	Ile	Ala
245								250				255			
Ala	Gly	Asp	Leu	Val	Leu	Asn	Lys	Asp	Thr	Asn	Pro	Val	Val	Leu	Ile
260								265				270			
Ser	Gln	Gly	Ile	Gly	Ser	Thr	Pro	Met	Val	Gly	Met	Leu	Ala	Gly	Met
275								280				285			
Asn	Pro	Glu	Arg	Asp	Val	Val	Val	Leu	His	Ala	Asp	Gln	Ala	Glu	Ser
290								295				300			
Thr	Tyr	Ala	Gln	Val	Glu	Glu	Val	Gln	Gly	Leu	Val	Glu	Lys	Leu	Pro
305								310				315			
Lys	Ala	Ala	Phe	Glu	Ile	Phe	Tyr	Arg	Asp	Asn	Asp	Gln	Trp	Leu	Glu
325								330				335			
Val	Ala	Gly	Arg	Ile	Pro	Ser	Gly	Ala	Ser	Val	Tyr	Leu	Cys	Gly	Gly
340								345				350			
Val	Glu	Phe	Leu	Lys	Asn	Val	Arg	Glu	Gln	Ile	Glu	Ala	Leu	Asp	Glu
355								360				365			
Gln	Pro	Arg	Asp	Val	Asn	Phe	Glu	Leu	Phe	Ala	Pro	Asn	Asp	Trp	Leu
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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(967)

<223> RXS02560

<400> 791

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ctt	aat	ctg	gca	gac	aac	agc	gag	aga	aag	aag	ccc	atg	ccg	tca	cca	163
Leu	Asn	Leu	Ala	Asp	Asn	Ser	Glu	Arg	Lys	Lys	Pro	Met	Pro	Ser	Pro	

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gga	gaa	ctt	tta	gcc	gcc	cgc	tac	gga	caa	cct	gca	acc	tgg	acg	cca	211
Gly	Glu	Leu	Leu	Ala	Ala	Arg	Tyr	Gly	Gln	Pro	Ala	Thr	Trp	Thr	Pro	
25				30				35								
ccg	cag	tgg	aat	gag	acg	ctt	gat	gtc	att	cac	cag	cat	cga	tca	gtt	259
Pro	Gln	Trp	Asn	Glu	Thr	Leu	Asp	Val	Ile	His	Gln	His	Arg	Ser	Val	
40				45				50								
cgc	agg	tgg	ttg	gat	aaa	ccg	gtt	gat	gat	gac	acc	atc	cgc	acc	att	307
Arg	Arg	Trp	Leu	Asp	Lys	Pro	Val	Asp	Asp	Asp	Thr	Ile	Arg	Thr	Ile	
55				60				65								
att	tcc	gcc	gca	caa	tcg	gct	gga	acc	tct	tcc	aat	aag	cag	gtc	att	355
Ile	Ser	Ala	Ala	Gln	Ser	Ala	Gly	Thr	Ser	Ser	Asn	Lys	Gln	Val	Ile	
70				75				80								
tct	gtc	atc	gtg	gtt	aaa	gat	cct	gag	ctg	agg	aaa	ggc	ctc	gcg	ggg	403
Ser	Val	Ile	Val	Val	Lys	Asp	Pro	Glu	Leu	Arg	Lys	Gly	Leu	Ala	Gly	
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Ile	Thr	Arg	Gln	Met	Phe	Pro	His	Leu	Glu	Gln	Val	Pro	Ala	Val	Leu	
105				110				115								
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Ile	Trp	Leu	Ile	Asp	Tyr	Ser	Arg	Ile	Ser	Ala	Val	Ala	Ala	Arg	Glu	
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Asp	Leu	Pro	Thr	Gly	Ala	Leu	Asp	Tyr	Leu	Asp	Glu	Ala	Ala	Trp	Gly	
135				140				145								
ttc	ctc	gac	gcc	gga	atc	gca	gct	caa	aac	gct	gca	att	gct	gcg	gag	595
Phe	Leu	Asp	Ala	Gly	Ile	Ala	Ala	Gln	Asn	Ala	Ala	Ile	Ala	Ala	Glu	
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Ser	Leu	Gly	Leu	Gly	Thr	Leu	Tyr	Leu	Gly	Ser	Val	Arg	Asn	Asp	Ala	
170				175				180								
gaa	gcc	gtg	cac	aaa	ttg	ctt	ggc	ctt	cca	cct	gag	atc	gtg	cct	gtc	691
Glu	Ala	Val	His	Lys	Leu	Leu	Gly	Leu	Pro	Pro	Glu	Ile	Val	Pro	Val	
185				190				195								
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Val	Gly	Leu	Glu	Met	Gly	His	Ala	Asp	Pro	Pro	Glu	Pro	Ala	Gly	Ile	
200				205				210								
aaa	cct	ccc	ctg	cca	caa	gaa	gcc	att	gtt	cac	tgg	gat	acc	tac	acc	787
Lys	Pro	Pro	Leu	Pro	Gln	Glu	Ala	Ile	Val	His	Trp	Asp	Thr	Tyr	Thr	
215				220				225								
gag	aaa	aac	ctc	gaa	ctt	atc	gat	tcc	tac	gac	cgc	gcc	ctc	gac	act	835
Glu	Lys	Asn	Leu	Glu	Leu	Ile	Asp	Ser	Tyr	Asp	Arg	Ala	Leu	Asp	Thr	
230				235				240								
tac	tat	tct	cgc	tac	ggc	cag	cac	cag	ctc	tgg	tcg	aag	cag	acg	gcg	883
Tyr	Tyr	Ser	Arg	Tyr	Gly	Gln	His	Gln	Leu	Trp	Ser	Lys	Gln	Thr	Ala	
250				255				260								

cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt 931
 His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu
 265 270 275

agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977
 Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg
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<210> 792

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 792

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 20 25 30

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 35 40 45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
 50 55 60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65 70 75 80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
 85 90 95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
 100 105 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
 115 120 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
 130 135 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
 145 150 155 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
 165 170 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
 180 185 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
 195 200 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp

225		230		235		240									
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				245					250					255	
Ser	Lys	Gln	Thr	Ala	His	Arg	Ala	Ala	Ser	Lys	Ser	Phe	Ser	Lys	Thr
			260					265					270		
Asn	Arg	Gln	Phe	Leu	Arg	Gly	Val	Phe	Glu	Arg	Ala	Gly	Phe	Gly	Leu
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Arg

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 <211> 1425
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1402)
 <223> RXA00382

<400> 793
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ctggattggc ttcacagatt gaattaatac aatgacgcac atg aca tcg tcc aat 115
 Met Thr Ser Ser Asn
 1 5

acg gct cga tcc gca gag tgg ttt gaa aag gct cag aag ctc acc cct 163
 Thr Ala Arg Ser Ala Glu Trp Phe Glu Lys Ala Gln Lys Leu Thr Pro
 10 15 20

ggt ggt gtg aat tct cct gtt cgc gct ttc ggt tca gtt ggc gga caa 211
 Gly Gly Val Asn Ser Pro Val Arg Ala Phe Gly Ser Val Gly Gly Gln
 25 30 35

gcc cgt ttc atc gaa aaa gct cac ggt tca acg ctg atc gat gtg gac 259
 Ala Arg Phe Ile Glu Lys Ala His Gly Ser Thr Leu Ile Asp Val Asp
 40 45 50

gga aat gaa tac gtt gac ctg gtc tgt tct tgg ggc ccc atg ctg atg 307
 Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp Gly Pro Met Leu Met
 55 60 65

ggt cac gct cac cca gca gtg gtc gag gct gtg cag aag gcc gtc gtg 355
 Gly His Ala His Pro Ala Val Val Glu Ala Val Gln Lys Ala Val Val
 70 75 80 85

gat ggt ctt tct ttc ggc gct ccc acc atc ggt gag gtt gag ttg gcc 403
 Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly Glu Val Glu Leu Ala
 90 95 100

caa gat atc gtc aag cgc act tct gtg gag gaa gtc cgc ctg gtc aac 451
 Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu Val Arg Leu Val Asn
 105 110 115

tcc ggc act gag gcc acc atg tcg gcg gtt cgt ctg gcg cgc ggt tac 499

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Thr	Gln	Arg	Ser	Lys	Ile	Leu	Lys	Phe	Glu	Gly	Cys	Tyr	His	Gly	His		
	135					140					145						
gtc	gat	gcg	ctg	ctc	gca	tct	gct	ggg	tct	ggg	gtc	gca	act	ttc	gct	595	
Val	Asp	Ala	Leu	Leu	Ala	Ser	Ala	Gly	Ser	Gly	Val	Ala	Thr	Phe	Ala		
	150				155					160					165		
ctg	cct	gat	tcc	cca	ggc	atc	acc	ggc	gct	cag	act	tct	gac	act	att	643	
Leu	Pro	Asp	Ser	Pro	Gly	Ile	Thr	Gly	Ala	Gln	Thr	Ser	Asp	Thr	Ile		
				170				175						180			
gtt	gtt	cct	tac	aac	gac	att	gaa	gcc	gtg	cgc	aac	gct	ttt	gcg	gag	691	
Val	Val	Pro	Tyr	Asn	Asp	Ile	Glu	Ala	Val	Arg	Asn	Ala	Phe	Ala	Glu		
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Tyr	Pro	Gly	Glu	Ile	Ala	Cys	Ile	Ile	Ala	Glu	Ala	Ala	Gly	Gly	Asn		
		200					205					210					
atg	ggc	acc	gtc	gct	cca	aag	gac	aac	ttt	aac	gac	aag	ctt	ctc	gcg	787	
Met	Gly	Thr	Val	Ala	Pro	Lys	Asp	Asn	Phe	Asn	Asp	Lys	Leu	Leu	Ala		
	215					220					225						
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Ile	Ala	His	Ala	Asp	Gly	Ala	Leu	Leu	Ile	Leu	Asp	Glu	Val	Met	Thr		
	230				235					240					245		
ggc	ttc	cgc	acc	tct	tac	cgt	ggc	tgg	ttc	ggc	gta	gac	aag	gtt	gcc	883	
Gly	Phe	Arg	Thr	Ser	Tyr	Arg	Gly	Trp	Phe	Gly	Val	Asp	Lys	Val	Ala		
				250				255						260			
gct	gac	ctg	gtc	acc	ttc	ggc	aag	gtc	gtc	tcc	ggc	ggc	cta	cct	gcc	931	
Ala	Asp	Leu	Val	Thr	Phe	Gly	Lys	Val	Val	Ser	Gly	Gly	Leu	Pro	Ala		
			265					270					275				
gca	gcg	ttt	ggc	ggc	aag	gct	gaa	atc	atg	aac	atg	ctg	gcc	cca	cag	979	
Ala	Ala	Phe	Gly	Gly	Lys	Ala	Glu	Ile	Met	Asn	Met	Leu	Ala	Pro	Gln		
		280					285					290					
ggc	ccc	gtc	tac	caa	gca	ggc	aca	ctg	tcc	ggc	aac	ccg	gtt	gcg	gtc		
1027																	
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gca	gct	ggg	cgg	gca	tcg	ctt	aag	ctt	gcc	gac	gaa	tcc	ctc	tac	aca		
1075																	
Ala	Ala	Gly	Arg	Ala	Ser	Leu	Lys	Leu	Ala	Asp	Glu	Ser	Leu	Tyr	Thr		
	310				315				320						325		
acc	atc	aac	gcc	aac	gca	gat	cgt	ctc	cac	ggg	ttg	atc	tct	gat	gcc		
1123																	
Thr	Ile	Asn	Ala	Asn	Ala	Asp	Arg	Leu	His	Gly	Leu	Ile	Ser	Asp	Ala		
				330				335						340			
tta	acc	cac	gaa	ggc	gta	gcc	cac	cac	att	cag	cgt	gcc	tca	aac	atg		
1171																	
Leu	Thr	His	Glu	Gly	Val	Ala	His	His	Ile	Gln	Arg	Ala	Ser	Asn	Met		

345 350 355
 ctg tct atc cgt ttt gca gaa ggt gag ggc cac aac ttc tct gat atg
 1219
 Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His Asn Phe Ser Asp Met
 360 365 370
 aag gca gcc gac atc ttc cgc ttc gca ccg ttc ttc cac act ttg ctg
 1267
 Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe Phe His Thr Leu Leu
 375 380 385
 gac aac ggc gtc tac gca cca cca agc gtt ttc gaa acc tgg ttt gtg
 1315
 Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe Glu Thr Trp Phe Val
 390 395 400 405
 tct tcc gct ctc acg gac gat gat ttc tcc aag atc gag cag gca ctc
 1363
 Ser Ser Ala Leu Thr Asp Asp Asp Phe Ser Lys Ile Glu Gln Ala Leu
 410 415 420
 aag ccc gcc gca cgt gca gca gca gaa gcg aag gca tca tgacgcaaac
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 Lys Pro Ala Ala Arg Ala Ala Ala Glu Ala Lys Ala Ser
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 1425

<210> 794

<211> 434

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 794

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 35 40 45
 Leu Ile Asp Val Asp Gly Asn Glu Tyr Val Asp Leu Val Cys Ser Trp
 50 55 60
 Gly Pro Met Leu Met Gly His Ala His Pro Ala Val Val Glu Ala Val
 65 70 75 80
 Gln Lys Ala Val Val Asp Gly Leu Ser Phe Gly Ala Pro Thr Ile Gly
 85 90 95
 Glu Val Glu Leu Ala Gln Asp Ile Val Lys Arg Thr Ser Val Glu Glu
 100 105 110
 Val Arg Leu Val Asn Ser Gly Thr Glu Ala Thr Met Ser Ala Val Arg
 115 120 125

Leu Ala Arg Gly Tyr Thr Gln Arg Ser Lys Ile Leu Lys Phe Glu Gly
 130 135 140
 Cys Tyr His Gly His Val Asp Ala Leu Leu Ala Ser Ala Gly Ser Gly
 145 150 155 160
 Val Ala Thr Phe Ala Leu Pro Asp Ser Pro Gly Ile Thr Gly Ala Gln
 165 170 175
 Thr Ser Asp Thr Ile Val Val Pro Tyr Asn Asp Ile Glu Ala Val Arg
 180 185 190
 Asn Ala Phe Ala Glu Tyr Pro Gly Glu Ile Ala Cys Ile Ile Ala Glu
 195 200 205
 Ala Ala Gly Gly Asn Met Gly Thr Val Ala Pro Lys Asp Asn Phe Asn
 210 215 220
 Asp Lys Leu Leu Ala Ile Ala His Ala Asp Gly Ala Leu Leu Ile Leu
 225 230 235 240
 Asp Glu Val Met Thr Gly Phe Arg Thr Ser Tyr Arg Gly Trp Phe Gly
 245 250 255
 Val Asp Lys Val Ala Ala Asp Leu Val Thr Phe Gly Lys Val Val Ser
 260 265 270
 Gly Gly Leu Pro Ala Ala Ala Phe Gly Gly Lys Ala Glu Ile Met Asn
 275 280 285
 Met Leu Ala Pro Gln Gly Pro Val Tyr Gln Ala Gly Thr Leu Ser Gly
 290 295 300
 Asn Pro Val Ala Val Ala Ala Gly Arg Ala Ser Leu Lys Leu Ala Asp
 305 310 315 320
 Glu Ser Leu Tyr Thr Thr Ile Asn Ala Asn Ala Asp Arg Leu His Gly
 325 330 335
 Leu Ile Ser Asp Ala Leu Thr His Glu Gly Val Ala His His Ile Gln
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 Arg Ala Ser Asn Met Leu Ser Ile Arg Phe Ala Glu Gly Glu Gly His
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 Asn Phe Ser Asp Met Lys Ala Ala Asp Ile Phe Arg Phe Ala Pro Phe
 370 375 380
 Phe His Thr Leu Leu Asp Asn Gly Val Tyr Ala Pro Pro Ser Val Phe
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 Ala Ser

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Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser Phe Gly Gly Pro Glu
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Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn Val Thr His Gly Arg
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ggg att ccg ccg gaa cgt cta gat gaa gtg gcg gtt cat tac cac cac 259
Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala Val His Tyr His His
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Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His Lys Leu Pro Val Tyr
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Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn Glu Ala Ala Glu Gln
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atg gct gat gac ggc gtg aaa aac gcg ctg gtg ttg gca act tcc gct 451
Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val Leu Ala Thr Ser Ala
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Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln Glu Asp Ile Gln Gly
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Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp Glu Leu Arg Asp Glu
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gct gcg gga acc cct gag gat ggc tcc ttg tat tcc aca cag gtc aag 739
 Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr Ser Thr Gln Val Lys
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gaa gcg tca gca ctg att gct gag gct gtt ggt gtg tca gat ttt gat 787
 Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly Val Ser Asp Phe Asp
 215 220 225

gtg gtg tgg cag tcc cgc tcg ggt agc ccg cac act ccg tgg ctg gag 835
 Val Val Trp Gln Ser Arg Ser Gly Ser Pro His Thr Pro Trp Leu Glu
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cct gac atc gtg gat cac gca gtg gag ctc aac gag aag ggt caa aaa 883
 Pro Asp Ile Val Asp His Ala Val Glu Leu Asn Glu Lys Gly Gln Lys
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gcg ctc gtt gtc tgc cct gta ggc ttt att tct gat cat atg gaa gtc 931
 Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser Asp His Met Glu Val
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att tgg gat ctt gat tcc gag ctg atg gaa gaa gcc gag aag cgc aac 979
 Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu Ala Glu Lys Arg Asn
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 295 300 305

gcc ctt gtg gtt gat ctc atc gag gag gca gag ctc aag cgc gtt atc
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 Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu Leu Lys Arg Val Ile
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 Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser Ser Val Asn Gly Ala
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<212> PRT

<213> Corynebacterium glutamicum

<400> 796

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Val	His	Tyr	His	His	Phe	Gly	Gly	Ile	Ser	Pro	Ile	Asn	Ala	Leu	Asn
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Lys	Leu	Pro	Val	Tyr	Phe	Gly	Asn	Arg	Asn	Trp	Lys	Pro	Phe	Asp	Asn
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145					150					155					160
Ser	Thr	Met	Ala	Gln	Leu	Val	Gln	Asp	Ser	Tyr	Ala	Lys	Leu	Pro	Asp
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Glu	Leu	Arg	Asp	Glu	Ala	Arg	Leu	Val	Phe	Thr	Ala	His	Ser	Ile	Pro
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Leu	Thr	Ala	Asp	Asn	Ala	Ala	Gly	Thr	Pro	Glu	Asp	Gly	Ser	Leu	Tyr
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Val	Ser	Asp	Phe	Asp	Val	Val	Trp	Gln	Ser	Arg	Ser	Gly	Ser	Pro	His
225					230					235					240
Thr	Pro	Trp	Leu	Glu	Pro	Asp	Ile	Val	Asp	His	Ala	Val	Glu	Leu	Asn
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Asp	His	Met	Glu	Val	Ile	Trp	Asp	Leu	Asp	Ser	Glu	Leu	Met	Glu	Glu
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Thr	Asp	Glu	Phe	Ala	Ala	Leu	Val	Val	Asp	Leu	Ile	Glu	Glu	Ala	Glu
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Leu Lys Arg Val Ile Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser
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His Lys Thr Ala Arg Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala
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Ala Asn
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<222> (101)..(787)

<223> RXA00624

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 Met Ser Gly Arg Leu
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ctt gtt tca gtt tct agt att ttc gac cag acc cga tcg gcg gct gac 163
 Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr Arg Ser Ala Ala Asp
 10 15 20

agg ctc att tca gac ctg cga gcc gac ggc atc gag gtc tca tta ctt 211
 Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile Glu Val Ser Leu Leu
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gtc gca ccc cgc atc gat ggg gac tgg cgt ctc gcc aaa gac aaa ggg 259
 Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu Ala Lys Asp Lys Gly
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acc ctc gcg tgg atg gaa caa caa cgc gaa cgc ggc cac gaa ctc atc 307
 Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg Gly His Glu Leu Ile
 55 60 65

ctc aac ggt ttc gac caa gca gtt cag gga cgt cgc tca gaa ttc gcc 355
 Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg Arg Ser Glu Phe Ala
 70 75 80 85

aac ctt gaa cgg cac gaa gca cgt ctt cgc ctt acc ggt gcc att agg 403
 Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu Thr Gly Ala Ile Arg
 90 95 100

caa atg cag aaa att ggc ttc gaa ttc caa atc ttt gcc cca cct cgt 451
 Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile Phe Ala Pro Pro Arg
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Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn Leu Asp Thr Gly Glu			
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Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu Gly Phe Gly Ala Ala			
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aaa tgg tgg cgc aag aat gtc atc aag gct gtc act cgt gga gcg gaa			643
Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val Thr Arg Gly Ala Glu			
	170	175	180
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Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala Arg Asn Leu Thr Asn			
	185	190	195
cct aaa gtc gca gct gac ttc cgg gaa gct gca tta gct gcc ttg gat			739
Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala Leu Ala Ala Leu Asp			
	200	205	210
ttg ggt gct cag gtg caa acc tat tct cag gcg gcc gca caa ctg gcc			787
Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala Ala Ala Gln Leu Ala			
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Ala	Lys	Asp	Lys	Gly	Thr	Leu	Ala	Trp	Met	Glu	Gln	Gln	Arg	Glu	Arg
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Gly	His	Glu	Leu	Ile	Leu	Asn	Gly	Phe	Asp	Gln	Ala	Val	Gln	Gly	Arg
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Arg	Ser	Glu	Phe	Ala	Asn	Leu	Glu	Arg	His	Glu	Ala	Arg	Leu	Arg	Leu
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Phe	Ala	Pro	Pro	Arg	Trp	Arg	Met	Ser	Glu	Gly	Thr	Phe	Ala	Val	Leu
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Pro	Glu	Phe	Asp	Phe	Asn	Val	Ala	Ala	Ser	Thr	Arg	Gly	Leu	His	Asn
	130					135					140				

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 Gly Phe Gly Ala Ala Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val
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 Thr Arg Gly Ala Glu Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala
 180 185 190
 Arg Asn Leu Thr Asn Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala
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 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
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 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
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 Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
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 aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg 240
 Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
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 gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt 288
 Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95
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 Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
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 Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu

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gac	gag	gcg	gat	gag	aaa	tcc	gat	atc	ttg	gct	gaa	tcc	atg	acc	cag	528		
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Tyr	Phe	Glu	Asp	Pro	Leu	Gly	Pro	Glu	Ile	Glu	Glu	Tyr	Phe	Thr	Arg			
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Thr	Ala	Trp	Leu	Arg	Glu	Gln	Thr	Arg	Asp	Ser	Ile	Leu	Ser	Ser	Arg			
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Phe	Lys	Val	Arg	Pro	Gly	Val	Ala	Arg	Glu	Gln	Ile	Ser	Leu	Ala	Asp			
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Thr	Asp	Gly	Pro	Arg	Trp	Ser	His	Asp	Val	Asp	Glu	His	Val	Ala	Ser			
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Glu	Met	Tyr	Ala	Met	Ala	Gln	Gly	Ile	Glu	Gly	Glu	Ser	Leu	His	Asn			
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Gly	Ala	Ile	Ala	Ala	Leu	Val	Asp	Leu	Ile	Arg	His	Gly	Leu	Val	Leu			
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Thr	Ala	Trp	Leu	Arg	Glu	Gln	Thr	Arg	Asp	Ser	Ile	Leu	Ser	Ser	Arg														
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Phe	Lys	Val	Arg	Pro	Gly	Val	Ala	Arg	Glu	Gln	Ile	Ser	Leu	Ala	Asp														
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Ile	Val	Ala	Gly	Leu	Asn	Pro	His	Gly	Leu	Pro	Phe	Glu	Glu	Ile	Leu														
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Glu	Met	Tyr	Ala	Met	Ala	Gln	Gly	Ile	Glu	Gly	Glu	Ser	Leu	His	Asn														
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Met Ser Val Phe Gly
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Val Tyr Ile His Val Pro Phe Cys Ser Thr Arg Cys Gly Tyr Cys Asp
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ttc aac acc tat act gct ggg gaa tta ggt agt act gca ggc ccg gac 211
Phe Asn Thr Tyr Thr Ala Gly Glu Leu Gly Ser Thr Ala Gly Pro Asp
25 30 35

acc tat ctt gac tcg ttg gaa gtt gag ttg gag atg gct gtg gct tcg 259
Thr Tyr Leu Asp Ser Leu Glu Val Glu Leu Glu Met Ala Val Ala Ser
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ctg gat aat cct cgg cag gcg gaa act atc ttt att ggc ggg ggt acc 307
Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe Ile Gly Gly Gly Thr
55 60 65

ccg tcg ttg att ggt gcg gac ggt ttg gcc agg gtt ttg ggg gct gtg 355
Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg Val Leu Gly Ala Val
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Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu Val Thr Thr Glu Ser
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aat ccg gag tct acc tcg cct gag ttt ttt gat ggc ctg cgt gag gcg 451
Asn Pro Glu Ser Thr Ser Pro Glu Phe Phe Asp Gly Leu Arg Glu Ala
105 110 115

ggc tac aac agg att tcg tta ggg atg cag tcg gcg tcg tca agc gtt 499
Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser Ala Ser Ser Ser Val
120 125 130

ttg aag gtg ctg gac cgc acg cac acc cca ggg cgc ccg gtg gcg gcg 547
Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly Arg Pro Val Ala Ala
135 140 145

gcc aag gag gca cgt gag gcg ggg ttt gag cat gtc aat ttg gac atg 595
Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His Val Asn Leu Asp Met
150 155 160 165

att tat ggc acg ccg aca gag acc gat gat gat gtc cgc aag acg ctg 643
Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp Val Arg Lys Thr Leu
170 175 180

aat gcg gtg ctc gaa gcg aac gtg gat cac gtg tct gcc tat tcc ttg 691
Asn Ala Val Leu Glu Ala Asn Val Asp His Val Ser Ala Tyr Ser Leu
185 190 195

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atc gtg aaa gat ggc acg gcg atg gcg cgc aag gtg cac aag ggc gag 739
 Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys Val His Lys Gly Glu
 200 205 210

ctg cca gcg ccg gac gag gat gtc tac gct gat cgt ttt gag ctt atc 787
 Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp Arg Phe Glu Leu Ile
 215 220 225

gac gct cgc ctg cgc tca gct ggt ttc gat tgg tac gag gtg tcc aac 835
 Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp Tyr Glu Val Ser Asn
 230 235 240 245

tgg gcg aaa ccc ggc gga gaa tgc aag cac aac atg ggc tat tgg gtc 883
 Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn Met Gly Tyr Trp Val
 250 255 260

gac ggc gac tgg tgg ggc gcg ggc ccg ggc gcg cac tcg cac atc ggc 931
 Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala His Ser His Ile Gly
 265 270 275

gac cgc cgc ttc tac aac atc aag cac cca gcg cgt tac tcc gcg cag 979
 Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala Arg Tyr Ser Ala Gln
 280 285 290

att gcg gcc ggc gag ctg ccc att aag gaa aca gag cgg ctg acg gcg
 1027
 Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr Glu Arg Leu Thr Ala
 295 300 305

gaa gat cac cac acc gag cgc gtc atg ctt ggt ttg cgc ctg aaa caa
 1075
 Glu Asp His His Thr Glu Arg Val Met Leu Gly Leu Arg Leu Lys Gln
 310 315 320 325

ggc gtg ccg ctg aac ctt ttc gca ccc gca gcg cgc ccg gtc atc gac
 1123
 Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala Arg Pro Val Ile Asp
 330 335 340

cgt cat atc gca ggg ggc ctg ctg cac gtc aat gcg ctg ggc aac ctg
 1171
 Arg His Ile Ala Gly Gly Leu Leu His Val Asn Ala Leu Gly Asn Leu
 345 350 355

gcg gtg acc gat gcg gga cgt ttg ctt gcc gac ggc atc atc gcc gac
 1219
 Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp Gly Ile Ile Ala Asp
 360 365 370

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 1263
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 375 380

<210> 802

<211> 380

<212> PRT

<213> Corynebacterium glutamicum

<400> 802

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 20 25 30
 Thr Ala Gly Pro Asp Thr Tyr Leu Asp Ser Leu Glu Val Glu Leu Glu
 35 40 45
 Met Ala Val Ala Ser Leu Asp Asn Pro Arg Gln Ala Glu Thr Ile Phe
 50 55 60
 Ile Gly Gly Gly Thr Pro Ser Leu Ile Gly Ala Asp Gly Leu Ala Arg
 65 70 75 80
 Val Leu Gly Ala Val Arg Asn Thr Phe Gly Ile Ala Asp Gly Ala Glu
 85 90 95
 Val Thr Thr Glu Ser Asn Pro Glu Ser Thr Ser Pro Glu Phe Phe Asp
 100 105 110
 Gly Leu Arg Glu Ala Gly Tyr Asn Arg Ile Ser Leu Gly Met Gln Ser
 115 120 125
 Ala Ser Ser Ser Val Leu Lys Val Leu Asp Arg Thr His Thr Pro Gly
 130 135 140
 Arg Pro Val Ala Ala Ala Lys Glu Ala Arg Glu Ala Gly Phe Glu His
 145 150 155 160
 Val Asn Leu Asp Met Ile Tyr Gly Thr Pro Thr Glu Thr Asp Asp Asp
 165 170 175
 Val Arg Lys Thr Leu Asn Ala Val Leu Glu Ala Asn Val Asp His Val
 180 185 190
 Ser Ala Tyr Ser Leu Ile Val Lys Asp Gly Thr Ala Met Ala Arg Lys
 195 200 205
 Val His Lys Gly Glu Leu Pro Ala Pro Asp Glu Asp Val Tyr Ala Asp
 210 215 220
 Arg Phe Glu Leu Ile Asp Ala Arg Leu Arg Ser Ala Gly Phe Asp Trp
 225 230 235 240
 Tyr Glu Val Ser Asn Trp Ala Lys Pro Gly Gly Glu Cys Lys His Asn
 245 250 255
 Met Gly Tyr Trp Val Asp Gly Asp Trp Trp Gly Ala Gly Pro Gly Ala
 260 265 270
 His Ser His Ile Gly Asp Arg Arg Phe Tyr Asn Ile Lys His Pro Ala
 275 280 285
 Arg Tyr Ser Ala Gln Ile Ala Ala Gly Glu Leu Pro Ile Lys Glu Thr
 290 295 300
 Glu Arg Leu Thr Ala Glu Asp His His Thr Glu Arg Val Met Leu Gly
 305 310 315 320
 Leu Arg Leu Lys Gln Gly Val Pro Leu Asn Leu Phe Ala Pro Ala Ala

	325		330		335
Arg Pro Val Ile Asp Arg His Ile Ala Gly Gly Leu Leu His Val Asn					
	340		345		350
Ala Leu Gly Asn Leu Ala Val Thr Asp Ala Gly Arg Leu Leu Ala Asp					
	355		360		365
Gly Ile Ile Ala Asp Ile Leu Leu Ser Glu Glu Asp					
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<210> 803

<211> 522

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(499)

<223> RXN02503

<400> 803

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ttegtgaacg caccttctgc cacacaaacg agggagtaac	atg acc tta aaa att	115
	Met Thr Leu Lys Ile	
	1 5	

ggt acc cga gga tcc aaa ctt gcc acc acc caa gct ggc acc atc cgc	163
Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln Ala Gly Thr Ile Arg	
10 15 20	

gac cag ctg aaa cac tac gga cgc gac gct gaa ctg cac atc gtg acc	211
Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu Leu His Ile Val Thr	
25 30 35	

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc	259
Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly	
40 45 50	

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat	307
Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp	
55 60 65	

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga	355
Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg	
70 75 80 85	

ttc cac ctg gtc gtg cca act cgt gcg gac tcg cgc gag gcc ctt atc	403
Phe His Leu Val Val Pro Thr Arg Ala Asp Ser Arg Glu Ala Leu Ile	
90 95 100	

gcc cgc gac ggc ctg act ctg gct gag ctt cca gaa agg cgc aaa ggt	451
Ala Arg Asp Gly Leu Thr Leu Ala Glu Leu Pro Glu Arg Arg Lys Gly	
105 110 115	

ggg aac ttc cgc tcc tcg acg cat ctc cca gct caa ggc aat ccg ccc	499
Gly Asn Phe Arg Ser Ser Thr His Leu Pro Ala Gln Gly Asn Pro Pro	
120 125 130	

tgacctggag attctccac tgc

522

<210> 804

<211> 133

<212> PRT

<213> Corynebacterium glutamicum

<400> 804

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Ala	Gly	Thr	Ile	Arg	Asp	Gln	Leu	Lys	His	Tyr	Gly	Arg	Asp	Ala	Glu
			20					25					30		

Leu	His	Ile	Val	Thr	Thr	Pro	Gly	Asp	Val	Asn	Met	Ser	Pro	Val	Glu
		35					40					45			

Arg	Ile	Gly	Val	Gly	Val	Phe	Thr	Gln	Ala	Leu	Arg	Asp	Val	Leu	His
	50					55					60				

Ser	Gly	Glu	Cys	Asp	Val	Ala	Val	His	Ser	Met	Lys	Asp	Leu	Pro	Thr
65					70					75					80

Ala	Thr	Asp	Pro	Arg	Phe	His	Leu	Val	Val	Pro	Thr	Arg	Ala	Asp	Ser
				85					90					95	

Arg	Glu	Ala	Leu	Ile	Ala	Arg	Asp	Gly	Leu	Thr	Leu	Ala	Glu	Leu	Pro
			100					105					110		

Glu	Arg	Arg	Lys	Gly	Gly	Asn	Phe	Arg	Ser	Ser	Thr	His	Leu	Pro	Ala
			115				120					125			

Gln	Gly	Asn	Pro	Pro
	130			

<210> 805

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA02503

<400> 805

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ttcgtgaacg	caccttctgc	cacacaaacg	aggagtaac	atg	acc	tta	aaa	att	115
				Met	Thr	Leu	Lys	Ile	
				1				5	

ggt	acc	cga	gga	tcc	aaa	ctt	gcc	acc	acc	caa	gct	ggc	acc	atc	cgc	163
Gly	Thr	Arg	Gly	Ser	Lys	Leu	Ala	Thr	Thr	Gln	Ala	Gly	Thr	Ile	Arg	
				10				15						20		

gac	cag	ctg	aaa	cac	tac	gga	cgc	gac	gct	gaa	ctg	cac	atc	gtg	acc	211
Asp	Gln	Leu	Lys	His	Tyr	Gly	Arg	Asp	Ala	Glu	Leu	His	Ile	Val	Thr	
			25				30						35			

acc cct ggt gat gtc aac atg tcc cca gtc gag cgt atc ggc gtc ggc 259
 Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu Arg Ile Gly Val Gly
 40 45 50

gtg ttc acc cag gcg ctg cgc gat gtg ttg cat tcc ggt gaa tgc gat 307
 Val Phe Thr Gln Ala Leu Arg Asp Val Leu His Ser Gly Glu Cys Asp
 55 60 65

gtg gct gtg cac tcc atg aag gat ctg ccg acc gcc acc gat cct cga 355
 Val Ala Val His Ser Met Lys Asp Leu Pro Thr Ala Thr Asp Pro Arg
 70 75 80 85

ttc cac ctg gtc gtg cca act cgt gcg gac tck cgc cga ggs cct tat 403
 Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa Arg Arg Xaa Pro Tyr
 90 95 100

cgc ccn cga cgg sct gan ttt kgg ttr agc tty caa aar gsg saa agg 451
 Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa Gln Xaa Xaa Xaa Arg
 105 110 115

tgg gaa ctt tcc gct cct cga cgc atc tcc cag ctc aag gca atc cgc 499
 Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg
 120 125 130

cct gac ctg gag att ctc cca ctt gcg cgg aaa cat tgacaccggc 545
 Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys His
 135 140 145

atgggcaagg tca 558

<210> 806

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 806

Met Thr Leu Lys Ile Gly Thr Arg Gly Ser Lys Leu Ala Thr Thr Gln
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Ala Gly Thr Ile Arg Asp Gln Leu Lys His Tyr Gly Arg Asp Ala Glu
 20 25 30

Leu His Ile Val Thr Thr Pro Gly Asp Val Asn Met Ser Pro Val Glu
 35 40 45

Arg Ile Gly Val Gly Val Phe Thr Gln Ala Leu Arg Asp Val Leu His
 50 55 60

Ser Gly Glu Cys Asp Val Ala Val His Ser Met Lys Asp Leu Pro Thr
 65 70 75 80

Ala Thr Asp Pro Arg Phe His Leu Val Val Pro Thr Arg Ala Asp Xaa
 85 90 95

Arg Arg Xaa Pro Tyr Arg Pro Arg Arg Xaa Xaa Phe Xaa Xaa Ser Xaa
 100 105 110

Gln Xaa Xaa Xaa Arg Trp Glu Leu Ser Ala Pro Arg Arg Ile Ser Gln
 115 120 125

Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile Leu Pro Leu Ala Arg Lys
 130 135 140

His
 145

<210> 807
 <211> 1245
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1222)
 <223> RXA00377

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 Val Trp Leu Leu Phe
 1 5

cta aat tgg gat aaa tgg ggc aag att gag cgc atg tct gct ctt act 163
 Leu Asn Trp Asp Lys Trp Gly Lys Ile Glu Arg Met Ser Ala Leu Thr
 10 15 20

att cca gct gcg cgt cgc acg cta aat aac gcg ccc att att gat gcc 211
 Ile Pro Ala Ala Arg Arg Thr Leu Asn Asn Ala Pro Ile Ile Asp Ala
 25 30 35

gct aat ggc aag acc ccg act cgc act ccg gtg tgg ttt atg cgc cag 259
 Ala Asn Gly Lys Thr Pro Thr Arg Thr Pro Val Trp Phe Met Arg Gln
 40 45 50

gcg ggt agg tcg ttg cct gag tac aag aag gtc cgt gag gga atc agc 307
 Ala Gly Arg Ser Leu Pro Glu Tyr Lys Lys Val Arg Glu Gly Ile Ser
 55 60 65

atg ttg gat tcc tgt ttc atg ccg gag ttg ttg gcg gag att act ttg 355
 Met Leu Asp Ser Cys Phe Met Pro Glu Leu Leu Ala Glu Ile Thr Leu
 70 75 80 85

cag ccg gtt cgt cgt cat gat gtg gat gct gcg att ttg ttc tct gac 403
 Gln Pro Val Arg Arg His Asp Val Asp Ala Ala Ile Leu Phe Ser Asp
 90 95 100

att gtg gtg ccg ttg cgt gct gcg ggt gtt ggt gtg gaa atc gtg gcg 451
 Ile Val Val Pro Leu Arg Ala Ala Gly Val Gly Val Glu Ile Val Ala
 105 110 115

ggt cgt gga cct gtg ttg gat gcg ccg gtg cgg agc cgt ggg gat gtg 499
 Gly Arg Gly Pro Val Leu Asp Ala Pro Val Arg Ser Arg Gly Asp Val
 120 125 130

ttg aat ctt cct att ttg gag ggc aac gtt ccg gag gtg gag cag ggt 547
 Leu Asn Leu Pro Ile Leu Glu Gly Asn Val Pro Glu Val Glu Gln Gly
 135 140 145

att ggc atc att ttg gat gag ttg tct gat tct cag gcg ttg att ggt Ile Gly Ile Ile Leu Asp Glu Leu Ser Asp Ser Gln Ala Leu Ile Gly 150 155 160 165	595
ttt gct ggt gcg ccg ttt acg ttg gcg agt tac ttg gtt gag ggt ggt Phe Ala Gly Ala Pro Phe Thr Leu Ala Ser Tyr Leu Val Glu Gly Gly 170 175 180	643
cct tcc aag aat cat gag aag acc aaa gca atg atg cat ggt gat cct Pro Ser Lys Asn His Glu Lys Thr Lys Ala Met Met His Gly Asp Pro 185 190 195	691
gag acg tgg cat gcg ttg atg gct cgt ttg gtg ccg acg att gtg aat Glu Thr Trp His Ala Leu Met Ala Arg Leu Val Pro Thr Ile Val Asn 200 205 210	739
tct ttg aag tcg cag atc gat gcg ggt atc gat gcg gtg cag ttg ttt Ser Leu Lys Ser Gln Ile Asp Ala Gly Ile Asp Ala Val Gln Leu Phe 215 220 225	787
gat tcg tgg gct ggg ttc ctc act gag cgt gat tac acc gag ttc gtg Asp Ser Trp Ala Gly Phe Leu Thr Glu Arg Asp Tyr Thr Glu Phe Val 230 235 240 245	835
ttg ccg tat tcc act gag att ttg gag gaa gtg ggc aag tac cag ctg Leu Pro Tyr Ser Thr Glu Ile Leu Glu Glu Val Gly Lys Tyr Gln Leu 250 255 260	883
cct cgt att cac ttt ggt gtg ggt act ggt gag ttg ctt ggt gcg atg Pro Arg Ile His Phe Gly Val Gly Thr Gly Glu Leu Leu Gly Ala Met 265 270 275	931
agc aag gct ggc tca gag gtc atg ggt gtg gat tgg cgg gtg ccg ttg Ser Lys Ala Gly Ser Glu Val Met Gly Val Asp Trp Arg Val Pro Leu 280 285 290	979
gat aag gct gcg gag cgt att gct gcg gta tca ggt cct aag gtg ttg 1027 Asp Lys Ala Ala Glu Arg Ile Ala Ala Val Ser Gly Pro Lys Val Leu 295 300 305	
cag ggt aac ctc gat cct gcg ttg ttg ttt gcg ggt cgc gca cct ttg 1075 Gln Gly Asn Leu Asp Pro Ala Leu Leu Phe Ala Gly Arg Ala Pro Leu 310 315 320 325	
act aag gaa att gag cgc atc aag gca gag gct cag act gct gtt gat 1123 Thr Lys Glu Ile Glu Arg Ile Lys Ala Glu Ala Gln Thr Ala Val Asp 330 335 340	
gca ggt cat gca acg ggc cat atc ttt aac ctt ggt cat ggt gtg ctt 1171 Ala Gly His Ala Thr Gly His Ile Phe Asn Leu Gly His Gly Val Leu 345 350 355	
cct aat acg gtg gcg gaa gat att act gaa gcc gtc tcc atc att cat 1219 Pro Asn Thr Val Ala Glu Asp Ile Thr Glu Ala Val Ser Ile Ile His 360 365 370	

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1245
Ser

<210> 808
<211> 374
<212> PRT
<213> Corynebacterium glutamicum

<400> 808

Val	Trp	Leu	Leu	Phe	Leu	Asn	Trp	Asp	Lys	Trp	Gly	Lys	Ile	Glu	Arg	1	5	10	15
Met	Ser	Ala	Leu	Thr	Ile	Pro	Ala	Ala	Arg	Arg	Thr	Leu	Asn	Asn	Ala	20	25	30	
Pro	Ile	Ile	Asp	Ala	Ala	Asn	Gly	Lys	Thr	Pro	Thr	Arg	Thr	Pro	Val	35	40	45	
Trp	Phe	Met	Arg	Gln	Ala	Gly	Arg	Ser	Leu	Pro	Glu	Tyr	Lys	Lys	Val	50	55	60	
Arg	Glu	Gly	Ile	Ser	Met	Leu	Asp	Ser	Cys	Phe	Met	Pro	Glu	Leu	Leu	65	70	75	80
Ala	Glu	Ile	Thr	Leu	Gln	Pro	Val	Arg	Arg	His	Asp	Val	Asp	Ala	Ala	85	90	95	
Ile	Leu	Phe	Ser	Asp	Ile	Val	Val	Pro	Leu	Arg	Ala	Ala	Gly	Val	Gly	100	105	110	
Val	Glu	Ile	Val	Ala	Gly	Arg	Gly	Pro	Val	Leu	Asp	Ala	Pro	Val	Arg	115	120	125	
Ser	Arg	Gly	Asp	Val	Leu	Asn	Leu	Pro	Ile	Leu	Glu	Gly	Asn	Val	Pro	130	135	140	
Glu	Val	Glu	Gln	Gly	Ile	Gly	Ile	Ile	Leu	Asp	Glu	Leu	Ser	Asp	Ser	145	150	155	160
Gln	Ala	Leu	Ile	Gly	Phe	Ala	Gly	Ala	Pro	Phe	Thr	Leu	Ala	Ser	Tyr	165	170	175	
Leu	Val	Glu	Gly	Gly	Pro	Ser	Lys	Asn	His	Glu	Lys	Thr	Lys	Ala	Met	180	185	190	
Met	His	Gly	Asp	Pro	Glu	Thr	Trp	His	Ala	Leu	Met	Ala	Arg	Leu	Val	195	200	205	
Pro	Thr	Ile	Val	Asn	Ser	Leu	Lys	Ser	Gln	Ile	Asp	Ala	Gly	Ile	Asp	210	215	220	
Ala	Val	Gln	Leu	Phe	Asp	Ser	Trp	Ala	Gly	Phe	Leu	Thr	Glu	Arg	Asp	225	230	235	240
Tyr	Thr	Glu	Phe	Val	Leu	Pro	Tyr	Ser	Thr	Glu	Ile	Leu	Glu	Glu	Val	245	250	255	
Gly	Lys	Tyr	Gln	Leu	Pro	Arg	Ile	His	Phe	Gly	Val	Gly	Thr	Gly	Glu				

	260		265		270										
Leu	Leu	Gly	Ala	Met	Ser	Lys	Ala	Gly	Ser	Glu	Val	Met	Gly	Val	Asp
	275						280					285			
Trp	Arg	Val	Pro	Leu	Asp	Lys	Ala	Ala	Glu	Arg	Ile	Ala	Ala	Val	Ser
	290					295					300				
Gly	Pro	Lys	Val	Leu	Gln	Gly	Asn	Leu	Asp	Pro	Ala	Leu	Leu	Phe	Ala
305					310					315					320
Gly	Arg	Ala	Pro	Leu	Thr	Lys	Glu	Ile	Glu	Arg	Ile	Lys	Ala	Glu	Ala
				325					330					335	
Gln	Thr	Ala	Val	Asp	Ala	Gly	His	Ala	Thr	Gly	His	Ile	Phe	Asn	Leu
			340					345					350		
Gly	His	Gly	Val	Leu	Pro	Asn	Thr	Val	Ala	Glu	Asp	Ile	Thr	Glu	Ala
	355						360					365			
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<210> 809
 <211> 681
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(658)
 <223> RXN02504

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 Val Gly Thr Ser Ala
 1 5
 cct cga cgc atc tcc cag ctc aag gca atc cgc cct gac ctg gag att 163
 Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg Pro Asp Leu Glu Ile
 10 15 20
 ctc cca ctg cgc gga aac att gac acc ggc atg ggc aag gtc acc tcc 211
 Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met Gly Lys Val Thr Ser
 25 30 35
 ggt gaa ctc gat gct gtg atg ctc gcc tac gca ggc ctc acc cgc gtc 259
 Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala Gly Leu Thr Arg Val
 40 45 50
 ggc atg cag gac cgc gca acg gaa gtt ttc gac gcc gac atc atc atg 307
 Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met
 55 60 65
 ccc gcc ccc gca cag ggc gca ctt gcg atc gaa tgc cgc gcc gac gac 355
 Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp
 70 75 80 85

act gaa acc gtc cgc gcg ctc aac atg ctg atg cac gcc gac acg ttt 403
 Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe
 90 95 100

 gtt tcc gcg gtt gca gaa cgc acc gtg ctc aac cgc ctc gaa gct ggc 451
 Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly
 105 110 115

 tgt acc gcg cct gtc gca gcg cac gcc acc ttg gac ggc tac tcc ggc 499
 Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly
 120 125 130

 gac acc atg act ctc acc gcc ggc gtc tac gca ctt gac ggc tct gac 547
 Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp
 135 140 145

 cag ctg gta ttc tcc gcc gaa ggt gac ggc gcc cgc cca gaa gag ctc 595
 Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu
 150 155 160 165

 ggc gag ctc gtt gca caa cag ctt atc gac gcc gga gcc gcc aat ttg 643
 Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu
 170 175 180

 ctc ggc gac cgc agc taattagggc ccgaaatttc cat 681
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<210> 810

<211> 186

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 810

Val Gly Thr Ser Ala Pro Arg Arg Ile Ser Gln Leu Lys Ala Ile Arg
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 Pro Asp Leu Glu Ile Leu Pro Leu Arg Gly Asn Ile Asp Thr Gly Met
 20 25 30

 Gly Lys Val Thr Ser Gly Glu Leu Asp Ala Val Met Leu Ala Tyr Ala
 35 40 45

 Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu Val Phe Asp
 50 55 60

 Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu Ala Ile Glu
 65 70 75 80

 Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn Met Leu Met
 85 90 95

 His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr Val Leu Asn
 100 105 110

 Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His Ala Thr Leu
 115 120 125

 Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly Val Tyr Ala
 130 135 140

Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly Asp Gly Ala
145 150 155 160

Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu Ile Asp Ala
165 170 175

Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser
180 185

<210> 811

<211> 561

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(538)

<223> FRXA02504

<400> 811

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Met Leu Val Met Leu
1 5

gcc tac gca ggc ctc acc cgc gtc ggc atg cag gac cgc gca acg gaa 163
Ala Tyr Ala Gly Leu Thr Arg Val Gly Met Gln Asp Arg Ala Thr Glu
10 15 20

gtt ttc gac gcc gac atc atc atg ccc gcc ccc gca cag ggc gca ctt 211
Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro Ala Gln Gly Ala Leu
25 30 35

gcg atc gaa tgc cgc gcc gac gac act gaa acc gtc cgc gcg ctc aac 259
Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr Val Arg Ala Leu Asn
40 45 50

atg ctg atg cac gcc gac acg ttt gtt tcc gcg gtt gca gaa cgc acc 307
Met Leu Met His Ala Asp Thr Phe Val Ser Ala Val Ala Glu Arg Thr
55 60 65

gtg ctc aac cgc ctc gaa gct ggc tgt acc gcg cct gtc gca gcg cac 355
Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala Pro Val Ala Ala His
70 75 80 85

gcc acc ttg gac ggc tac tcc ggc gac acc atg act ctc acc gcc ggc 403
Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met Thr Leu Thr Ala Gly
90 95 100

gtc tac gca ctt gac ggc tct gac cag ctg gta ttc tcc gcc gaa ggt 451
Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val Phe Ser Ala Glu Gly
105 110 115

gac ggc gcc cgc cca gaa gag ctc ggc gag ctc gtt gca caa cag ctt 499
Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu Val Ala Gln Gln Leu
120 125 130

atc gac gcc gga gcc gcc aat ttg ctc ggc gac cgc agc taattagggc 548

Ile Asp Ala Gly Ala Ala Asn Leu Leu Gly Asp Arg Ser
 135 140 145

ccgaaatttc cat

561

<210> 812

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 812

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Asp Arg Ala Thr Glu Val Phe Asp Ala Asp Ile Ile Met Pro Ala Pro
 20 25 30

Ala Gln Gly Ala Leu Ala Ile Glu Cys Arg Ala Asp Asp Thr Glu Thr
 35 40 45

Val Arg Ala Leu Asn Met Leu Met His Ala Asp Thr Phe Val Ser Ala
 50 55 60

Val Ala Glu Arg Thr Val Leu Asn Arg Leu Glu Ala Gly Cys Thr Ala
 65 70 75 80

Pro Val Ala Ala His Ala Thr Leu Asp Gly Tyr Ser Gly Asp Thr Met
 85 90 95

Thr Leu Thr Ala Gly Val Tyr Ala Leu Asp Gly Ser Asp Gln Leu Val
 100 105 110

Phe Ser Ala Glu Gly Asp Gly Ala Arg Pro Glu Glu Leu Gly Glu Leu
 115 120 125

Val Ala Gln Gln Leu Ile Asp Ala Gly Ala Ala Asn Leu Leu Gly Asp
 130 135 140

Arg Ser
 145

<210> 813

<211> 1449

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1426)

<223> RXN01162

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gtcgggggttt cacagtcact tattctatgc aggattcacc atg tat atc gtg ggg 115
 Met Tyr Ile Val Gly
 1 5

att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac 163

Ile	Cys	Leu	Gln	Leu	Val	Val	Met	Ser	Gln	Pro	Met	Ser	Ala	Pro	Asp	
				10					15					20		
tcc	gct	cca	gga	aca	gag	cgc	ggg	cat	gaa	cgc	acc	cat	ttt	gcg	gta	211
Ser	Ala	Pro	Gly	Thr	Glu	Arg	Gly	His	Glu	Arg	Thr	His	Phe	Ala	Val	
			25					30					35			
gtc	ggg	gac	tcc	cag	gat	cca	gca	cag	gca	aca	gct	cct	aga	gcg	cca	259
Val	Gly	Asp	Ser	Gln	Asp	Pro	Ala	Gln	Ala	Thr	Ala	Pro	Arg	Ala	Pro	
		40					45					50				
gca	gaa	tca	att	act	ttg	att	ggg	att	ggg	acc	gat	ggg	ttt	gag	ggg	307
Ala	Glu	Ser	Ile	Thr	Leu	Ile	Gly	Ile	Gly	Thr	Asp	Gly	Phe	Glu	Gly	
	55					60					65					
ctc	gga	ctc	aag	gca	cag	caa	gca	tta	caa	cgt	gcc	tct	gtg	gtg	att	355
Leu	Gly	Leu	Lys	Ala	Gln	Gln	Ala	Leu	Gln	Arg	Ala	Ser	Val	Val	Ile	
	70				75					80					85	
gga	tca	tgg	cgc	cag	ctc	aat	ctc	gta	cct	gat	gcc	att	aag	gca	gag	403
Gly	Ser	Trp	Arg	Gln	Leu	Asn	Leu	Val	Pro	Asp	Ala	Ile	Lys	Ala	Glu	
				90					95					100		
cgt	cgc	cca	tgg	ccg	ggg	aat	acc	aag	cat	cct	gat	tta	gat	gcc	ttg	451
Arg	Arg	Pro	Trp	Pro	Gly	Asn	Thr	Lys	His	Pro	Asp	Leu	Asp	Ala	Leu	
			105					110					115			
ttt	aaa	gag	ttc	ctc	ggg	cgg	cat	gtt	gct	gtt	ctg	gcc	tct	ggc	gat	499
Phe	Lys	Glu	Phe	Leu	Gly	Arg	His	Val	Ala	Val	Leu	Ala	Ser	Gly	Asp	
		120					125					130				
cca	ctg	ttt	tac	ggc	gtg	ggc	acc	gca	atg	gtc	cat	gtg	ctg	ggg	atg	547
Pro	Leu	Phe	Tyr	Gly	Val	Gly	Thr	Ala	Met	Val	His	Val	Leu	Gly	Met	
	135					140					145					
gat	aga	ctc	acg	gtt	att	ccg	gga	cca	tca	tcc	gcg	tcg	ctt	gct	tgc	595
Asp	Arg	Leu	Thr	Val	Ile	Pro	Gly	Pro	Ser	Ser	Ala	Ser	Leu	Ala	Cys	
	150				155					160					165	
gcc	cgc	ttg	ggg	tgg	aca	gtc	aac	cgc	aca	cgg	gtg	gtg	tac	cta	gga	643
Ala	Arg	Leu	Gly	Trp	Thr	Val	Asn	Arg	Thr	Arg	Val	Val	Tyr	Leu	Gly	
				170					175					180		
caa	gaa	ccc	att	gag	aca	ctc	atc	ccg	att	att	gaa	tca	ggc	gct	caa	691
Gln	Glu	Pro	Ile	Glu	Thr	Leu	Ile	Pro	Ile	Ile	Glu	Ser	Gly	Ala	Gln	
			185					190					195			
ttc	ctc	gtc	ttg	ggg	aaa	gat	gaa	ttc	agt	aca	gct	caa	gtt	gcc	acg	739
Phe	Leu	Val	Leu	Gly	Lys	Asp	Glu	Phe	Ser	Thr	Ala	Gln	Val	Ala	Thr	
		200					205					210				
ttg	ttg	aat	gaa	ctc	gga	ctg	ggg	gag	act	cca	ctg	act	gtg	ctc	agc	787
Leu	Leu	Asn	Glu	Leu	Gly	Leu	Gly	Glu	Thr	Pro	Leu	Thr	Val	Leu	Ser	
	215					220					225					
gat	ttg	ggc	agt	act	gat	gag	gag	atc	acc	caa	ggc	aca	gct	tca	cat	835
Asp	Leu	Gly	Ser	Thr	Asp	Glu	Glu	Ile	Thr	Gln	Gly	Thr	Ala	Ser	His	
	230				235					240					245	
cca	cca	gct	gca	gtg	tct	gtt	ctc	aac	gtg	att	gct	gtg	gga	gct	cgc	883
Pro	Pro	Ala	Ala	Val	Ser	Val	Leu	Asn	Val	Ile	Ala	Val	Gly	Ala	Arg	

	250		255		260	
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac						931
Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp						
	265		270		275	
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg						979
Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met						
	280		285		290	
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta						
1027						
Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu						
	295		300		305	
cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt						
1075						
Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val						
	310		315		320	325
gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt						
1123						
Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser						
	330		335		340	
gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta						
1171						
Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val						
	345		350		355	
caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc						
1219						
Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly						
	360		365		370	
cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct						
1267						
Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro						
	375		380		385	
gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag						
1315						
Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys						
	390		395		400	405
ctt cac aca ctc caa gaa caa cac ggc gga atc atc aaa cac atc cgc						
1363						
Leu His Thr Leu Gln Glu Gln His Gly Gly Ile Ile Lys His Ile Arg						
	410		415		420	
atc gac gac aca gac gtg cac caa tgg cga gtt aca aag ccg gtg act						
1411						
Ile Asp Asp Thr Asp Val His Gln Trp Arg Val Thr Lys Pro Val Thr						
	425		430		435	
cca gaa gcg gtg aat tagcatcaaaa aaccaacccc atg						
1449						
Pro Glu Ala Val Asn						
	440					

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 <213> Corynebacterium glutamicum

<400> 814

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			20					25					30		
Thr	His	Phe	Ala	Val	Val	Gly	Asp	Ser	Gln	Asp	Pro	Ala	Gln	Ala	Thr
		35					40					45			
Ala	Pro	Arg	Ala	Pro	Ala	Glu	Ser	Ile	Thr	Leu	Ile	Gly	Ile	Gly	Thr
	50					55					60				
Asp	Gly	Phe	Glu	Gly	Leu	Gly	Leu	Lys	Ala	Gln	Gln	Ala	Leu	Gln	Arg
65					70					75					80
Ala	Ser	Val	Val	Ile	Gly	Ser	Trp	Arg	Gln	Leu	Asn	Leu	Val	Pro	Asp
				85					90					95	
Ala	Ile	Lys	Ala	Glu	Arg	Arg	Pro	Trp	Pro	Gly	Asn	Thr	Lys	His	Pro
			100					105					110		
Asp	Leu	Asp	Ala	Leu	Phe	Lys	Glu	Phe	Leu	Gly	Arg	His	Val	Ala	Val
		115					120					125			
Leu	Ala	Ser	Gly	Asp	Pro	Leu	Phe	Tyr	Gly	Val	Gly	Thr	Ala	Met	Val
	130					135					140				
His	Val	Leu	Gly	Met	Asp	Arg	Leu	Thr	Val	Ile	Pro	Gly	Pro	Ser	Ser
145					150					155					160
Ala	Ser	Leu	Ala	Cys	Ala	Arg	Leu	Gly	Trp	Thr	Val	Asn	Arg	Thr	Arg
				165					170					175	
Val	Val	Tyr	Leu	Gly	Gln	Glu	Pro	Ile	Glu	Thr	Leu	Ile	Pro	Ile	Ile
			180					185					190		
Glu	Ser	Gly	Ala	Gln	Phe	Leu	Val	Leu	Gly	Lys	Asp	Glu	Phe	Ser	Thr
		195					200					205			
Ala	Gln	Val	Ala	Thr	Leu	Leu	Asn	Glu	Leu	Gly	Leu	Gly	Glu	Thr	Pro
	210					215					220				
Leu	Thr	Val	Leu	Ser	Asp	Leu	Gly	Ser	Thr	Asp	Glu	Glu	Ile	Thr	Gln
225					230					235					240
Gly	Thr	Ala	Ser	His	Pro	Pro	Ala	Ala	Val	Ser	Val	Leu	Asn	Val	Ile
				245					250					255	
Ala	Val	Gly	Ala	Arg	Thr	Ala	Met	Pro	Lys	Pro	His	Phe	Glu	Gly	Asp
			260					265					270		
Val	Ser	Asn	Glu	Asp	Leu	Arg	Ala	Leu	Thr	Val	Ala	Ala	Leu	Glu	Pro
		275					280					285			
Thr	Gln	Gly	Gln	Met	Leu	Trp	Thr	Phe	Gly	Asp	Ile	Gly	Ala	Ala	Leu

290	295	300
Ala Cys Asp Trp Leu Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser 305 310 315 320		
Phe Ala Ser Met Val Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly 325 330 335		
Val Ser Thr Leu Ser Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys 340 345 350		
Asp Ile Arg Tyr Val Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile 355 360 365		
Phe Met Asn Lys Gly Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp 370 375 380		
Met Met Leu Arg Pro Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu 385 390 395 400		
Asp Asn Ile Ala Lys Leu His Thr Leu Gln Glu Gln His Gly Gly Ile 405 410 415		
Ile Lys His Ile Arg Ile Asp Asp Thr Asp Val His Gln Trp Arg Val 420 425 430		
Thr Lys Pro Val Thr Pro Glu Ala Val Asn 435 440		

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 <222> (101)..(1345)
 <223> FRXA01162

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 Met Tyr Ile Val Gly
 1 5

att tgt cta caa tta gtg gtt atg agc caa ccg atg tca gca ccc gac 163
 Ile Cys Leu Gln Leu Val Val Met Ser Gln Pro Met Ser Ala Pro Asp
 10 15 20

tcc gct cca gga aca gag cgc ggt cat gaa cgc acc cat ttt gcg gta 211
 Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg Thr His Phe Ala Val
 25 30 35

gtc ggt gac tcc cag gat cca gca cag gca aca gct cct aga gcg cca 259
 Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr Ala Pro Arg Ala Pro
 40 45 50

gca gaa tca att act ttg att ggt att ggt acc gat ggg ttt gag ggg 307
 Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr Asp Gly Phe Glu Gly

55	60	65	
ctc gga ctc aag gca cag caa gca tta caa cgt gcc tct gtg gtg att Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg Ala Ser Val Val Ile 70 75 80 85			355
gga tca tgg cgc cag ctc aat ctc gta cct gat gcc att aag gca gag Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp Ala Ile Lys Ala Glu 90 95 100			403
cgt cgc cca tgg ccg ggt aat acc aag cat cct gat tta gat gcc ttg Arg Arg Pro Trp Pro Gly Asn Thr Lys His Pro Asp Leu Asp Ala Leu 105 110 115			451
ttt aaa gag ttc ctc ggt cgg cat gtt gct gtt ctg gcc tct ggc gat Phe Lys Glu Phe Leu Gly Arg His Val Ala Val Leu Ala Ser Gly Asp 120 125 130			499
cca ctg ttt tac ggc gtg ggc acc gca atg gtc cat gtg ctg ggg atg Pro Leu Phe Tyr Gly Val Gly Thr Ala Met Val His Val Leu Gly Met 135 140 145			547
gat aga ctc acg gtt att ccg gga cca tca tcc gcg tcg ctt gct tgc Asp Arg Leu Thr Val Ile Pro Gly Pro Ser Ser Ala Ser Leu Ala Cys 150 155 160 165			595
gcc cgc ttg ggt tgg aca gtc aac cgc aca cgg gtg gtg tac cta gga Ala Arg Leu Gly Trp Thr Val Asn Arg Thr Arg Val Val Tyr Leu Gly 170 175 180			643
caa gaa ccc att gag aca ctc atc ccg att att gaa tca ggc gct caa Gln Glu Pro Ile Glu Thr Leu Ile Pro Ile Ile Glu Ser Gly Ala Gln 185 190 195			691
ttc ctc gtc ttg ggt aaa gat gaa ttc agt aca gct caa gtt gcc acg Phe Leu Val Leu Gly Lys Asp Glu Phe Ser Thr Ala Gln Val Ala Thr 200 205 210			739
ttg ttg aat gaa ctc gga ctg ggg gag act cca ctg act gtg ctc agc Leu Leu Asn Glu Leu Gly Leu Gly Glu Thr Pro Leu Thr Val Leu Ser 215 220 225			787
gat ttg ggc agt act gat gag gag atc acc caa ggc aca gct tca cat Asp Leu Gly Ser Thr Asp Glu Glu Ile Thr Gln Gly Thr Ala Ser His 230 235 240 245			835
cca cca gct gca gtg tct gtt ctc aac gtg att gct gtg gga gct cgc Pro Pro Ala Ala Val Ser Val Leu Asn Val Ile Ala Val Gly Ala Arg 250 255 260			883
acc gca atg ccg aaa ccc cac ttt gaa ggc gac gta tca aac gaa gac Thr Ala Met Pro Lys Pro His Phe Glu Gly Asp Val Ser Asn Glu Asp 265 270 275			931
ctt cgg gca ctg acc gtg gca gct cta gaa ccc acc cag gga caa atg Leu Arg Ala Leu Thr Val Ala Ala Leu Glu Pro Thr Gln Gly Gln Met 280 285 290			979
ctg tgg acc ttc ggg gat att gga gca gca ctt gcc tgc gat tgg cta 1027 Leu Trp Thr Phe Gly Asp Ile Gly Ala Ala Leu Ala Cys Asp Trp Leu			

295	300	305
cgc gca gcc ggc aac aag gcg cac gcc att agt ttt gcc tcc atg gtt 1075		
Arg Ala Ala Gly Asn Lys Ala His Ala Ile Ser Phe Ala Ser Met Val 310 315 320 325		
gag caa agc caa agg aat gct cgc aaa cta ggt gta tcc acc ctc agt 1123		
Glu Gln Ser Gln Arg Asn Ala Arg Lys Leu Gly Val Ser Thr Leu Ser 330 335 340		
gtg aaa gag acc ctg tca ccc aaa acg ctc aaa gat atc cgc tat gta 1171		
Val Lys Glu Thr Leu Ser Pro Lys Thr Leu Lys Asp Ile Arg Tyr Val 345 350 355		
caa gga cca gaa tca gca agc cca cat gcc atc ttc atg aac aaa ggc 1219		
Gln Gly Pro Glu Ser Ala Ser Pro His Ala Ile Phe Met Asn Lys Gly 360 365 370		
cta ggc atc gat cta gtt cct gaa acc gca tgg atg atg ctg cgg cct 1267		
Leu Gly Ile Asp Leu Val Pro Glu Thr Ala Trp Met Met Leu Arg Pro 375 380 385		
gga gga aag ctc att gcg caa gcc tcc aca gaa gac aac atc gca aag 1315		
Gly Gly Lys Leu Ile Ala Gln Ala Ser Thr Glu Asp Asn Ile Ala Lys 390 395 400 405		
ctt cac aca ctc caa gaa caa cac ggc gga 1345		
Leu His Thr Leu Gln Glu Gln His Gly Gly 410 415		
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<213> Corynebacterium glutamicum		
<400> 816		
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Met Ser Ala Pro Asp Ser Ala Pro Gly Thr Glu Arg Gly His Glu Arg 20 25 30		
Thr His Phe Ala Val Val Gly Asp Ser Gln Asp Pro Ala Gln Ala Thr 35 40 45		
Ala Pro Arg Ala Pro Ala Glu Ser Ile Thr Leu Ile Gly Ile Gly Thr 50 55 60		
Asp Gly Phe Glu Gly Leu Gly Leu Lys Ala Gln Gln Ala Leu Gln Arg 65 70 75 80		
Ala Ser Val Val Ile Gly Ser Trp Arg Gln Leu Asn Leu Val Pro Asp 85 90 95		

Ala	Ile	Lys	Ala	Glu	Arg	Arg	Pro	Trp	Pro	Gly	Asn	Thr	Lys	His	Pro	100	105	110
Asp	Leu	Asp	Ala	Leu	Phe	Lys	Glu	Phe	Leu	Gly	Arg	His	Val	Ala	Val	115	120	125
Leu	Ala	Ser	Gly	Asp	Pro	Leu	Phe	Tyr	Gly	Val	Gly	Thr	Ala	Met	Val	130	135	140
His	Val	Leu	Gly	Met	Asp	Arg	Leu	Thr	Val	Ile	Pro	Gly	Pro	Ser	Ser	145	150	155
Ala	Ser	Leu	Ala	Cys	Ala	Arg	Leu	Gly	Trp	Thr	Val	Asn	Arg	Thr	Arg	165	170	175
Val	Val	Tyr	Leu	Gly	Gln	Glu	Pro	Ile	Glu	Thr	Leu	Ile	Pro	Ile	Ile	180	185	190
Glu	Ser	Gly	Ala	Gln	Phe	Leu	Val	Leu	Gly	Lys	Asp	Glu	Phe	Ser	Thr	195	200	205
Ala	Gln	Val	Ala	Thr	Leu	Leu	Asn	Glu	Leu	Gly	Leu	Gly	Glu	Thr	Pro	210	215	220
Leu	Thr	Val	Leu	Ser	Asp	Leu	Gly	Ser	Thr	Asp	Glu	Glu	Ile	Thr	Gln	225	230	235
Gly	Thr	Ala	Ser	His	Pro	Pro	Ala	Ala	Val	Ser	Val	Leu	Asn	Val	Ile	245	250	255
Ala	Val	Gly	Ala	Arg	Thr	Ala	Met	Pro	Lys	Pro	His	Phe	Glu	Gly	Asp	260	265	270
Val	Ser	Asn	Glu	Asp	Leu	Arg	Ala	Leu	Thr	Val	Ala	Ala	Leu	Glu	Pro	275	280	285
Thr	Gln	Gly	Gln	Met	Leu	Trp	Thr	Phe	Gly	Asp	Ile	Gly	Ala	Ala	Leu	290	295	300
Ala	Cys	Asp	Trp	Leu	Arg	Ala	Ala	Gly	Asn	Lys	Ala	His	Ala	Ile	Ser	305	310	315
Phe	Ala	Ser	Met	Val	Glu	Gln	Ser	Gln	Arg	Asn	Ala	Arg	Lys	Leu	Gly	325	330	335
Val	Ser	Thr	Leu	Ser	Val	Lys	Glu	Thr	Leu	Ser	Pro	Lys	Thr	Leu	Lys	340	345	350
Asp	Ile	Arg	Tyr	Val	Gln	Gly	Pro	Glu	Ser	Ala	Ser	Pro	His	Ala	Ile	355	360	365
Phe	Met	Asn	Lys	Gly	Leu	Gly	Ile	Asp	Leu	Val	Pro	Glu	Thr	Ala	Trp	370	375	380
Met	Met	Leu	Arg	Pro	Gly	Gly	Lys	Leu	Ile	Ala	Gln	Ala	Ser	Thr	Glu	385	390	395
Asp	Asn	Ile	Ala	Lys	Leu	His	Thr	Leu	Gln	Glu	Gln	His	Gly	Gly		405	410	415

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(850)
 <223> RXA01692

<400> 817

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 Met Thr Ile Ser Gln
 1 5

gaa aac cag cca ata atc cag cca gtc tcc tta att ggt gga ggt cct 163
 Glu Asn Gln Pro Ile Ile Gln Pro Val Ser Leu Ile Gly Gly Gly Pro
 10 15 20

ggg gca tgg gac tta att acg gtg cgt ggg atg aat cgc ctt cag gag 211
 Gly Ala Trp Asp Leu Ile Thr Val Arg Gly Met Asn Arg Leu Gln Glu
 25 30 35

gct gat gtc att ttg gct gat cac ttg ggg ccc act gat gag ttg gaa 259
 Ala Asp Val Ile Leu Ala Asp His Leu Gly Pro Thr Asp Glu Leu Glu
 40 45 50

aaa ttg tgc gac atc agc tcg aag act gtt gtt gat gtg tcc aag ctt 307
 Lys Leu Cys Asp Ile Ser Ser Lys Thr Val Val Asp Val Ser Lys Leu
 55 60 65

ccg tat ggg cgg cag gtc act cag gag cgt act aat gag atg ctt gtt 355
 Pro Tyr Gly Arg Gln Val Thr Gln Glu Arg Thr Asn Glu Met Leu Val
 70 75 80 85

gaa tac gca cag cag gga cta aag gtg gtt cgc ctt aaa ggt ggt gac 403
 Glu Tyr Ala Gln Gln Gly Leu Lys Val Val Arg Leu Lys Gly Gly Asp
 90 95 100

cct tat gtc ttc ggt cgg ggt ttt gaa gag ttg gag ttt ttg ggc gag 451
 Pro Tyr Val Phe Gly Arg Gly Phe Glu Glu Leu Glu Phe Leu Gly Glu
 105 110 115

cat gga att gaa tgc gag gtc att ccg ggt gtg acc agt gcg gtg tcc 499
 His Gly Ile Glu Cys Glu Val Ile Pro Gly Val Thr Ser Ala Val Ser
 120 125 130

gtt cca gcg gcg gca ggt att cct att act aat ccg gga gtg gtg cat 547
 Val Pro Ala Ala Ala Gly Ile Pro Ile Thr Asn Arg Gly Val Val His
 135 140 145

tcc ttt acc gtg gtg tct gga cat ttg cct cca ggc cat ccg aag tca 595
 Ser Phe Thr Val Val Ser Gly His Leu Pro Pro Gly His Pro Lys Ser
 150 155 160 165

ctg gtt gat tgg gct gcg ttg gcc aaa tcg ggt ggc acc ttg tcc atc 643
 Leu Val Asp Trp Ala Ala Leu Ala Lys Ser Gly Gly Thr Leu Ser Ile
 170 175 180

atc atg ggt gtg aaa aat gcg ggt gcg att gcc cag gcg ctc atg gac 691
 Ile Met Gly Val Lys Asn Ala Gly Ala Ile Ala Gln Ala Leu Met Asp
 185 190 195

 ggc ggg ctt gat gca gat act cca gca gct gtt att cag gaa ggc act 739
 Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val Ile Gln Glu Gly Thr
 200 205 210

 act gat gca caa cgc tca gtt cgg tgc acc ttg ggc aca ttg ggt gca 787
 Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu Gly Thr Leu Gly Ala
 215 220 225

 gtc atg gtg gag gaa gag att aag cct cca gct gtg tat gtc att gga 835
 Val Met Val Glu Glu Glu Ile Lys Pro Pro Ala Val Tyr Val Ile Gly
 230 235 240 245

 caa gtt gct ggc ctc taagcagatc gcctaagaat ggg 873
 Gln Val Ala Gly Leu
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<210> 818
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 818
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 Asn Arg Leu Gln Glu Ala Asp Val Ile Leu Ala Asp His Leu Gly Pro
 35 40 45

 Thr Asp Glu Leu Glu Lys Leu Cys Asp Ile Ser Ser Lys Thr Val Val
 50 55 60

 Asp Val Ser Lys Leu Pro Tyr Gly Arg Gln Val Thr Gln Glu Arg Thr
 65 70 75 80

 Asn Glu Met Leu Val Glu Tyr Ala Gln Gln Gly Leu Lys Val Val Arg
 85 90 95

 Leu Lys Gly Gly Asp Pro Tyr Val Phe Gly Arg Gly Phe Glu Glu Leu
 100 105 110

 Glu Phe Leu Gly Glu His Gly Ile Glu Cys Glu Val Ile Pro Gly Val
 115 120 125

 Thr Ser Ala Val Ser Val Pro Ala Ala Ala Gly Ile Pro Ile Thr Asn
 130 135 140

 Arg Gly Val Val His Ser Phe Thr Val Val Ser Gly His Leu Pro Pro
 145 150 155 160

 Gly His Pro Lys Ser Leu Val Asp Trp Ala Ala Leu Ala Lys Ser Gly
 165 170 175

Gly Thr Leu Ser Ile Ile Met Gly Val Lys Asn Ala Gly Ala Ile Ala
 180 185 190

Gln Ala Leu Met Asp Gly Gly Leu Asp Ala Asp Thr Pro Ala Ala Val
 195 200 205

Ile Gln Glu Gly Thr Thr Asp Ala Gln Arg Ser Val Arg Cys Thr Leu
 210 215 220

Gly Thr Leu Gly Ala Val Met Val Glu Glu Glu Ile Lys Pro Pro Ala
 225 230 235 240

Val Tyr Val Ile Gly Gln Val Ala Gly Leu
 245 250

<210> 819
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1894)
 <223> RXN00371

<400> 819
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acgttgggtcg ttttcgagac aagtactaga aaagatatatg atg act atc gcc cat 115
 Met Thr Ile Ala His
 1 5

aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163
 Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser
 10 15 20

gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211
 Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val
 25 30 35

tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259
 Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro
 40 45 50

ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307
 Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu
 55 60 65

aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355
 Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr
 70 75 80 85

gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403
 Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile
 90 95 100

cct gtg ccg gaa gat aag ctt cag gct gcg gaa gat gag tac gag cgc 451
 Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu Asp Glu Tyr Glu Arg
 105 110 115

atc tgc att gaa gcg aag gag aac ggt gca cgc cgt aag cct cct cgt	499
Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg Arg Lys Pro Pro Arg	
120 125 130	
cca gca cca cca acc gct gca gag atc acg gaa gtt tct gag gcg act	547
Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu Val Ser Glu Ala Thr	
135 140 145	
cca gct cag att gtt gag ctt gtg cag gat gct ctt tct tat ggt gga	595
Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala Leu Ser Tyr Gly Gly	
150 155 160 165	
gat gtt att cgt ctt gtc acc ggc aac cca ttg agc agc gat gcc aca	643
Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu Ser Ser Asp Ala Thr	
170 175 180	
ctg gct gag atc tct gca gtt tcc gag gct ggc ctg gag ttc cag gtg	691
Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly Leu Glu Phe Gln Val	
185 190 195	
gtt cca ggt atg tct ttg cct gca acg gtt cct gca ttt gcg gga att	739
Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro Ala Phe Ala Gly Ile	
200 205 210	
gcg ttg ggt tct acc tac acc gaa act gat gtc aac ggt caa aac ttg	787
Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val Asn Gly Gln Asn Leu	
215 220 225	
gac tgg gat cag ttg gct agc gca cct cag cct ttg gtg ctg cag gcc	835
Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro Leu Val Leu Gln Ala	
230 235 240 245	
cgc gtg gat gac ctt tcc cgt att gca cag gaa cta aag gcc cgc aat	883
Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu Leu Lys Ala Arg Asn	
250 255 260	
atg tct ttg gaa act cct gtt tct gtc acc gct aac ggc acc acc cgt	931
Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala Asn Gly Thr Thr Arg	
265 270 275	
ttg cag cgc acc tat gac acc act tta ggt ctg ttg cac aag ctt gat	979
Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu Leu His Lys Leu Asp	
280 285 290	
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Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu Gly Lys Gly Val Asp	
295 300 305	
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1075	
Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg Ala Leu Tyr Gly Trp	
310 315 320 325	
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1123	
Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala Ala Ser Met Ser Ala	
330 335 340	
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1171	

Arg	Leu	Ser	Ser	His	Gly	Ala	Ile	Pro	Gln	Glu	Val	Pro	Thr	Ile	Ser
			345					350					355		
gtc	gaa	cca	ccg	cgc	aac	cca	gcg	caa	atg	gaa	cgc	gcc	atc	aag	ggc
1219															
Val	Glu	Pro	Pro	Arg	Asn	Pro	Ala	Gln	Met	Glu	Arg	Ala	Ile	Lys	Gly
		360					365					370			
atc	gtc	gaa	gga	cgc	tac	cag	tgg	gtt	gtc	ctc	acc	agc	gtc	aac	gca
1267															
Ile	Val	Glu	Gly	Arg	Tyr	Gln	Trp	Val	Val	Leu	Thr	Ser	Val	Asn	Ala
	375					380					385				
gtg	aag	gca	gtc	tgg	gag	aaa	atc	acc	gaa	ttc	ggc	ctc	gat	tca	cgt
1315															
Val	Lys	Ala	Val	Trp	Glu	Lys	Ile	Thr	Glu	Phe	Gly	Leu	Asp	Ser	Arg
390					395					400					405
tcc	ttc	gcg	ggc	gtc	cgc	atc	gcc	gca	gtc	ggg	gaa	aaa	acc	gcc	gct
1363															
Ser	Phe	Ala	Gly	Val	Arg	Ile	Ala	Ala	Val	Gly	Glu	Lys	Thr	Ala	Ala
			410						415					420	
gag	atc	cgc	gcg	ctc	ggc	atc	acg	ccg	gag	ctt	ctg	cct	gca	cgt	acc
1411															
Glu	Ile	Arg	Ala	Leu	Gly	Ile	Thr	Pro	Glu	Leu	Leu	Pro	Ala	Arg	Thr
			425					430					435		
agg	caa	aat	gcg	caa	ggg	ctt	gtc	gac	gtg	ttc	ccc	gaa	tat	ttc	gaa
1459															
Arg	Gln	Asn	Ala	Gln	Gly	Leu	Val	Asp	Val	Phe	Pro	Glu	Tyr	Phe	Glu
		440					445					450			
gaa	ctc	gat	cca	gtc	ggc	cgt	gtc	ctc	ttg	ccg	cgc	gca	gat	atc	gca
1507															
Glu	Leu	Asp	Pro	Val	Gly	Arg	Val	Leu	Leu	Pro	Arg	Ala	Asp	Ile	Ala
	455					460					465				
acc	gac	gtg	ctt	gtc	gac	ggc	ctg	acc	cac	ctt	ggg	tgg	gaa	gtc	gaa
1555															
Thr	Asp	Val	Leu	Val	Asp	Gly	Leu	Thr	His	Leu	Gly	Trp	Glu	Val	Glu
470					475					480					485
gac	gtg	gtg	gct	tac	cgc	acc	gtc	cgc	gca	gca	cca	cca	agc	gct	gat
1603															
Asp	Val	Val	Ala	Tyr	Arg	Thr	Val	Arg	Ala	Ala	Pro	Pro	Ser	Ala	Asp
				490					495					500	
atc	cga	gat	atg	atc	aag	acc	ggc	gga	ttt	gat	gca	gtt	gcc	ttc	acc
1651															
Ile	Arg	Asp	Met	Ile	Lys	Thr	Gly	Gly	Phe	Asp	Ala	Val	Ala	Phe	Thr
			505					510					515		
tct	tcg	tcg	acc	gtg	aag	aac	ctc	gtt	ggg	atc	gcg	ggg	aaa	cca	cac
1699															
Ser	Ser	Ser	Thr	Val	Lys	Asn	Leu	Val	Gly	Ile	Ala	Gly	Lys	Pro	His
			520				525					530			
cca	cgc	acc	atc	gtc	gcg	tgc	atc	gga	ccc	atg	act	gca	gcg	acc	gct
1747															
Pro	Arg	Thr	Ile	Val	Ala	Cys	Ile	Gly	Pro	Met	Thr	Ala	Ala	Thr	Ala

535 540 545
 gaa gaa ctg gga ctg cgc gtt gat gtc atg cca gag atc gcc gaa gta
 1795
 Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile Ala Glu Val
 550 555 560 565

 cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat ctg cgc gct
 1843
 Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp Leu Arg Ala
 570 575 580

 aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt cga aaa gcg
 1891
 Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg Arg Lys Ala
 585 590 595

 tct taaaagggttt ttcactaggg tgt
 1917
 Ser

<210> 820
 <211> 598
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 820
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 20 25 30

 Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr
 35 40 45

 Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly
 50 55 60

 Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala
 65 70 75 80

 Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe
 85 90 95

 Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu
 100 105 110

 Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg
 115 120 125

 Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu
 130 135 140

 Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala
 145 150 155 160

 Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu
 165 170 175

Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly
 180 185 190
 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro
 195 200 205
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val
 210 215 220
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro
 225 230 235 240
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu
 245 250 255
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala
 260 265 270
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu
 275 280 285
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu
 290 295 300
 Gly Lys Gly Val Asp Asp Arg Ser Lys Tyr Ser Trp Trp Glu Asn Arg
 305 310 315 320
 Ala Leu Tyr Gly Trp Arg Val Leu Val Pro Arg Ala Arg Glu Gln Ala
 325 330 335
 Ala Ser Met Ser Ala Arg Leu Ser Ser His Gly Ala Ile Pro Gln Glu
 340 345 350
 Val Pro Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu
 355 360 365
 Arg Ala Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu
 370 375 380
 Thr Ser Val Asn Ala Val Lys Ala Val Trp Glu Lys Ile Thr Glu Phe
 385 390 395 400
 Gly Leu Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly
 405 410 415
 Glu Lys Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu
 420 425 430
 Leu Pro Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe
 435 440 445
 Pro Glu Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro
 450 455 460
 Arg Ala Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu
 465 470 475 480
 Gly Trp Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala
 485 490 495

Pro Pro Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp
 500 505 510

Ala Val Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile
 515 520 525

Ala Gly Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met
 530 535 540

Thr Ala Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro
 545 550 555 560

Glu Ile Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val
 565 570 575

Ala Asp Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg
 580 585 590

Arg Arg Arg Lys Ala Ser
 595

<210> 821
 <211> 1024
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1024)
 <223> FRXA00371

<400> 821
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 Met Thr Ile Ala His
 1 5

aag ccc gag atg gct gaa act acc ggg atc gag acc aac cag gtt tcc 163
 Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu Thr Asn Gln Val Ser
 10 15 20

gaa acc atc ggg gtt gaa tcg ctc acg cac gga aac tta cgt cct gtt 211
 Glu Thr Ile Gly Val Glu Ser Leu Thr His Gly Asn Leu Arg Pro Val
 25 30 35

tca tct ttt gag gga cag cat gag gga caa acg gaa gag tta ctt cca 259
 Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr Glu Glu Leu Leu Pro
 40 45 50

ggc aaa gtc att ttt gtt ggg gcc ggt ccc ggt aac cct gat ctt ctt 307
 Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly Asn Pro Asp Leu Leu
 55 60 65

aca gtt cgt gcc cgt gaa gtt ctg ggc aac gcg gtt cgt gcg att act 355
 Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala Val Arg Ala Ile Thr
 70 75 80 85

gat gaa caa gta cta agc ggc gtt cga gct ttt gtc gcc act gaa att 403
 Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe Val Ala Thr Glu Ile

90								95					100					
cct	gtg	ccg	gaa	gat	aag	ctt	cag	gct	gcg	gaa	gat	gag	tac	gag	cgc	451		
Pro	Val	Pro	Glu	Asp	Lys	Leu	Gln	Ala	Ala	Glu	Asp	Glu	Tyr	Glu	Arg			
			105					110					115					
atc	tgc	att	gaa	gcg	aag	gag	aac	ggt	gca	cgc	cgt	aag	cct	cct	cgt	499		
Ile	Cys	Ile	Glu	Ala	Lys	Glu	Asn	Gly	Ala	Arg	Arg	Lys	Pro	Pro	Arg			
		120					125					130						
cca	gca	cca	cca	acc	gct	gca	gag	atc	acg	gaa	gtt	tct	gag	gcg	act	547		
Pro	Ala	Pro	Pro	Thr	Ala	Ala	Glu	Ile	Thr	Glu	Val	Ser	Glu	Ala	Thr			
	135					140					145							
cca	gct	cag	att	gtt	gag	ctt	gtg	cag	gat	gct	ctt	tct	tat	ggt	gga	595		
Pro	Ala	Gln	Ile	Val	Glu	Leu	Val	Gln	Asp	Ala	Leu	Ser	Tyr	Gly	Gly			
150					155				160						165			
gat	gtt	att	cgt	ctt	gtc	acc	ggc	aac	cca	ttg	agc	agc	gat	gcc	aca	643		
Asp	Val	Ile	Arg	Leu	Val	Thr	Gly	Asn	Pro	Leu	Ser	Ser	Asp	Ala	Thr			
				170					175					180				
ctg	gct	gag	atc	tct	gca	gtt	tcc	gag	gct	ggc	ctg	gag	ttc	cag	gtg	691		
Leu	Ala	Glu	Ile	Ser	Ala	Val	Ser	Glu	Ala	Gly	Leu	Glu	Phe	Gln	Val			
			185					190					195					
gtt	cca	ggt	atg	tct	ttg	cct	gca	acg	gtt	cct	gca	ttt	gcg	gga	att	739		
Val	Pro	Gly	Met	Ser	Leu	Pro	Ala	Thr	Val	Pro	Ala	Phe	Ala	Gly	Ile			
		200					205					210						
gcg	ttg	ggt	tct	acc	tac	acc	gaa	act	gat	gtc	aac	ggt	caa	aac	ttg	787		
Ala	Leu	Gly	Ser	Thr	Tyr	Thr	Glu	Thr	Asp	Val	Asn	Gly	Gln	Asn	Leu			
	215					220					225							
gac	tgg	gat	cag	ttg	gct	agc	gca	cct	cag	cct	ttg	gtg	ctg	cag	gcc	835		
Asp	Trp	Asp	Gln	Leu	Ala	Ser	Ala	Pro	Gln	Pro	Leu	Val	Leu	Gln	Ala			
230					235				240					245				
cgc	gtg	gat	gac	ctt	tcc	cgt	att	gca	cag	gaa	cta	aag	gcc	cgc	aat	883		
Arg	Val	Asp	Asp	Leu	Ser	Arg	Ile	Ala	Gln	Glu	Leu	Lys	Ala	Arg	Asn			
				250				255					260					
atg	tct	ttg	gaa	act	cct	gtt	tct	gtc	acc	gct	aac	ggc	acc	acc	cgt	931		
Met	Ser	Leu	Glu	Thr	Pro	Val	Ser	Val	Thr	Ala	Asn	Gly	Thr	Thr	Arg			
			265					270					275					
ttg	cag	cgc	acc	tat	gac	acc	act	tta	ggt	ctg	ttg	cac	aag	ctt	gat	979		
Leu	Gln	Arg	Thr	Tyr	Asp	Thr	Thr	Leu	Gly	Leu	Leu	His	Lys	Leu	Asp			
		280					285					290						
gct	gaa	cta	agc	gga	cct	ttg	gtt	gtt	acc	ttg	ggc	aag	ggt	gtg				
1024																		
Ala	Glu	Leu	Ser	Gly	Pro	Leu	Val	Val	Thr	Leu	Gly	Lys	Gly	Val				
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<210> 822

<211> 308

<212> PRT

<213> Corynebacterium glutamicum

<400> 822

Met Thr Ile Ala His Lys Pro Glu Met Ala Glu Thr Thr Gly Ile Glu
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 20 25 30
 Asn Leu Arg Pro Val Ser Ser Phe Glu Gly Gln His Glu Gly Gln Thr
 35 40 45
 Glu Glu Leu Leu Pro Gly Lys Val Ile Phe Val Gly Ala Gly Pro Gly
 50 55 60
 Asn Pro Asp Leu Leu Thr Val Arg Ala Arg Glu Val Leu Gly Asn Ala
 65 70 75 80
 Val Arg Ala Ile Thr Asp Glu Gln Val Leu Ser Gly Val Arg Ala Phe
 85 90 95
 Val Ala Thr Glu Ile Pro Val Pro Glu Asp Lys Leu Gln Ala Ala Glu
 100 105 110
 Asp Glu Tyr Glu Arg Ile Cys Ile Glu Ala Lys Glu Asn Gly Ala Arg
 115 120 125
 Arg Lys Pro Pro Arg Pro Ala Pro Pro Thr Ala Ala Glu Ile Thr Glu
 130 135 140
 Val Ser Glu Ala Thr Pro Ala Gln Ile Val Glu Leu Val Gln Asp Ala
 145 150 155 160
 Leu Ser Tyr Gly Gly Asp Val Ile Arg Leu Val Thr Gly Asn Pro Leu
 165 170 175
 Ser Ser Asp Ala Thr Leu Ala Glu Ile Ser Ala Val Ser Glu Ala Gly
 180 185 190
 Leu Glu Phe Gln Val Val Pro Gly Met Ser Leu Pro Ala Thr Val Pro
 195 200 205
 Ala Phe Ala Gly Ile Ala Leu Gly Ser Thr Tyr Thr Glu Thr Asp Val
 210 215 220
 Asn Gly Gln Asn Leu Asp Trp Asp Gln Leu Ala Ser Ala Pro Gln Pro
 225 230 235 240
 Leu Val Leu Gln Ala Arg Val Asp Asp Leu Ser Arg Ile Ala Gln Glu
 245 250 255
 Leu Lys Ala Arg Asn Met Ser Leu Glu Thr Pro Val Ser Val Thr Ala
 260 265 270
 Asn Gly Thr Thr Arg Leu Gln Arg Thr Tyr Asp Thr Thr Leu Gly Leu
 275 280 285
 Leu His Lys Leu Asp Ala Glu Leu Ser Gly Pro Leu Val Val Thr Leu
 290 295 300
 Gly Lys Gly Val
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<210> 823
 <211> 755
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(732)
 <223> FRXA00374

<400> 823
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 atc aag ggc atc gtc gaa gga cgc tac cag tgg gtt gtc ctc aca agc 96
 Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser
 20 25 30
 gtc aac gca gtg aag gca gtc tgg aag aaa atc acc gaa ttc ggc ctc 144
 Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu
 35 40 45
 gat tca cgt tcc ttc gcg ggc gtc cgc atc gcc gca gtc ggt gaa aaa 192
 Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys
 50 55 60
 acc gcc gct gag atc cgc gcg ctc ggc atc acg ccg gag ctt ctg cct 240
 Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro
 65 70 75 80
 gca cgt acc agg caa aat gcg caa ggg ctt gtc gac gtg ttc ccc gaa 288
 Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu
 85 90 95
 tat ttc gaa gaa ctc gat cca gtc ggc cgt gtc ctc ttg ccg cgc gca 336
 Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala
 100 105 110
 gat atc gca acc gac gtg ctt gtc gac ggc ctg acc cac ctt ggt tgg 384
 Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp
 115 120 125
 gaa gtc gaa gac gtg gtg gct tac cgc acc gtc cgc gca gca cca cca 432
 Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro
 130 135 140
 agc gct gat atc cga gat atg atc aag acc ggc gga ttt gat gca gtt 480
 Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val
 145 150 155 160
 gcc ttc acc tct tcg tcg acc gtg aag aac ctc gtt ggt atc gcg ggt 528
 Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly
 165 170 175
 aaa cca cac cca cgc acc atc gtc gcg tgc atc gga ccc atg act gca 576
 Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala
 180 185 190
 gcg acc gct gaa gaa ctg gga ctg cgc gtt gat gtc atg cca gag atc 624

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile
 195 200 205

gcc gaa gta cca gaa ctg atc gac gct ctt gcg gaa cac gtg gcg gat 672
 Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp
 210 215 220

ctg cgc gct aag ggc gag ctg ccg ccg ccg agg aag aaa cgc agg cgt 720
 Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg
 225 230 235 240

cga aaa gcg tct taaaagggttt ttcactaggg tgt 755
 Arg Lys Ala Ser

<210> 824
 <211> 244
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 824

Thr Ile Ser Val Glu Pro Pro Arg Asn Pro Ala Gln Met Glu Arg Ala
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Ile Lys Gly Ile Val Glu Gly Arg Tyr Gln Trp Val Val Leu Thr Ser
 20 25 30

Val Asn Ala Val Lys Ala Val Trp Lys Lys Ile Thr Glu Phe Gly Leu
 35 40 45

Asp Ser Arg Ser Phe Ala Gly Val Arg Ile Ala Ala Val Gly Glu Lys
 50 55 60

Thr Ala Ala Glu Ile Arg Ala Leu Gly Ile Thr Pro Glu Leu Leu Pro
 65 70 75 80

Ala Arg Thr Arg Gln Asn Ala Gln Gly Leu Val Asp Val Phe Pro Glu
 85 90 95

Tyr Phe Glu Glu Leu Asp Pro Val Gly Arg Val Leu Leu Pro Arg Ala
 100 105 110

Asp Ile Ala Thr Asp Val Leu Val Asp Gly Leu Thr His Leu Gly Trp
 115 120 125

Glu Val Glu Asp Val Val Ala Tyr Arg Thr Val Arg Ala Ala Pro Pro
 130 135 140

Ser Ala Asp Ile Arg Asp Met Ile Lys Thr Gly Gly Phe Asp Ala Val
 145 150 155 160

Ala Phe Thr Ser Ser Ser Thr Val Lys Asn Leu Val Gly Ile Ala Gly
 165 170 175

Lys Pro His Pro Arg Thr Ile Val Ala Cys Ile Gly Pro Met Thr Ala
 180 185 190

Ala Thr Ala Glu Glu Leu Gly Leu Arg Val Asp Val Met Pro Glu Ile
 195 200 205

Ala Glu Val Pro Glu Leu Ile Asp Ala Leu Ala Glu His Val Ala Asp
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Leu Arg Ala Lys Gly Glu Leu Pro Pro Pro Arg Lys Lys Arg Arg Arg
 225 230 235 240

Arg Lys Ala Ser

<210> 825
 <211> 1467
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1444)
 <223> RXN00383

<400> 825
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 Met Arg Phe Ala Ile
 1 5

atc ggt gca ggc ctt gcg ggt ctg act gct gca tat gag atc cat aaa 163
 Ile Gly Ala Gly Leu Ala Gly Leu Thr Ala Ala Tyr Glu Ile His Lys
 10 15 20

gct gat ccc act gcc caa atc gat gtg ttg gaa gca ggc gaa cgc att 211
 Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu Ala Gly Glu Arg Ile
 25 30 35

ggc ggc aag ctt ttt acg gtg ccg ttt gct tcc gga cct acc gat att 259
 Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser Gly Pro Thr Asp Ile
 40 45 50

gga gcg gag gcg ttt tta gct gcg cgt tcc gat gcg gtg gag ttt ttt 307
 Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp Ala Val Glu Phe Phe
 55 60 65

act gag ctt ggg ttg gct gat tct ttg gtc agc ccg tct gct gcg aag 355
 Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser Pro Ser Ala Ala Lys
 70 75 80 85

tct cag tat ttc gcg ggc ggt gcg ctg cat gcg ttc ccc gca ggt gga 403
 Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala Phe Pro Ala Gly Gly
 90 95 100

gtg atg ggt att cca agc aat cca cca gca ggc gcg caa gac acc gct 451
 Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly Ala Gln Asp Thr Ala
 105 110 115

ttt gat tgg act cct ggc caa gac att tct gtt ggc gcc tta gtg cgc 499
 Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val Gly Ala Leu Val Arg
 120 125 130

cgt cag tat ggc gat gag atc gtc gat act gtg gtg tct tcg ctg ctt 547
 Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val Val Ser Ser Leu Leu

135	140	145	
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ccg gtg act ctg tca gct gcg gtc aag gcc gtg gaa gct cag cgg gaa Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val Glu Ala Gln Arg Glu 185 190 195			691
gcc gca aaa aca act tca gaa acc cgc ccc gtt ttc cag acc ttc aag Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val Phe Gln Thr Phe Lys 200 205 210			739
ggc gga tac gcg gag ctg tac gaa gcg ttg gca gag caa tgc ggt gca Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala Glu Gln Cys Gly Ala 215 220 225			787
gat att cac ttg gat agt ttc gtt tcc gcc atc acc aaa gat ggt gaa Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile Thr Lys Asp Gly Glu 230 235 240 245			835
ggt ttt gcc atc aag ggc ggt ggc gaa ggc acc tac gac aag gtg att Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr Tyr Asp Lys Val Ile 250 255 260			883
ttg gcg gtt ccc gct cca acc gcc gct gtg ctg ctc cgc gac ttg gca Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu Leu Arg Asp Leu Ala 265 270 275			931
ccg gcc gca gcg cca cat ttg cgc gca att aag ttg gct tct tca gca Pro Ala Ala Pro His Leu Arg Ala Ile Lys Leu Ala Ser Ser Ala 280 285 290			979
gtc gtc ggc atg cgt ttc gat tcc agc gag ggc ctg ccc gac aac tcc 1027 Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly Leu Pro Asp Asn Ser 295 300 305			
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acg ttc tcc tca aag aag tgg cct cac ctg gag gct cgc ggg ggc gcg 1123 Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu Ala Arg Gly Gly Ala 330 335 340			
ctc gtg cgc gcg tcg ttc ggc agg cta ggc gat gag gcg tcg gca cgc 1171 Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp Glu Ala Ser Ala Arg 345 350 355			
atg gac gag gat ttg ctt gtc gac gcc gcc ctc gac gat ctc ctc acc 1219 Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu Asp Asp Leu Leu Thr			

360 365 370
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 Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu Gly Glu Ile Phe Val
 375 380 385
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 1315
 Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly Val Asp His Ile Ala
 390 395 400 405
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 1363
 Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala Val Pro Gly Val Glu
 410 415 420
 gca att ggc gcg tgg gct ggg gga gtg gga gtt ccc gca gtt atc gca
 1411
 Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val Pro Ala Val Ile Ala
 425 430 435
 gat gcc cag gca gca gta cac agg ttg ctg gga taagcaccca aaaacactat
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 Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly
 440 445
 tga
 1467

<210> 826
 <211> 448
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 826
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 Ala Gly Glu Arg Ile Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser
 35 40 45
 Gly Pro Thr Asp Ile Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp
 50 55 60
 Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser
 65 70 75 80
 Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu His Ala
 85 90 95
 Phe Pro Ala Gly Gly Val Met Gly Ile Pro Ser Asn Pro Pro Ala Gly
 100 105 110
 Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile Ser Val
 115 120 125

Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp Thr Val
 130 135 140
 Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp Asp Leu
 145 150 155 160
 Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Leu Asp Gln Leu
 165 170 175
 Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys Ala Val
 180 185 190
 Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg Pro Val
 195 200 205
 Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala Leu Ala
 210 215 220
 Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser Ala Ile
 225 230 235 240
 Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu Gly Thr
 245 250 255
 Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala Val Leu
 260 265 270
 Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala Ile Lys
 275 280 285
 Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser Glu Gly
 290 295 300
 Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro Gly Ile
 305 310 315 320
 Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His Leu Glu
 325 330 335
 Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu Gly Asp
 340 345 350
 Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala Ala Leu
 355 360 365
 Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala Gly Leu
 370 375 380
 Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala Tyr Gly
 385 390 395 400
 Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile Ala Ala
 405 410 415
 Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val Gly Val
 420 425 430
 Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu Leu Gly
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<210> 827
<211> 382
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(382)  
<223> FRXA00376
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ag	cc	gt	tct	cc	at	catt	catt	ct	taa	act	aa	gag	gag	ttt	c	atg	cgt	ttt	gcc	atc	115			
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																1								
atc	ggt	gca	ggc	ctt	gcg	ggt	ctg	act	gct	gca	tat	gag	atc	cat	aaa	163								
Ile	Gly	Ala	Gly	Leu	Ala	Gly	Leu	Thr	Ala	Ala	Tyr	Glu	Ile	His	Lys									
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gct	gat	ccc	act	gcc	caa	atc	gat	gtg	ttg	gaa	gca	ggc	gaa	cgc	att	211								
Ala	Asp	Pro	Thr	Ala	Gln	Ile	Asp	Val	Leu	Glu	Ala	Gly	Glu	Arg	Ile									
				25					30					35										
ggc	ggc	aag	ctt	ttt	acg	gtg	ccg	ttt	gct	tcc	gga	cct	acc	gat	att	259								
Gly	Gly	Lys	Leu	Phe	Thr	Val	Pro	Phe	Ala	Ser	Gly	Pro	Thr	Asp	Ile									
		40			45			50																
gga	gcg	gag	gcg	ttt	tta	gct	gcg	cgt	tcc	gat	gcg	gtg	gag	ttt	ttt	307								
Gly	Ala	Glu	Ala	Phe	Leu	Ala	Ala	Arg	Ser	Asp	Ala	Val	Glu	Phe	Phe									
		55			60			65																
act	gag	ctt	ggg	ttg	gct	gat	tct	ttg	gtc	agc	ccg	tct	gct	gcg	aag	355								
Thr	Glu	Leu	Gly	Leu	Ala	Asp	Ser	Leu	Val	Ser	Pro	Ser	Ala	Ala	Lys									
70					75					80					85									
tct	cag	tat	ttc	gcg	ggc	ggt	gcg	ctg	382															
Ser	Gln	Tyr	Phe	Ala	Gly	Gly	Ala	Leu																
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<210> 828
<211> 94
<212> PRT
<213> Corynebacterium glutamicum
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Tyr Glu Ile His Lys Ala Asp Pro Thr Ala Gln Ile Asp Val Leu Glu
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Ala Gly Glu Arg Ile Gly Gly Lys Leu Phe Thr Val Pro Phe Ala Ser
             35             40             45

Gly Pro Thr Asp Ile Gly Ala Glu Ala Phe Leu Ala Ala Arg Ser Asp

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50 55 60
 Ala Val Glu Phe Phe Thr Glu Leu Gly Leu Ala Asp Ser Leu Val Ser
 65 70 75 80
 Pro Ser Ala Ala Lys Ser Gln Tyr Phe Ala Gly Gly Ala Leu
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 <210> 829
 <211> 1037
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
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 <222> (1)..(1014)
 <223> FRXA00383

 <400> 829
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 Ala Gly Ala Gln Asp Thr Ala Phe Asp Trp Thr Pro Gly Gln Asp Ile
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 tct gtt ggc gcc tta gtg cgc cgt cag tat ggc gat gag atc gtc gat 96
 Ser Val Gly Ala Leu Val Arg Arg Gln Tyr Gly Asp Glu Ile Val Asp
 20 25 30

 act gtg gtg tct tcg ctg ctt ggt ggc gtt tat tcc tcc acc gct gat 144
 Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp
 35 40 45

 gat ctg ggt gtg cgc gct tcc gtg ccg gca ctt gct gca gcc ctt gat 192
 Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp
 50 55 60

 cag ctg gct gag gcc ggc gag ccg gtg act ctg tca gct gcg gtc aag 240
 Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys
 65 70 75 80

 gcc gtg gaa gct cag cgg gaa gcc gca aaa aca act tca gaa acc cgc 288
 Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg
 85 90 95

 ccc gtt ttc cag acc ttc aag ggc gga tac gcg gag ctg tac gaa gcg 336
 Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala
 100 105 110

 ttg gca gag caa tgc ggt gca gat att cac ttg gat agt ttc gtt tcc 384
 Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser
 115 120 125

 gcc atc acc aaa gat ggt gaa ggt ttt gcc atc aag ggc ggt ggc gaa 432
 Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu
 130 135 140

 ggc acc tac gac aag gtg att ttg gcg gtt ccc gct cca acc gcc gct 480
 Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala
 145 150 155 160

 gtg ctg ctc cgc gac ttg gca ccg gcc gca gcg cca cat ttg cgc gca 528

Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala
 165 170 175
 att aag ttg gct tct tca gca gtc gtc ggc atg cgt ttc gat tcc agc 576
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser
 180 185 190
 gag ggc ctg ccc gac aac tcc ggc gtc ctg gtc gct gtt aat gag ccg 624
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro
 195 200 205
 ggc atc acg gcg aag gcc ttc acg ttc tcc tca aag aag tgg cct cac 672
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His
 210 215 220
 ctg gag gct cgc ggg ggc gcg ctc gtg cgc gcg tcg ttc ggc agg cta 720
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu
 225 230 235 240
 ggc gat gag gcg tcg gca cgc atg gac gag gat ttg ctt gtc gac gcc 768
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala
 245 250 255
 gcc ctc gac gat ctc ctc acc ata acc ggg ttc gac ggc cgg gct gcc 816
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala
 260 265 270
 gga ctg ggt gaa att ttc gtg cag cgc tgg ttc ggt ggg ctc cca gcc 864
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala
 275 280 285
 tat gga gtt gat cac att gct acc gtt tcg gct gcg cgt gca gag atc 912
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile
 290 295 300
 gca gcc gtg cct ggc gtg gaa gca att ggc gcg tgg gct ggg gga gtg 960
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val
 305 310 315 320
 gga gtt ccc gca gtt atc gca gat gcc cag gca gca gta cac agg ttg
 1008
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu
 325 330 335
 ctg gga taagcaccca aaaacactat tga
 1037
 Leu Gly

<210> 830

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 830

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 20 25 30

Thr Val Val Ser Ser Leu Leu Gly Gly Val Tyr Ser Ser Thr Ala Asp
 35 40 45
 Asp Leu Gly Val Arg Ala Ser Val Pro Ala Leu Ala Ala Ala Leu Asp
 50 55 60
 Gln Leu Ala Glu Ala Gly Glu Pro Val Thr Leu Ser Ala Ala Val Lys
 65 70 75 80
 Ala Val Glu Ala Gln Arg Glu Ala Ala Lys Thr Thr Ser Glu Thr Arg
 85 90 95
 Pro Val Phe Gln Thr Phe Lys Gly Gly Tyr Ala Glu Leu Tyr Glu Ala
 100 105 110
 Leu Ala Glu Gln Cys Gly Ala Asp Ile His Leu Asp Ser Phe Val Ser
 115 120 125
 Ala Ile Thr Lys Asp Gly Glu Gly Phe Ala Ile Lys Gly Gly Gly Glu
 130 135 140
 Gly Thr Tyr Asp Lys Val Ile Leu Ala Val Pro Ala Pro Thr Ala Ala
 145 150 155 160
 Val Leu Leu Arg Asp Leu Ala Pro Ala Ala Ala Pro His Leu Arg Ala
 165 170 175
 Ile Lys Leu Ala Ser Ser Ala Val Val Gly Met Arg Phe Asp Ser Ser
 180 185 190
 Glu Gly Leu Pro Asp Asn Ser Gly Val Leu Val Ala Val Asn Glu Pro
 195 200 205
 Gly Ile Thr Ala Lys Ala Phe Thr Phe Ser Ser Lys Lys Trp Pro His
 210 215 220
 Leu Glu Ala Arg Gly Gly Ala Leu Val Arg Ala Ser Phe Gly Arg Leu
 225 230 235 240
 Gly Asp Glu Ala Ser Ala Arg Met Asp Glu Asp Leu Leu Val Asp Ala
 245 250 255
 Ala Leu Asp Asp Leu Leu Thr Ile Thr Gly Phe Asp Gly Arg Ala Ala
 260 265 270
 Gly Leu Gly Glu Ile Phe Val Gln Arg Trp Phe Gly Gly Leu Pro Ala
 275 280 285
 Tyr Gly Val Asp His Ile Ala Thr Val Ser Ala Ala Arg Ala Glu Ile
 290 295 300
 Ala Ala Val Pro Gly Val Glu Ala Ile Gly Ala Trp Ala Gly Gly Val
 305 310 315 320
 Gly Val Pro Ala Val Ile Ala Asp Ala Gln Ala Ala Val His Arg Leu
 325 330 335
 Leu Gly

tcc gaa aac acc gac gac caa cgc caa caa ttc gcc gaa ggc gcc gtc 691
 Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe Ala Glu Gly Ala Val
 185 190 195
 caa ggc agc atc atc gcc acc tac atg cac ggc ccc gca ctc gcc cga 739
 Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly Pro Ala Leu Ala Arg
 200 205 210
 aac ccc caa ctc gcc gac ctc atg ctc gca aaa gca atg ggt gtc gcg 787
 Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys Ala Met Gly Val Ala
 215 220 225
 ctg aaa gac ctg gag cct ttg gac atc gac gtc atc gac cgc ctc cgc 835
 Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val Ile Asp Arg Leu Arg
 230 235 240 245
 gcc gaa cgc ctg gcg tagcccccttc taaaccgggt cta 873
 Ala Glu Arg Leu Ala
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<210> 832

<211> 250

<212> PRT

<213> Corynebacterium glutamicum

<400> 832

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 20 25 30
 Arg Gly Ile Asn Ala Glu Ile Gln Arg Val Thr Leu Asp Asp Ala Val
 35 40 45
 Pro Ser Thr Leu Asp Leu Tyr Cys Leu Gly Gly Gly Glu Asp Thr Ala
 50 55 60
 Gln Ile Leu Ala Thr Glu His Leu Thr Lys Asp Gly Gly Leu Gln Thr
 65 70 75 80
 Ala Ala Ala Ala Gly Arg Pro Ile Phe Ala Val Cys Ala Gly Leu Gln
 85 90 95
 Val Leu Gly Asp Ser Phe Arg Ala Ala Gly Arg Val Ile Asp Gly Leu
 100 105 110
 Gly Leu Ile Asp Ala Thr Thr Val Ser Leu Gln Lys Arg Ala Ile Gly
 115 120 125
 Glu Val Glu Thr Thr Pro Thr Arg Ala Gly Phe Thr Ala Glu Leu Thr
 130 135 140
 Glu Arg Leu Thr Gly Phe Glu Asn His Met Gly Ala Thr Leu Leu Gly
 145 150 155 160
 Pro Asp Ala Glu Pro Leu Gly Arg Val Val Arg Gly Glu Gly Asn Thr
 165 170 175

Asp Val Trp Ala Ala Ser Glu Asn Thr Asp Asp Gln Arg Gln Gln Phe
 180 185 190
 Ala Glu Gly Ala Val Gln Gly Ser Ile Ile Ala Thr Tyr Met His Gly
 195 200 205
 Pro Ala Leu Ala Arg Asn Pro Gln Leu Ala Asp Leu Met Leu Ala Lys
 210 215 220
 Ala Met Gly Val Ala Leu Lys Asp Leu Glu Pro Leu Asp Ile Asp Val
 225 230 235 240
 Ile Asp Arg Leu Arg Ala Glu Arg Leu Ala
 245 250

<210> 833
 <211> 1044
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1021)
 <223> RXA02134

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 Met Ser Gly Lys Ala
 1 5
 ggc ttt acc ccc gaa gat ccc gaa gac tca gac aac cgc cac ggg aac 163
 Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp Asn Arg His Gly Asn
 10 15 20
 ccc ctt ttc gaa ggt atc ttt acc gca ctt aat tgg atg acc gtt ctc 211
 Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn Trp Met Thr Val Leu
 25 30 35
 ccc gtc ccc ggc gca tca gtt ttt gat cgc acc acg ggc gcc cgg gta 259
 Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr Thr Gly Ala Arg Val
 40 45 50
 atg gcc tct ttg ccc ttt gtt ggc ttc gtt ttc gga atg ttc acc gcg 307
 Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe Gly Met Phe Thr Ala
 55 60 65
 atc atc atg tgg gct atc ggc ccc att tca ggg gtg atc cac gtc gat 355
 Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly Val Ile His Val Asp
 70 75 80 85
 gga ctt tta gtt gcc gtt ctg atc gtc gcg ttc tgg gaa ctt ctt aat 403
 Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe Trp Glu Leu Leu Asn
 90 95 100
 cgg ttt atg cac ctc gac ggc ctc gca gat gtc tcc gat gct ttg ggt 451
 Arg Phe Met His Leu Asp Gly Leu Ala Asp Val Ser Asp Ala Leu Gly
 105 110 115

tcc tac gca gcc cca cca cgc gca cga gaa atc ctt gcc gat ccc cgc 499
 Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile Leu Ala Asp Pro Arg
 120 125 130

acc gga ctt ttc ggc ctc gcc acc gcc atg ctt tcc gtt ctc ctg cag 547
 Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu Ser Val Leu Leu Gln
 135 140 145

gtc gct gca gtc gca tcg ctt gtc gat tca acc gtg tgg tgg atg atc 595
 Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr Val Trp Trp Met Ile
 150 155 160 165

tgc ttc atc ccc gtt ctc ggc cgc atc gct gga caa gta acc gca ctg 643
 Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly Gln Val Thr Ala Leu
 170 175 180

aaa aac cac aac gcc ttc tcc ccc acc ggc ttt ggc gca cta gtc atc 691
 Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe Gly Ala Leu Val Ile
 185 190 195

gga acg gtg aaa ttt tgg tgg atc gcg ctg tgg ctc ttg gtt act gct 739
 Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp Leu Leu Val Thr Ala
 200 205 210

gcg ttg gct ttt tgg tgc gca gaa tta att tct cca ctt tca ccg ctg 787
 Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser Pro Leu Ser Pro Leu
 215 220 225

acc agt gtt aac act ccc ttt gtc gct gga cct ttc ccc gct gca atc 835
 Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro Phe Pro Ala Ala Ile
 230 235 240 245

aac ccc gcc tgg ctt gga ggc tgg gtt gcg ata acc gca gtc gtg gca 883
 Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile Thr Ala Val Val Ala
 250 255 260

tgt gtt ttc gca gca ctt ttc agc cgc cgc tta tca cga agt ttc ggt 931
 Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu Ser Arg Ser Phe Gly
 265 270 275

gga ctc aac gga gac tgc atc ggc gca tgc att cat ctc ggg gcg tcg 979
 Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile His Leu Gly Ala Ser
 280 285 290

att tct gca gtg atg ttt gct gtt gtc gcc aat gca atg gtg
 1021
 Ile Ser Ala Val Met Phe Ala Val Val Ala Asn Ala Met Val
 295 300 305

taaagcgggtg gcgtcttttg gga
 1044

<210> 834

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 834

Met Ser Gly Lys Ala Gly Phe Thr Pro Glu Asp Pro Glu Asp Ser Asp
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Asn Arg His Gly Asn Pro Leu Phe Glu Gly Ile Phe Thr Ala Leu Asn
 20 25 30
 Trp Met Thr Val Leu Pro Val Pro Gly Ala Ser Val Phe Asp Arg Thr
 35 40 45
 Thr Gly Ala Arg Val Met Ala Ser Leu Pro Phe Val Gly Phe Val Phe
 50 55 60
 Gly Met Phe Thr Ala Ile Ile Met Trp Ala Ile Gly Pro Ile Ser Gly
 65 70 75 80
 Val Ile His Val Asp Gly Leu Leu Val Ala Val Leu Ile Val Ala Phe
 85 90 95
 Trp Glu Leu Leu Asn Arg Phe Met His Leu Asp Gly Leu Ala Asp Val
 100 105 110
 Ser Asp Ala Leu Gly Ser Tyr Ala Ala Pro Pro Arg Ala Arg Glu Ile
 115 120 125
 Leu Ala Asp Pro Arg Thr Gly Leu Phe Gly Leu Ala Thr Ala Met Leu
 130 135 140
 Ser Val Leu Leu Gln Val Ala Ala Val Ala Ser Leu Val Asp Ser Thr
 145 150 155 160
 Val Trp Trp Met Ile Cys Phe Ile Pro Val Leu Gly Arg Ile Ala Gly
 165 170 175
 Gln Val Thr Ala Leu Lys Asn His Asn Ala Phe Ser Pro Thr Gly Phe
 180 185 190
 Gly Ala Leu Val Ile Gly Thr Val Lys Phe Trp Trp Ile Ala Leu Trp
 195 200 205
 Leu Leu Val Thr Ala Ala Leu Ala Phe Trp Cys Ala Glu Leu Ile Ser
 210 215 220
 Pro Leu Ser Pro Leu Thr Ser Val Asn Thr Pro Phe Val Ala Gly Pro
 225 230 235 240
 Phe Pro Ala Ala Ile Asn Pro Ala Trp Leu Gly Gly Trp Val Ala Ile
 245 250 255
 Thr Ala Val Val Ala Cys Val Phe Ala Ala Leu Phe Ser Arg Arg Leu
 260 265 270
 Ser Arg Ser Phe Gly Gly Leu Asn Gly Asp Cys Ile Gly Ala Cys Ile
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 His Leu Gly Ala Ser Ile Ser Ala Val Met Phe Ala Val Val Ala Asn
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 Ala Met Val
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<210> 835

<211> 1197

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1174)

<223> RXA02135

<400> 835

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				Met	Val	Pro	Ala	Glu	
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ctt	ttt	gcg	cgt	gtg	gaa	ttt	ccg	gat	cat	aaa	atc	ctg	gct	cag	acg	163
Leu	Phe	Ala	Arg	Val	Glu	Phe	Pro	Asp	His	Lys	Ile	Leu	Ala	Gln	Thr	
				10					15					20		

aag	gat	ttc	cat	gac	tcc	ctc	acc	aag	cca	ccc	gga	tct	ttg	ggc	aag	211
Lys	Asp	Phe	His	Asp	Ser	Leu	Thr	Lys	Pro	Pro	Gly	Ser	Leu	Gly	Lys	
			25					30					35			

ttg	gag	cag	atc	ggc	tgt	ttc	att	tcc	gca	tgc	cag	ggc	cag	att	ccg	259
Leu	Glu	Gln	Ile	Gly	Cys	Phe	Ile	Ser	Ala	Cys	Gln	Gly	Gln	Ile	Pro	
		40					45					50				

cca	cgt	cca	ctc	aac	aac	tca	aag	atc	gtt	gtt	ttc	gct	ggc	gat	cac	307
Pro	Arg	Pro	Leu	Asn	Asn	Ser	Lys	Ile	Val	Val	Phe	Ala	Gly	Asp	His	
	55					60					65					

ggc	gtt	gca	act	aaa	ggc	gtg	tcc	gcg	tac	cca	tcc	tca	gta	agc	ttg	355
Gly	Val	Ala	Thr	Lys	Gly	Val	Ser	Ala	Tyr	Pro	Ser	Ser	Val	Ser	Leu	
70					75					80					85	

cag	atg	gct	gaa	aac	att	aca	aac	ggg	ggc	gcc	gcc	atc	aac	gtg	att	403
Gln	Met	Ala	Glu	Asn	Ile	Thr	Asn	Gly	Gly	Ala	Ala	Ile	Asn	Val	Ile	
				90				95						100		

gca	cgc	acc	acc	ggc	acg	tcc	gtc	cga	ctt	att	gat	acc	tcc	ctc	gac	451
Ala	Arg	Thr	Thr	Gly	Thr	Ser	Val	Arg	Leu	Ile	Asp	Thr	Ser	Leu	Asp	
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cac	gaa	gca	tgg	ggc	gac	gag	cgc	gta	tct	agg	tcc	tgc	gga	tcc	atc	499
His	Glu	Ala	Trp	Gly	Asp	Glu	Arg	Val	Ser	Arg	Ser	Cys	Gly	Ser	Ile	
	120					125						130				

gat	gtt	gaa	gac	gcc	atg	acc	caa	gaa	cag	gtc	gaa	cgc	gca	ctg	aag	547
Asp	Val	Glu	Asp	Ala	Met	Thr	Gln	Glu	Gln	Val	Glu	Arg	Ala	Leu	Lys	
	135					140					145					

atc	ggg	aag	cgc	att	gcg	gat	caa	gaa	gtg	gac	gca	ggc	gcc	gac	att	595
Ile	Gly	Lys	Arg	Ile	Ala	Asp	Gln	Glu	Val	Asp	Ala	Gly	Ala	Asp	Ile	
150					155					160					165	

tta	atc	ccc	ggc	gat	tta	gga	att	ggc	aac	acc	acc	acc	gcc	gct	gcc	643
Leu	Ile	Pro	Gly	Asp	Leu	Gly	Ile	Gly	Asn	Thr	Thr	Thr	Ala	Ala	Ala	
				170				175						180		

ctc	gtt	gga	acg	ttc	acc	ctc	gca	gag	cct	gtt	gtt	gtc	gta	ggc	cgc	691
Leu	Val	Gly	Thr	Phe	Thr	Leu	Ala	Glu	Pro	Val	Val	Val	Val	Gly	Arg	

185								190				195				
ggc	acc	gga	atc	gac	gat	gaa	gcc	tgg	aaa	ctc	aaa	gtc	tcc	gcg	atc	739
Gly	Thr	Gly	Ile	Asp	Asp	Glu	Ala	Trp	Lys	Leu	Lys	Val	Ser	Ala	Ile	
		200					205					210				
cgc	gac	gcc	atg	ttc	cgc	gcc	cgc	gac	ctg	cgc	caa	gac	ccc	atc	gcc	787
Arg	Asp	Ala	Met	Phe	Arg	Ala	Arg	Asp	Leu	Arg	Gln	Asp	Pro	Ile	Ala	
		215				220					225					
atc	gcc	cgg	aaa	atc	tct	tcc	cca	gac	ctt	gca	gcc	atg	gca	gca	ttc	835
Ile	Ala	Arg	Lys	Ile	Ser	Ser	Pro	Asp	Leu	Ala	Ala	Met	Ala	Ala	Phe	
230					235					240					245	
att	gcc	caa	gca	gca	gtt	cga	cgc	acc	ccc	gtg	ctt	ctc	gac	ggc	gtt	883
Ile	Ala	Gln	Ala	Ala	Val	Arg	Arg	Thr	Pro	Val	Leu	Leu	Asp	Gly	Val	
				250					255					260		
gta	gtc	acc	gcc	gca	gcc	ctc	cta	gcc	aac	aaa	ctg	gcc	cca	ggt	gcc	931
Val	Val	Thr	Ala	Ala	Ala	Leu	Leu	Ala	Asn	Lys	Leu	Ala	Pro	Gly	Ala	
			265					270					275			
agg	cgt	tgg	ttc	atc	gca	gga	cac	cgc	tcc	acc	gaa	cca	gcg	cat	tcc	979
Arg	Arg	Trp	Phe	Ile	Ala	Gly	His	Arg	Ser	Thr	Glu	Pro	Ala	His	Ser	
		280					285					290				
gta	gct	cta	aac	gca	ctg	gcc	ctt	gat	ccc	atc	ctg	gaa	ctt	gga	atg	
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Val	Ala	Leu	Asn	Ala	Leu	Ala	Leu	Asp	Pro	Ile	Leu	Glu	Leu	Gly	Met	
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tcc	ctt	ggc	gaa	ggc	tcc	ggc	gca	gcc	acc	gca	ctc	ccc	ctg	gtc	aag	
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Ser	Leu	Gly	Glu	Gly	Ser	Gly	Ala	Ala	Thr	Ala	Leu	Pro	Leu	Val	Lys	
310					315				320						325	
att	gcc	gtt	gac	ctg	atg	aac	gac	atg	tcg	aca	ttt	tct	tcc	gcc	ggc	
1123																
Ile	Ala	Val	Asp	Leu	Met	Asn	Asp	Met	Ser	Thr	Phe	Ser	Ser	Ala	Gly	
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gtc	gat	gga	ccc	cta	aac	gcc	tct	tcc	gaa	gcg	ccc	gag	caa	aac	acg	
1171																
Val	Asp	Gly	Pro	Leu	Asn	Ala	Ser	Ser	Glu	Ala	Pro	Glu	Gln	Asn	Thr	
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1197																
Glu																

<210> 836

<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 836

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Ile	Leu	Ala	Gln	Thr	Lys	Asp	Phe	His	Asp	Ser	Leu	Thr	Lys	Pro	Pro
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Gly	Ser	Leu	Gly	Lys	Leu	Glu	Gln	Ile	Gly	Cys	Phe	Ile	Ser	Ala	Cys
		35					40					45			
Gln	Gly	Gln	Ile	Pro	Pro	Arg	Pro	Leu	Asn	Asn	Ser	Lys	Ile	Val	Val
	50					55					60				
Phe	Ala	Gly	Asp	His	Gly	Val	Ala	Thr	Lys	Gly	Val	Ser	Ala	Tyr	Pro
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Ser	Ser	Val	Ser	Leu	Gln	Met	Ala	Glu	Asn	Ile	Thr	Asn	Gly	Gly	Ala
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Ala	Ile	Asn	Val	Ile	Ala	Arg	Thr	Thr	Gly	Thr	Ser	Val	Arg	Leu	Ile
			100					105					110		
Asp	Thr	Ser	Leu	Asp	His	Glu	Ala	Trp	Gly	Asp	Glu	Arg	Val	Ser	Arg
		115					120					125			
Ser	Cys	Gly	Ser	Ile	Asp	Val	Glu	Asp	Ala	Met	Thr	Gln	Glu	Gln	Val
	130					135					140				
Glu	Arg	Ala	Leu	Lys	Ile	Gly	Lys	Arg	Ile	Ala	Asp	Gln	Glu	Val	Asp
145					150					155					160
Ala	Gly	Ala	Asp	Ile	Leu	Ile	Pro	Gly	Asp	Leu	Gly	Ile	Gly	Asn	Thr
				165					170					175	
Thr	Thr	Ala	Ala	Ala	Leu	Val	Gly	Thr	Phe	Thr	Leu	Ala	Glu	Pro	Val
			180					185					190		
Val	Val	Val	Gly	Arg	Gly	Thr	Gly	Ile	Asp	Asp	Glu	Ala	Trp	Lys	Leu
		195					200					205			
Lys	Val	Ser	Ala	Ile	Arg	Asp	Ala	Met	Phe	Arg	Ala	Arg	Asp	Leu	Arg
	210					215					220				
Gln	Asp	Pro	Ile	Ala	Ile	Ala	Arg	Lys	Ile	Ser	Ser	Pro	Asp	Leu	Ala
225					230					235					240
Ala	Met	Ala	Ala	Phe	Ile	Ala	Gln	Ala	Ala	Val	Arg	Arg	Thr	Pro	Val
				245				250						255	
Leu	Leu	Asp	Gly	Val	Val	Val	Thr	Ala	Ala	Ala	Leu	Leu	Ala	Asn	Lys
			260					265					270		
Leu	Ala	Pro	Gly	Ala	Arg	Arg	Trp	Phe	Ile	Ala	Gly	His	Arg	Ser	Thr
		275					280					285			
Glu	Pro	Ala	His	Ser	Val	Ala	Leu	Asn	Ala	Leu	Ala	Leu	Asp	Pro	Ile
	290					295					300				
Leu	Glu	Leu	Gly	Met	Ser	Leu	Gly	Glu	Gly	Ser	Gly	Ala	Ala	Thr	Ala
305					310					315					320
Leu	Pro	Leu	Val	Lys	Ile	Ala	Val	Asp	Leu	Met	Asn	Asp	Met	Ser	Thr
				325				330						335	
Phe	Ser	Ser	Ala	Gly	Val	Asp	Gly	Pro	Leu	Asn	Ala	Ser	Ser	Glu	Ala

340

345

350

Pro Glu Gln Asn Thr Glu
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<210> 837

<211> 645

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(622)

<223> RXA02136

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Met Arg Thr Leu Val
1 5

ctt ggc ggg gcc agg tct ggt aag tct gct ttt gca gaa tca ctt gtt 163
Leu Gly Gly Ala Arg Ser Gly Lys Ser Ala Phe Ala Glu Ser Leu Val
10 15 20

gga tct ggt ccc gtt ttg tat gtc gca acg gca agg cct tcg gga gat 211
Gly Ser Gly Pro Val Leu Tyr Val Ala Thr Ala Arg Pro Ser Gly Asp
25 30 35

gat cct gaa ttc gcc gag cgc att gcg gtt cat gcg gag cgg cgc cca 259
Asp Pro Glu Phe Ala Glu Arg Ile Ala Val His Ala Glu Arg Arg Pro
40 45 50

acg tct tgg gtg ttg gac gag gag ggg gac gtc gat aag ctt ctt gcc 307
Thr Ser Trp Val Leu Asp Glu Glu Gly Asp Val Asp Lys Leu Leu Ala
55 60 65

tcg cca ccg gcc atg ccg gtg ctc gtt gat gac ctg ggc acc tgg ctc 355
Ser Pro Pro Ala Met Pro Val Leu Val Asp Asp Leu Gly Thr Trp Leu
70 75 80 85

acg cac gcc acc gat gcg tgc gac ggt tgg gag gcg agt tcg gcg cag 403
Thr His Ala Thr Asp Ala Cys Asp Gly Trp Glu Ala Ser Ser Ala Gln
90 95 100

ctt gag gcc aag atg gat ttg ctt atc gac gcc atc ctc cac ttt cag 451
Leu Glu Ala Lys Met Asp Leu Leu Ile Asp Ala Ile Leu His Phe Gln
105 110 115

ggc gaa gat ctg gta att gtt tca cct gaa gtt ggt atg gga atc gtc 499
Gly Glu Asp Leu Val Ile Val Ser Pro Glu Val Gly Met Gly Ile Val
120 125 130

ccg gaa tat aaa tct ggg cgc ctt ttt cgt gat cgc atc ggc aca ctt 547
Pro Glu Tyr Lys Ser Gly Arg Leu Phe Arg Asp Arg Ile Gly Thr Leu
135 140 145

aat cag cgt gtc gca gcg att tgc gag agg gtt gtc ttc gtg gtt gct 595
Asn Gln Arg Val Ala Ala Ile Cys Glu Arg Val Val Phe Val Val Ala

150		155		160		165	
ggt	ctg	cca	cta	gag	ttg	aaa	acg ttt taagaaaaca gtcggtttga
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agg 645

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<210> 838
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<212> PRT
<213> Corynebacterium glutamicum
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			20					25					30			
Arg	Pro	Ser	Gly	Asp	Asp	Pro	Glu	Phe	Ala	Glu	Arg	Ile	Ala	Val	His	
		35					40					45				
Ala	Glu	Arg	Arg	Pro	Thr	Ser	Trp	Val	Leu	Asp	Glu	Glu	Gly	Asp	Val	
	50					55					60					
Asp	Lys	Leu	Leu	Ala	Ser	Pro	Pro	Ala	Met	Pro	Val	Leu	Val	Asp	Asp	
65					70					75					80	
Leu	Gly	Thr	Trp	Leu	Thr	His	Ala	Thr	Asp	Ala	Cys	Asp	Gly	Trp	Glu	
				85					90					95		
Ala	Ser	Ser	Ala	Gln	Leu	Glu	Ala	Lys	Met	Asp	Leu	Leu	Ile	Asp	Ala	
			100					105					110			
Ile	Leu	His	Phe	Gln	Gly	Glu	Asp	Leu	Val	Ile	Val	Ser	Pro	Glu	Val	
		115					120					125				
Gly	Met	Gly	Ile	Val	Pro	Glu	Tyr	Lys	Ser	Gly	Arg	Leu	Phe	Arg	Asp	
	130					135					140					
Arg	Ile	Gly	Thr	Leu	Asn	Gln	Arg	Val	Ala	Ala	Ile	Cys	Glu	Arg	Val	
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Val	Phe	Val	Val	Ala	Gly	Leu	Pro	Leu	Glu	Leu	Lys	Thr	Phe			
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<213> Corynebacterium glutamicum
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<222> (1)..(552)  
<223> RXN03114
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cgc	cgc	gag	ttg	acg	gtg	ggg	ttg	gat	gct	ggg	gac	ggg	ccg	att	tta		96
Arg	Arg	Glu	Leu	Thr 20	Val	Gly	Leu	Asp 25	Ala	Gly	Asp	Gly	Pro 30	Ile	Leu		
agg	cag	agc	ttt	gat	gtt	ggg	ttt	ttg	ctt	gtc	gac	gcc	tcc	ttc	cac		144
Arg	Gln	Ser 35	Phe	Asp	Val	Gly	Phe 40	Leu	Leu	Val	Asp	Ala 45	Ser	Phe	His		
att	cat	atc	aat	ggc	gtg	tct	act	ggg	cag	tcg	gtt	gcg	ccg	gat	gat		192
Ile	His 50	Ile	Asn	Gly	Val	Ser 55	Thr	Gly	Gln	Ser	Val 60	Ala	Pro	Asp	Asp		
gta	gtt	gag	gtg	gtg	cgt	ggg	ttg	gct	gat	gct	tcg	gag	ttg	tcc	gtg		240
Val	Val	Glu	Val	Val	Arg 70	Gly	Leu	Ala	Asp	Ala 75	Ser	Glu	Leu	Ser	Val 80		
gaa	agt	gtt	gct	gag	ttg	tgt	act	ccc	gtg	gca	ccg	gtt	tca	tta	tct		288
Glu	Ser	Val	Ala	Glu 85	Leu	Cys	Thr	Pro 90	Val	Ala	Pro	Val	Ser	Leu 95	Ser		
gag	gca	cag	ggg	aat	cct	gcg	cct	att	ggg	tgg	ttg	gag	cat	gat	ggc		336
Glu	Ala	Gln	Gly 100	Asn	Pro	Ala	Pro	Ile 105	Gly	Trp	Leu	Glu	His 110	Asp	Gly		
gtg	gtg	tcg	ttg	ggg	gcg	ggg	att	cca	ggg	ggg	cgg	gtg	gag	gct	cgt		384
Val	Val	Ser 115	Leu	Gly	Ala	Gly	Ile 120	Pro	Gly	Gly	Arg	Val 125	Glu	Ala	Arg		
tta	gcg	cgt	ttt	att	gcg	gtg	att	gag	gcg	gag	acc	act	att	acc	cca		432
Leu	Ala	Arg	Phe	Ile 130	Ala	Val	Ile 135	Glu	Ala	Glu	Thr 140	Thr	Ile	Thr	Pro		
tgg	aat	tcg	ttg	atc	att	cat	gat	ttg	tat	gag	ggg	gtt	gca	gaa	cag		480
Trp	Asn	Ser	Leu	Ile 145	Ile	His	Asp	Leu	Tyr	Glu 155	Gly	Val	Ala	Glu	Gln 160		
gtg	gtg	aag	gtt	ctg	gct	ccc	atg	ggg	ttg	gtt	ttt	gat	gct	aat	tca		528
Val	Val	Lys	Val	Leu 165	Ala	Pro	Met	Gly	Leu	Val 170	Phe	Asp	Ala	Asn 175	Ser		
ccg	ctt	ctg	gag	tca	ccg	gct	ttg	taactcgcca	ttggtgcacg	tct							575
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<210> 840

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 840

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Arg	Arg	Glu	Leu	Thr 20	Val	Gly	Leu	Asp 25	Ala	Gly	Asp	Gly	Pro 30	Ile	Leu		
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Arg	Gln	Ser	Phe	Asp	Val	Gly	Phe	Leu	Leu	Val	Asp	Ala	Ser	Phe	His		
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35	40	45
Ile His Ile Asn Gly Val Ser Thr Gly Gln Ser Val Ala Pro Asp Asp		
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Val Val Glu Val Val Arg Gly Leu Ala Asp Ala Ser Glu Leu Ser Val		
65	70	75
Glu Ser Val Ala Glu Leu Cys Thr Pro Val Ala Pro Val Ser Leu Ser		
	85	90
Glu Ala Gln Gly Asn Pro Ala Pro Ile Gly Trp Leu Glu His Asp Gly		
	100	105
Val Val Ser Leu Gly Ala Gly Ile Pro Gly Gly Arg Val Glu Ala Arg		
	115	120
Leu Ala Arg Phe Ile Ala Val Ile Glu Ala Glu Thr Thr Ile Thr Pro		
	130	135
Trp Asn Ser Leu Ile Ile His Asp Leu Tyr Glu Gly Val Ala Glu Gln		
145	150	155
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Pro Leu Leu Glu Ser Pro Ala Leu		
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<210> 841

<211> 1200

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1177)

<223> RXN01810

<400> 841

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gcttcaccgt cggcaaccgc actggaaaat aaggcttcac atg aat aac gct ttt 115
                                     Met Asn Asn Ala Phe
                                     1                               5

cga cgc acc ctt aca tcc gta gtc ctc gcc gct agc ttg gcc tta acg 163
Arg Arg Thr Leu Thr Ser Val Val Leu Ala Ala Ser Leu Ala Leu Thr
                                     10                               15                               20

gcc tgc gca agc tgg gat tca cct acg gca tct tcc aat ggt gat ctg 211
Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser Ser Asn Gly Asp Leu
                                     25                               30                               35

att gag gag atc cag gca agc tcc acc tca aca gat ccg cgc acc ttc 259
Ile Glu Glu Ile Gln Ala Ser Ser Thr Ser Thr Asp Pro Arg Thr Phe
                                     40                               45                               50

aca ggc ttg agc atc gtg gaa gat atc ggc gat gtg gtt ccc gta acc 307
Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp Val Val Pro Val Thr

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aac gac gtg gtg gtg gag aac gtg tcc cgc atc ctc cca ctg gat ctc Asn Asp Val Val Val Glu Asn Val Ser Arg Ile Leu Pro Leu Asp Leu 90 95 100			403
tac gga acc tat tcc aaa acc atc gct ggc ctg gga ctc gtg gac aat Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu Gly Leu Val Asp Asn 105 110 115			451
att gtg ggt cgt act gtt agt tcc acc gag cct gca ttg gcg gac att Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro Ala Leu Ala Asp Ile 120 125 130			499
gag gtg gtc acc act ggc gga cac acc ctc aat gct gaa gcg atc ctt Glu Val Val Thr Thr Gly Gly His Thr Leu Asn Ala Glu Ala Ile Leu 135 140 145			547
aat tta cat ccg act ttg gtg atc atc gac cac tcg atc ggc cca cgc Asn Leu His Pro Thr Leu Val Ile Ile Asp His Ser Ile Gly Pro Arg 150 155 160 165			595
gaa gtc atc gat cag atc cgc gca gct ggt gtc gcc acg gtg atc atg Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val Ala Thr Val Ile Met 170 175 180			643
tcg ccg cag cgt tcc att gcc tca att ggc gac gac atc cgc gac atc Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp Asp Ile Arg Asp Ile 185 190 195			691
gcc tcc gtc gtt gga ctt cct gaa gaa ggg gag aag ctc gcg gaa cgt Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu Lys Leu Ala Glu Arg 200 205 210			739
tcc gtt gct gaa gtc gaa gag gcc agc acg gtt gtc gat gaa ctc acc Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val Val Asp Glu Leu Thr 215 220 225			787
cca gaa gat ccc ctc aaa atg gta ttc ctc tat gcc cgc gga act ggt Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr Ala Arg Gly Thr Gly 230 235 240 245			835
gga gtg ttc ttc att ttg ggc gat gcc tat ggt gga cgc gat ctc att Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly Gly Arg Asp Leu Ile 250 255 260			883
gaa ggc ctg ggc ggc gtc gac atg gct gct gaa aag ggc atc atg gat Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu Lys Gly Ile Met Asp 265 270 275			931
ctg gca cca gcc aac gcg gaa gca ctt gcc gaa cta aat cca gac gtc Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu Leu Asn Pro Asp Val 280 285 290			979
ttc gtg atg atg tcg gaa gga cta gtc tcg aca gga ggt atc gac ggt 1027 Phe Val Met Met Ser Glu Gly Leu Val Ser Thr Gly Gly Ile Asp Gly			

295 300 305
 ctt atg gaa cgc ccc ggc att gct cag aca acc gcc gga caa aac caa
 1075
 Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr Ala Gly Gln Asn Gln
 310 315 320 325
 cga gta ctg gcg ctt ccc gat ggt caa tca ttg gcc ttt ggt gcc caa
 1123
 Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu Ala Phe Gly Ala Gln
 330 335 340
 act ggc gag ttg ttg ctc cgc gca tcc cgc gaa ctg tat gtg cag ggc
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 Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu Leu Tyr Val Gln Gly
 345 350 355
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 Gly Glu

<210> 842
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 842
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 Ser Leu Ala Leu Thr Ala Cys Ala Ser Trp Asp Ser Pro Thr Ala Ser
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 35 40 45
 Asp Pro Arg Thr Phe Thr Gly Leu Ser Ile Val Glu Asp Ile Gly Asp
 50 55 60
 Val Val Pro Val Thr Asp Asn Ala Ser Pro Ala Leu Pro Val Ser Leu
 65 70 75 80
 Thr Asp Ala Asp Gly Asn Asp Val Val Val Glu Asn Val Ser Arg Ile
 85 90 95
 Leu Pro Leu Asp Leu Tyr Gly Thr Tyr Ser Lys Thr Ile Ala Gly Leu
 100 105 110
 Gly Leu Val Asp Asn Ile Val Gly Arg Thr Val Ser Ser Thr Glu Pro
 115 120 125
 Ala Leu Ala Asp Ile Glu Val Val Thr Thr Gly Gly His Thr Leu Asn
 130 135 140
 Ala Glu Ala Ile Leu Asn Leu His Pro Thr Leu Val Ile Ile Asp His
 145 150 155 160
 Ser Ile Gly Pro Arg Glu Val Ile Asp Gln Ile Arg Ala Ala Gly Val
 165 170 175

Ala Thr Val Ile Met Ser Pro Gln Arg Ser Ile Ala Ser Ile Gly Asp
 180 185 190

Asp Ile Arg Asp Ile Ala Ser Val Val Gly Leu Pro Glu Glu Gly Glu
 195 200 205

Lys Leu Ala Glu Arg Ser Val Ala Glu Val Glu Glu Ala Ser Thr Val
 210 215 220

Val Asp Glu Leu Thr Pro Glu Asp Pro Leu Lys Met Val Phe Leu Tyr
 225 230 235 240

Ala Arg Gly Thr Gly Gly Val Phe Phe Ile Leu Gly Asp Ala Tyr Gly
 245 250 255

Gly Arg Asp Leu Ile Glu Gly Leu Gly Gly Val Asp Met Ala Ala Glu
 260 265 270

Lys Gly Ile Met Asp Leu Ala Pro Ala Asn Ala Glu Ala Leu Ala Glu
 275 280 285

Leu Asn Pro Asp Val Phe Val Met Met Ser Glu Gly Leu Val Ser Thr
 290 295 300

Gly Gly Ile Asp Gly Leu Met Glu Arg Pro Gly Ile Ala Gln Thr Thr
 305 310 315 320

Ala Gly Gln Asn Gln Arg Val Leu Ala Leu Pro Asp Gly Gln Ser Leu
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Ala Phe Gly Ala Gln Thr Gly Glu Leu Leu Leu Arg Ala Ser Arg Glu
 340 345 350

Leu Tyr Val Gln Gly Gly Glu
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<210> 843
 <211> 963
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(933)
 <223> RXS03205

<400> 843

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Val	Arg	Gly	Arg	Thr	Phe	Asp	Arg	Ile	Ile	Ala	Asn	Pro	Pro	Phe	Val	
			20					25					30			
gtg	gga	cca	ccg	gaa	att	ggg	cat	gtg	tac	cgc	gat	tcc	ggc	atg	gat	144
Val	Gly	Pro	Pro	Glu	Ile	Gly	His	Val	Tyr	Arg	Asp	Ser	Gly	Met	Asp	
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cta	gac	ggc	gcg	acc	gcg	ttg	gtg	gtc	aaa	gaa	gcc	tgc	gcg	cat	ctc	192
Leu	Asp	Gly	Ala	Thr	Ala	Leu	Val	Val	Lys	Glu	Ala	Cys	Ala	His	Leu	
	50					55					60					
aac	cct	ggc	ggc	acc	gct	cac	ctg	ctc	ggc	gca	tgg	gtg	cat	tcc	gcg	240
Asn	Pro	Gly	Gly	Thr	Ala	His	Leu	Leu	Gly	Ala	Trp	Val	His	Ser	Ala	
	65				70					75					80	
gat	caa	tcg	tgg	cag	cag	cgc	gtt	gca	gaa	tgg	ttg	ccg	gat	aac	ggc	288
Asp	Gln	Ser	Trp	Gln	Gln	Arg	Val	Ala	Glu	Trp	Leu	Pro	Asp	Asn	Gly	
				85					90					95		
tat	gtt	gct	tgg	gtt	att	gag	cgc	gac	gcc	gtg	agc	ccc	gcg	cag	tat	336
Tyr	Val	Ala	Trp	Val	Ile	Glu	Arg	Asp	Ala	Val	Ser	Pro	Ala	Gln	Tyr	
			100					105					110			
gtg	ggc	acg	tgg	ctt	agt	gat	gag	tcc	ctc	gat	ctg	cgt	agc	ccc	gag	384
Val	Gly	Thr	Trp	Leu	Ser	Asp	Glu	Ser	Leu	Asp	Leu	Arg	Ser	Pro	Glu	
		115					120					125				
gca	gca	gca	cgc	acc	acc	gcg	tgg	ctt	aac	cac	ttt	gaa	aaa	gcc	aag	432
Ala	Ala	Ala	Arg	Thr	Thr	Ala	Trp	Leu	Asn	His	Phe	Glu	Lys	Ala	Lys	
		130				135					140					
gtt	caa	ggc	gtt	ggc	ttt	ggc	ttc	atc	gcc	atc	caa	cgt	ctg	gag	gaa	480
Val	Gln	Gly	Val	Gly	Phe	Gly	Phe	Ile	Ala	Ile	Gln	Arg	Leu	Glu	Glu	
					150				155					160		
gac	gag	gcg	gat	gag	aaa	tcc	gat	atc	ttg	gct	gaa	tcc	atg	acc	cag	528
Asp	Glu	Ala	Asp	Glu	Lys	Ser	Asp	Ile	Leu	Ala	Glu	Ser	Met	Thr	Gln	
				165					170					175		
tac	ttc	gag	gat	cct	ctc	ggc	cct	gaa	att	gag	gag	tac	ttc	acc	cgc	576
Tyr	Phe	Glu	Asp	Pro	Leu	Gly	Pro	Glu	Ile	Glu	Glu	Tyr	Phe	Thr	Arg	
			180					185					190			
acc	gca	tgg	ctt	cgt	gaa	caa	act	cgc	gat	tcc	att	ctg	agc	tcc	cgc	624
Thr	Ala	Trp	Leu	Arg	Glu	Gln	Thr	Arg	Asp	Ser	Ile	Leu	Ser	Ser	Arg	
		195					200					205				
ttc	aaa	gtt	cgc	cct	ggc	gtg	gcc	cgg	gaa	caa	atc	agc	ctg	gcc	gat	672
Phe	Lys	Val	Arg	Pro	Gly	Val	Ala	Arg	Glu	Gln	Ile	Ser	Leu	Ala	Asp	
	210					215					220					
gcg	gaa	gaa	ggc	atg	ggc	ttt	agt	cct	gtc	acg	ttg	agg	ctc	acc	cgc	720
Ala	Glu	Glu	Gly	Met	Gly	Phe	Ser	Pro	Val	Thr	Leu	Arg	Leu	Thr	Arg	
	225				230					235					240	
acc	gat	ggc	cct	cgt	tgg	tcc	cat	gat	gtt	gat	gag	cat	gtg	gct	tcc	768
Thr	Asp	Gly	Pro	Arg	Trp	Ser	His	Asp	Val	Asp	Glu	His	Val	Ala	Ser	
				245					250					255		
atc	gtc	gca	gga	ctt	aac	cca	cat	gga	ctc	ccc	ttt	gaa	gaa	atc	ctg	816
Ile	Val	Ala	Gly	Leu	Asn	Pro	His	Gly	Leu	Pro	Phe	Glu	Glu	Ile	Leu	
			260					265					270			
gaa	atg	tac	gcg	atg	gct	caa	ggc	atc	gag	gga	gaa	tcc	ctg	cac	aac	864
Glu	Met	Tyr	Ala	Met	Ala	Gln	Gly	Ile	Glu	Gly	Glu	Ser	Leu	His	Asn	
		275					280					285				
ggc	gcc	att	gcg	gcg	ttg	gtg	gat	ctc	atc	cgc	cac	gga	ttg	gtg	ttg	912

Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
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ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aagccgtttt 963
 Pro Ala Asp Leu Leu Asp Ser
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<210> 844

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 844

Asp Ser Gly Ile Pro Thr Gln Leu Val Glu Gly Ser Trp Phe Glu Pro
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Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60

Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80

Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95

Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110

Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu
 115 120 125

Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys
 130 135 140

Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
 145 150 155 160

Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
 165 170 175

Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190

Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205

Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220

Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240

Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255

Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270

Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285

Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
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Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 845
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(933)
 <223> FRXA00306

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gtt cgc ggg cgc acc ttt gac cgc atc atc gcc aac ccg ccg ttc gtg 96
 Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

gtg gga cca ccg gaa att ggg cat gtg tac cgc gat tcc ggc atg gat 144
 Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

cta gac ggc gcg acc gcg ttg gtg gtc aaa gaa gcc tgc gcg cat ctc 192
 Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu
 50 55 60

aac cct ggt ggc acc gct cac ctg ctc ggc gca tgg gtg cat tcc gcg 240
 Asn Pro Gly Gly Thr Ala His Leu Leu Gly Ala Trp Val His Ser Ala
 65 70 75 80

gat caa tcg tgg cag cag cgc gtt gca gaa tgg ttg ccg gat aac ggt 288
 Asp Gln Ser Trp Gln Gln Arg Val Ala Glu Trp Leu Pro Asp Asn Gly
 85 90 95

tat gtt gct tgg gtt att gag cgc gac gcc gtg agc ccc gcg cag tat 336
 Tyr Val Ala Trp Val Ile Glu Arg Asp Ala Val Ser Pro Ala Gln Tyr
 100 105 110

gtg ggc acg tgg ctt agt gat gag tcc ctc gat ctg cgt agc ccc gag 384
 Val Gly Thr Trp Leu Ser Asp Glu Ser Leu Asp Leu Arg Ser Pro Glu
 115 120 125

gca gca gca cgc acc acc gcg tgg ctt aac cac ttt gaa aaa gcc aag 432
 Ala Ala Ala Arg Thr Thr Ala Trp Leu Asn His Phe Glu Lys Ala Lys
 130 135 140

gtt caa ggc gtt ggt ttt ggt ttc atc gcc atc caa cgt ctg gag gaa 480
 Val Gln Gly Val Gly Phe Gly Phe Ile Ala Ile Gln Arg Leu Glu Glu
 145 150 155 160
 gac gag gcg gat gag aaa tcc gat atc ttg gct gaa tcc atg acc cag 528
 Asp Glu Ala Asp Glu Lys Ser Asp Ile Leu Ala Glu Ser Met Thr Gln
 165 170 175
 tac ttc gag gat cct ctc ggc cct gaa att gag gag tac ttc acc cgc 576
 Tyr Phe Glu Asp Pro Leu Gly Pro Glu Ile Glu Glu Tyr Phe Thr Arg
 180 185 190
 acc gca tgg ctt cgt gaa caa act cgc gat tcc att ctg agc tcc cgc 624
 Thr Ala Trp Leu Arg Glu Gln Thr Arg Asp Ser Ile Leu Ser Ser Arg
 195 200 205
 ttc aaa gtt cgc cct ggc gtg gcc cgg gaa caa atc agc ctg gcc gat 672
 Phe Lys Val Arg Pro Gly Val Ala Arg Glu Gln Ile Ser Leu Ala Asp
 210 215 220
 gcg gaa gaa ggc atg ggc ttt agt cct gtc acg ttg agg ctc acc cgc 720
 Ala Glu Glu Gly Met Gly Phe Ser Pro Val Thr Leu Arg Leu Thr Arg
 225 230 235 240
 acc gat ggt cct cgt tgg tcc cat gat gtt gat gag cat gtg gct tcc 768
 Thr Asp Gly Pro Arg Trp Ser His Asp Val Asp Glu His Val Ala Ser
 245 250 255
 atc gtc gca gga ctt aac cca cat gga ctc ccc ttt gaa gaa atc ctg 816
 Ile Val Ala Gly Leu Asn Pro His Gly Leu Pro Phe Glu Glu Ile Leu
 260 265 270
 gaa atg tac gcg atg gct caa ggt atc gag gga gaa tcc ctg cac aac 864
 Glu Met Tyr Ala Met Ala Gln Gly Ile Glu Gly Glu Ser Leu His Asn
 275 280 285
 ggc gcc att gcg gcg ttg gtg gat ctc atc cgc cac gga ttg gtg ttg 912
 Gly Ala Ile Ala Ala Leu Val Asp Leu Ile Arg His Gly Leu Val Leu
 290 295 300
 ccc gct gat ctt ctc gat tct taaataagga ctgattgtga aag 956
 Pro Ala Asp Leu Leu Asp Ser
 305 310

<210> 846

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 846

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Val Arg Gly Arg Thr Phe Asp Arg Ile Ile Ala Asn Pro Pro Phe Val
 20 25 30

Val Gly Pro Pro Glu Ile Gly His Val Tyr Arg Asp Ser Gly Met Asp
 35 40 45

Leu Asp Gly Ala Thr Ala Leu Val Val Lys Glu Ala Cys Ala His Leu

50					55					60					
Asn	Pro	Gly	Gly	Thr	Ala	His	Leu	Leu	Gly	Ala	Trp	Val	His	Ser	Ala
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Asp	Gln	Ser	Trp	Gln	Gln	Arg	Val	Ala	Glu	Trp	Leu	Pro	Asp	Asn	Gly
				85					90					95	
Tyr	Val	Ala	Trp	Val	Ile	Glu	Arg	Asp	Ala	Val	Ser	Pro	Ala	Gln	Tyr
			100					105					110		
Val	Gly	Thr	Trp	Leu	Ser	Asp	Glu	Ser	Leu	Asp	Leu	Arg	Ser	Pro	Glu
			115				120					125			
Ala	Ala	Ala	Arg	Thr	Thr	Ala	Trp	Leu	Asn	His	Phe	Glu	Lys	Ala	Lys
			130			135					140				
Val	Gln	Gly	Val	Gly	Phe	Gly	Phe	Ile	Ala	Ile	Gln	Arg	Leu	Glu	Glu
145				150					155					160	
Asp	Glu	Ala	Asp	Glu	Lys	Ser	Asp	Ile	Leu	Ala	Glu	Ser	Met	Thr	Gln
				165				170						175	
Tyr	Phe	Glu	Asp	Pro	Leu	Gly	Pro	Glu	Ile	Glu	Glu	Tyr	Phe	Thr	Arg
			180					185					190		
Thr	Ala	Trp	Leu	Arg	Glu	Gln	Thr	Arg	Asp	Ser	Ile	Leu	Ser	Ser	Arg
			195				200					205			
Phe	Lys	Val	Arg	Pro	Gly	Val	Ala	Arg	Glu	Gln	Ile	Ser	Leu	Ala	Asp
			210			215					220				
Ala	Glu	Glu	Gly	Met	Gly	Phe	Ser	Pro	Val	Thr	Leu	Arg	Leu	Thr	Arg
225				230						235				240	
Thr	Asp	Gly	Pro	Arg	Trp	Ser	His	Asp	Val	Asp	Glu	His	Val	Ala	Ser
				245				250						255	
Ile	Val	Ala	Gly	Leu	Asn	Pro	His	Gly	Leu	Pro	Phe	Glu	Glu	Ile	Leu
			260					265					270		
Glu	Met	Tyr	Ala	Met	Ala	Gln	Gly	Ile	Glu	Gly	Glu	Ser	Leu	His	Asn
		275					280					285			
Gly	Ala	Ile	Ala	Ala	Leu	Val	Asp	Leu	Ile	Arg	His	Gly	Leu	Val	Leu
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Pro	Ala	Asp	Leu	Leu	Asp	Ser									
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<211> 819

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(796)

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Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile Ala Asp Leu Ile Lys

215 220 225
 gtt ctt cct taaaagctgc ttttctaaac gat 819
 Val Leu Pro
 230

 <210> 848
 <211> 232
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 848
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 Gln Trp Ala Val Phe Arg Ala Ile Pro Gly Ala Leu Asp Asp Asp Arg
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 Thr Glu Val Thr Asp Gln Ala Ala Lys Phe Phe Ala Asp Leu Glu Ala
 35 40 45
 Glu Gly Lys Val Thr Val Arg Gly Ile Tyr Asn Ala Ser Gly Leu Arg
 50 55 60
 Ala Asp Ala Asp Tyr Met Ile Trp Trp His Ala Glu Glu Phe Glu Asp
 65 70 75 80
 Ile Gln Lys Ala Phe Ala Asp Phe Arg Arg Thr Thr Ile Leu Gly Gln
 85 90 95
 Val Ser Glu Val Phe Trp Ile Gly Asn Ala Leu His Arg Pro Ser Glu
 100 105 110
 Phe Asn Lys Ala His Leu Pro Ser Phe Ile Met Gly Glu Glu Ala Lys
 115 120 125
 Asp Trp Ile Thr Val Tyr Pro Phe Val Arg Ser Tyr Asp Trp Tyr Ile
 130 135 140
 Met Glu Pro Leu Lys Arg Ser Arg Ile Leu Arg Glu His Gly Gln Ala
 145 150 155 160
 Ala Val Glu Phe Pro Asp Val Arg Ala Asn Thr Val Pro Ala Phe Ala
 165 170 175
 Leu Gly Asp Tyr Glu Trp Val Leu Ala Phe Glu Ala Asp Glu Leu His
 180 185 190
 Arg Ile Val Asp Leu Met His Lys Met Arg Tyr Thr Glu Ala Arg Leu
 195 200 205
 His Val Arg Glu Glu Leu Pro Phe Ile Ser Gly Gln Arg Val Asp Ile
 210 215 220
 Ala Asp Leu Ile Lys Val Leu Pro
 225 230

 <210> 849
 <211> 1587

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1564)

<223> RXN00420

<400> 849

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				Met	Asn	Ser	Ser	His	
				1				5	

ggc	acg	tcc	agc	tcc	ggc	gct	tcg	gcc	ggg	gcc	cac	gga	gcc	ctt	ccc	163
Gly	Thr	Ser	Ser	Ser	Gly	Ala	Ser	Ala	Gly	Ala	His	Gly	Ala	Leu	Pro	
				10					15					20		

cta	gaa	gct	cag	aaa	ctg	aac	ggg	tgg	ggc	cgc	aca	gcc	ccc	acc	acc	211
Leu	Glu	Ala	Gln	Lys	Leu	Asn	Gly	Trp	Gly	Arg	Thr	Ala	Pro	Thr	Thr	
			25					30					35			

gct	gag	gta	ctt	acc	acc	cca	gac	cta	gac	atc	att	gtg	gat	gca	gtc	259
Ala	Glu	Val	Leu	Thr	Thr	Pro	Asp	Leu	Asp	Ile	Ile	Val	Asp	Ala	Val	
		40					45					50				

cgc	caa	gtc	gct	gaa	caa	aac	gac	tcc	aag	ccg	gac	tac	ctc	aag	cgc	307
Arg	Gln	Val	Ala	Glu	Gln	Asn	Asp	Ser	Lys	Pro	Asp	Tyr	Leu	Lys	Arg	
	55					60					65					

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Gly	Val	Ile	Ala	Arg	Gly	Met	Gly	Arg	Ser	Tyr	Gly	Asp	Pro	Ala	Gln	
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aac	gcc	ggg	ggc	ctt	gtc	att	gac	atg	cag	cca	ctg	aac	aaa	atc	cac	403
Asn	Ala	Gly	Gly	Leu	Val	Ile	Asp	Met	Gln	Pro	Leu	Asn	Lys	Ile	His	
				90					95					100		

tcg	att	gat	cct	gat	tct	gcg	atc	gtc	gat	gta	gat	ggc	ggc	gtc	acc	451
Ser	Ile	Asp	Pro	Asp	Ser	Ala	Ile	Val	Asp	Val	Asp	Gly	Gly	Val	Thr	
			105					110						115		

ctc	gat	cag	ctc	atg	aag	gct	gcc	ctg	cca	tat	ggc	ctc	tgg	gtt	cct	499
Leu	Asp	Gln	Leu	Met	Lys	Ala	Ala	Leu	Pro	Tyr	Gly	Leu	Trp	Val	Pro	
		120					125					130				

gtc	ctt	ccc	ggc	acc	cgc	caa	gtc	acc	atc	ggg	ggc	gca	atc	gga	cca	547
Val	Leu	Pro	Gly	Thr	Arg	Gln	Val	Thr	Ile	Gly	Gly	Ala	Ile	Gly	Pro	
	135					140					145					

gac	atc	cac	ggg	aag	aac	cac	cac	tct	gca	ggg	tcc	ttc	ggc	gac	cac	595
Asp	Ile	His	Gly	Lys	Asn	His	His	Ser	Ala	Gly	Ser	Phe	Gly	Asp	His	
150					155					160					165	

gtg	gtc	tcc	atg	gaa	ctc	ctc	gtt	gca	gac	gga	cgc	atc	ctg	cac	ctc	643
Val	Val	Ser	Met	Glu	Leu	Leu	Val	Ala	Asp	Gly	Arg	Ile	Leu	His	Leu	
				170					175					180		

gag	cca	gaa	ggc	acc	gcc	gaa	gac	cca	cag	ggc	gac	ctg	ttc	tgg	gca	691
Glu	Pro	Glu	Gly	Thr	Ala	Glu	Asp	Pro	Gln	Gly	Asp	Leu	Phe	Trp	Ala	

185							190					195					
acc gtt ggt ggc atg ggc ctg	acc ggc atc atc gtc cgt gca cgc atc	739															
Thr Val Gly Gly Met Gly Leu	Thr Gly Ile Ile Val Arg Ala Arg Ile																
200	205 210																
cgc atg acc aag acg gaa acc gcc tac ttc att gcg gac acc gac cgc	787																
Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile Ala Asp Thr Asp Arg																	
215 220 225																	
acc aac aac ttg gaa gaa acc gtt gcg ttc cac tcc gac gga tca gag	835																
Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His Ser Asp Gly Ser Glu																	
230 235 240 245																	
cac aac tac acc tat tct tct gcg tgg ttc gat gtc atc agc cct gag	883																
His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp Val Ile Ser Pro Glu																	
250 255 260																	
cca aag ctt ggc cgc tcc acc atc tcc cgt ggt tcc ctg gca aca ctt	931																
Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly Ser Leu Ala Thr Leu																	
265 270 275																	
gct cag ctg gaa gaa ttg gca cca aag ctg gcc aag gat cca ctg aag	979																
Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala Lys Asp Pro Leu Lys																	
280 285 290																	
ttt aat gct cca cag ctg atg aag gtt cca gat atc ttc cca tcc tgg																	
1027 Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp Ile Phe Pro Ser Trp																	
295 300 305																	
act ttg aac aag ctg acc ctt tcc gca gtc ggt gtg gct tac tac gcc																	
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1123 Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe Tyr																	
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caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc aag																	
1171 Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser Lys																	
345 350 355																	
ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag cct																	
1219 Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu Pro																	
360 365 370																	
ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc gca																	
1267 Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser Ala																	
375 380 385																	
ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg tcc																	
1315 Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu Ser																	
390 395 400 405																	

tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc cca
 1363
 Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg Pro
 410 415 420

ggt ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa ttc
 1411
 Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu Phe
 425 430 435

ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag aac
 1459
 Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu Asn
 440 445 450

ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga aat
 1507
 Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg Asn
 455 460 465

gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga ctt
 1555
 Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg Leu
 470 475 480 485

gag ctt tct taagaaaggg cttgaactaa aca
 1587
 Glu Leu Ser

<210> 850
 <211> 488
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 850
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 20 25 30
 Thr Ala Pro Thr Thr Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile
 35 40 45
 Ile Val Asp Ala Val Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro
 50 55 60
 Asp Tyr Leu Lys Arg Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr
 65 70 75 80
 Gly Asp Pro Ala Gln Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro
 85 90 95
 Leu Asn Lys Ile His Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val
 100 105 110
 Asp Gly Gly Val Thr Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr
 115 120 125

Gly Leu Trp Val Pro Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly
 130 135 140
 Gly Ala Ile Gly Pro Asp Ile His Gly Lys Asn His His Ser Ala Gly
 145 150 155 160
 Ser Phe Gly Asp His Val Val Ser Met Glu Leu Leu Val Ala Asp Gly
 165 170 175
 Arg Ile Leu His Leu Glu Pro Glu Gly Thr Ala Glu Asp Pro Gln Gly
 180 185 190
 Asp Leu Phe Trp Ala Thr Val Gly Gly Met Gly Leu Thr Gly Ile Ile
 195 200 205
 Val Arg Ala Arg Ile Arg Met Thr Lys Thr Glu Thr Ala Tyr Phe Ile
 210 215 220
 Ala Asp Thr Asp Arg Thr Asn Asn Leu Glu Glu Thr Val Ala Phe His
 225 230 235 240
 Ser Asp Gly Ser Glu His Asn Tyr Thr Tyr Ser Ser Ala Trp Phe Asp
 245 250 255
 Val Ile Ser Pro Glu Pro Lys Leu Gly Arg Ser Thr Ile Ser Arg Gly
 260 265 270
 Ser Leu Ala Thr Leu Ala Gln Leu Glu Glu Leu Ala Pro Lys Leu Ala
 275 280 285
 Lys Asp Pro Leu Lys Phe Asn Ala Pro Gln Leu Met Lys Val Pro Asp
 290 295 300
 Ile Phe Pro Ser Trp Thr Leu Asn Lys Leu Thr Leu Ser Ala Val Gly
 305 310 315 320
 Val Ala Tyr Tyr Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn
 325 330 335
 Leu Thr Gln Phe Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg
 340 345 350
 Gly Tyr Gly Ser Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr
 355 360 365
 Glu Ala Val Glu Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser
 370 375 380
 Gly His Tyr Ser Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn
 385 390 395 400
 Arg Ala Pro Leu Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp
 405 410 415
 Phe Pro Ile Arg Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys
 420 425 430
 Arg Val Met Glu Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg
 435 440 445
 Thr Ser Ala Glu Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp

450 455 460
 Leu Lys Thr Arg Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp
 465 470 475 480
 Met Ser Arg Arg Leu Glu Leu Ser
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<210> 851
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> FRXA00420

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 gcc atg ggt gca cca gcg aaa aac cag gtg aaa aac ctc acc cag ttc 96
 Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe
 20 25 30
 tac caa cca ctg gat ttg atc ggc gaa tgg aac cgt ggc tac ggc tcc 144
 Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser
 35 40 45
 aag ggc ttc ctg cag tac cag ttc gtg gtc ccc aca gaa gct gtt gag 192
 Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu
 50 55 60
 cct ttc aag gac atc atc cgc gat atg caa aag tcc ggc cac tac tcc 240
 Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser
 65 70 75 80
 gca ctc aac gtg ttc aaa ctg ttt ggc cca ggc aac cgc gca cca ctg 288
 Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu
 85 90 95
 tcc tac cca atg cca ggc tgg aac gtc tgc gtt gac ttc cct atc cgc 336
 Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg
 100 105 110
 cca ggt ctg gga gct ttc ttg gac gat ctg gac aag cgc gtc atg gaa 384
 Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu
 115 120 125
 ttc ggc ggc cgc ctc tac ctg gcc aag gaa tcc cgc acc tcc gca gag 432
 Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu
 130 135 140
 aac ttc cac gcc atg tac cca ggt atg gaa ggc tgg ttg aag act cga 480
 Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg
 145 150 155 160
 aat gag atc gac cca acc gga gtc ttt gca tct gac atg tcc cgc cga 528

Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg
 165 170 175

ctt gag ctt tct taagaaaggg cttgaactaa aca
 Leu Glu Leu Ser
 180

563

<210> 852

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 852

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Ala Met Gly Ala Pro Ala Lys Asn Gln Val Lys Asn Leu Thr Gln Phe
 20 25 30

Tyr Gln Pro Leu Asp Leu Ile Gly Glu Trp Asn Arg Gly Tyr Gly Ser
 35 40 45

Lys Gly Phe Leu Gln Tyr Gln Phe Val Val Pro Thr Glu Ala Val Glu
 50 55 60

Pro Phe Lys Asp Ile Ile Arg Asp Met Gln Lys Ser Gly His Tyr Ser
 65 70 75 80

Ala Leu Asn Val Phe Lys Leu Phe Gly Pro Gly Asn Arg Ala Pro Leu
 85 90 95

Ser Tyr Pro Met Pro Gly Trp Asn Val Cys Val Asp Phe Pro Ile Arg
 100 105 110

Pro Gly Leu Gly Ala Phe Leu Asp Asp Leu Asp Lys Arg Val Met Glu
 115 120 125

Phe Gly Gly Arg Leu Tyr Leu Ala Lys Glu Ser Arg Thr Ser Ala Glu
 130 135 140

Asn Phe His Ala Met Tyr Pro Gly Met Glu Gly Trp Leu Lys Thr Arg
 145 150 155 160

Asn Glu Ile Asp Pro Thr Gly Val Phe Ala Ser Asp Met Ser Arg Arg
 165 170 175

Leu Glu Leu Ser
 180

<210> 853

<211> 622

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(622)

<223> FRXA00426

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ttcaccacct gaaaattttc gggggtaacc tttaaaggcg atg aac agt tct cac 115
 Met Asn Ser Ser His
 1 5

ggc acg tcc agc tcc ggc gct tcg gcc ggt gcc cac gga gcc ctt ccc 163
 Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala His Gly Ala Leu Pro
 10 15 20

cta gaa gct cag aaa ctg aac ggt tgg ggc cgc aca gcc ccc acc acc 211
 Leu Glu Ala Gln Lys Leu Asn Gly Trp Gly Arg Thr Ala Pro Thr Thr
 25 30 35

gct gag gta ctt acc acc cca gac cta gac atc att gtg gat gca gtc 259
 Ala Glu Val Leu Thr Thr Pro Asp Leu Asp Ile Ile Val Asp Ala Val
 40 45 50

cgc caa gtc gct gaa caa aac gac tcc aag ccg gac tac ctc aag cgc 307
 Arg Gln Val Ala Glu Gln Asn Asp Ser Lys Pro Asp Tyr Leu Lys Arg
 55 60 65

ggc gtg att gcc cgt ggc atg ggt cgt tcc tat ggt gac cca gcc caa 355
 Gly Val Ile Ala Arg Gly Met Gly Arg Ser Tyr Gly Asp Pro Ala Gln
 70 75 80 85

aac gcc ggt ggc ctt gtc att gac atg cag cca ctg aac aaa atc cac 403
 Asn Ala Gly Gly Leu Val Ile Asp Met Gln Pro Leu Asn Lys Ile His
 90 95 100

tcg att gat cct gat tct gcg atc gtc gat gta gat ggc ggc gtc acc 451
 Ser Ile Asp Pro Asp Ser Ala Ile Val Asp Val Asp Gly Gly Val Thr
 105 110 115

ctc gat cag ctc atg aag gct gcc ctg cca tat ggc ctc tgg gtt cct 499
 Leu Asp Gln Leu Met Lys Ala Ala Leu Pro Tyr Gly Leu Trp Val Pro
 120 125 130

gtc ctt ccc ggc acc cgc caa gtc acc atc ggt ggc gca atc gga cca 547
 Val Leu Pro Gly Thr Arg Gln Val Thr Ile Gly Gly Ala Ile Gly Pro
 135 140 145

gac atc cac ggt aag aac cac cac tct gca ggt tcc ttc ggc gac cac 595
 Asp Ile His Gly Lys Asn His His Ser Ala Gly Ser Phe Gly Asp His
 150 155 160 165

gtg gtc tcc atg gaa ctc ctc gtt gca 622
 Val Val Ser Met Glu Leu Leu Val Ala
 170

<210> 854

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 854

Met Asn Ser Ser His Gly Thr Ser Ser Ser Gly Ala Ser Ala Gly Ala
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			20					25					30		
Thr	Ala	Pro	Thr	Thr	Ala	Glu	Val	Leu	Thr	Thr	Pro	Asp	Leu	Asp	Ile
		35					40					45			
Ile	Val	Asp	Ala	Val	Arg	Gln	Val	Ala	Glu	Gln	Asn	Asp	Ser	Lys	Pro
	50					55					60				
Asp	Tyr	Leu	Lys	Arg	Gly	Val	Ile	Ala	Arg	Gly	Met	Gly	Arg	Ser	Tyr
65					70					75					80
Gly	Asp	Pro	Ala	Gln	Asn	Ala	Gly	Gly	Leu	Val	Ile	Asp	Met	Gln	Pro
				85					90					95	
Leu	Asn	Lys	Ile	His	Ser	Ile	Asp	Pro	Asp	Ser	Ala	Ile	Val	Asp	Val
			100					105					110		
Asp	Gly	Gly	Val	Thr	Leu	Asp	Gln	Leu	Met	Lys	Ala	Ala	Leu	Pro	Tyr
		115					120					125			
Gly	Leu	Trp	Val	Pro	Val	Leu	Pro	Gly	Thr	Arg	Gln	Val	Thr	Ile	Gly
	130					135					140				
Gly	Ala	Ile	Gly	Pro	Asp	Ile	His	Gly	Lys	Asn	His	His	Ser	Ala	Gly
145					150					155					160
Ser	Phe	Gly	Asp	His	Val	Val	Ser	Met	Glu	Leu	Leu	Val	Ala		
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<210> 855
<211> 930
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101) .. (907)  
<223> RXN00708
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taccgateccc ctccctgaa gtttcgctaa cctggcgtac  atg  act  ctt  tcc  ctt      115
                                     Met Thr Leu Ser Leu
                                     1      5

cct cca att ggt ttc ggc acc gtt cat ctt gat ggc gca cct ggc gtt      163
Pro Pro Ile Gly Phe Gly Thr Val His Leu Asp Gly Ala Pro Gly Val
                10                        15                        20

gaa gcc atc gct act gcc att gat gct ggt tac cgc ctc atc gac acc      211
Glu Ala Ile Ala Thr Ala Ile Asp Ala Gly Tyr Arg Leu Ile Asp Thr
                25                        30                        35

gcg tac aac tat gaa aat gaa ggt acc gtg ggc aag gct gtc cgc gag      259
Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly Lys Ala Val Arg Glu
                40                        45                        50

tcg ggt gtc ccc cgc gag gaa ttg att gtt acc agt aag ctc cct ggc      307

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Ser	Gly	Val	Pro	Arg	Glu	Glu	Leu	Ile	Val	Thr	Ser	Lys	Leu	Pro	Gly	
55						60					65					
cgc	ttc	cat	gct	cgc	gat	cta	gga	cgc	gtc	cgc	att	gag	gaa	agt	cta	355
Arg	Phe	His	Ala	Arg	Asp	Leu	Gly	Arg	Val	Arg	Ile	Glu	Glu	Ser	Leu	
70					75					80					85	
tac	cgc	ctc	aac	tta	gat	tac	atc	gat	ctc	ctc	ttg	att	cac	tgg	cct	403
Tyr	Arg	Leu	Asn	Leu	Asp	Tyr	Ile	Asp	Leu	Leu	Leu	Ile	His	Trp	Pro	
				90					95					100		
aat	ccc	agc	aag	gat	ctc	tac	gtc	gag	gcg	tgg	gaa	acg	ctg	att	gaa	451
Asn	Pro	Ser	Lys	Asp	Leu	Tyr	Val	Glu	Ala	Trp	Glu	Thr	Leu	Ile	Glu	
			105					110					115			
gtc	cgc	gat	gct	ggc	ctg	gtc	aag	cac	atc	gga	gtg	tct	aac	ttc	ctt	499
Val	Arg	Asp	Ala	Gly	Leu	Val	Lys	His	Ile	Gly	Val	Ser	Asn	Phe	Leu	
			120				125						130			
cca	aat	cac	att	gat	cgc	ctg	cgc	cgc	gaa	acc	ggt	gaa	ctg	ccg	gcc	547
Pro	Asn	His	Ile	Asp	Arg	Leu	Arg	Arg	Glu	Thr	Gly	Glu	Leu	Pro	Ala	
			135			140					145					
gtt	aac	cag	atc	gag	ttg	cac	ccc	tat	ttc	ccg	cag	gtg	gag	cag	gta	595
Val	Asn	Gln	Ile	Glu	Leu	His	Pro	Tyr	Phe	Pro	Gln	Val	Glu	Gln	Val	
150					155					160					165	
gat	ttc	cac	gat	gag	ctg	ggc	atc	att	acc	gag	gcc	tgg	agc	ccg	ctc	643
Asp	Phe	His	Asp	Glu	Leu	Gly	Ile	Ile	Thr	Glu	Ala	Trp	Ser	Pro	Leu	
				170					175					180		
agc	aac	ggt	cgc	gga	ctc	gtc	gaa	gag	cca	ttg	ctc	aag	gaa	atc	ggc	691
Ser	Asn	Gly	Arg	Gly	Leu	Val	Glu	Glu	Pro	Leu	Leu	Lys	Glu	Ile	Gly	
			185					190					195			
gag	cgc	tac	ggg	gtc	ggc	agc	ggc	gaa	atc	gcc	ctc	gct	tgg	cat	cac	739
Glu	Arg	Tyr	Gly	Val	Gly	Ser	Gly	Glu	Ile	Ala	Leu	Ala	Trp	His	His	
			200				205					210				
gcc	agg	gga	atc	gtt	ccg	att	cca	cgc	tcc	acc	aac	ccg	gcc	agg	cag	787
Ala	Arg	Gly	Ile	Val	Pro	Ile	Pro	Arg	Ser	Thr	Asn	Pro	Ala	Arg	Gln	
			215			220					225					
cgc	agc	aac	ttg	gag	gcg	gta	aag	att	tcg	ctt	atc	gac	gaa	gac	gtc	835
Arg	Ser	Asn	Leu	Glu	Ala	Val	Lys	Ile	Ser	Leu	Ile	Asp	Glu	Asp	Val	
230					235					240					245	
cag	gcg	att	acc	gct	ttg	gcg	cgc	aaa	aac	ggc	cgg	atc	aaa	gat	caa	883
Gln	Ala	Ile	Thr	Ala	Leu	Ala	Arg	Lys	Asn	Gly	Arg	Ile	Lys	Asp	Gln	
				250					255					260		
gat	cca	gcc	gtc	tat	gaa	gaa	ttc	tagatagtt	catcaagg	ttc	ccg					930
Asp	Pro	Ala	Val	Tyr	Glu	Glu	Phe									
			265													

<210> 856

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 856

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Arg Leu Ile Asp Thr Ala Tyr Asn Tyr Glu Asn Glu Gly Thr Val Gly
          35          40          45

Lys Ala Val Arg Glu Ser Gly Val Pro Arg Glu Glu Leu Ile Val Thr
          50          55          60

Ser Lys Leu Pro Gly Arg Phe His Ala Arg Asp Leu Gly Arg Val Arg
          65          70          75          80

Ile Glu Glu Ser Leu Tyr Arg Leu Asn Leu Asp Tyr Ile Asp Leu Leu
          85          90          95

Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val Glu Ala Trp
          100          105          110

Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys His Ile Gly
          115          120          125

Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg Arg Glu Thr
          130          135          140

Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro Tyr Phe Pro
          145          150          155          160

Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile Ile Thr Glu
          165          170          175

Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu Glu Pro Leu
          180          185          190

Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly Glu Ile Ala
          195          200          205

Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro Arg Ser Thr
          210          215          220

Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys Ile Ser Leu
          225          230          235          240

Ile Asp Glu Asp Val Gln Ala Ile Thr Ala Leu Ala Arg Lys Asn Gly
          245          250          255

Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
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<211> 695

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (672)

<223> FRXA00708

<400> 857

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Thr	Val	Gly	Lys	Ala	Val	Arg	Glu	Ser	Gly	Val	Pro	Arg	Glu	Glu	Leu	
1				5					10					15		
att	gtt	acc	agt	aag	ctc	cct	ggc	cgc	ttc	cat	gct	cgc	gat	cta	gga	96
Ile	Val	Thr	Ser	Lys	Leu	Pro	Gly	Arg	Phe	His	Ala	Arg	Asp	Leu	Gly	
			20					25					30			
cgc	gtc	cgc	att	gag	gaa	agt	cta	tac	cgc	ctc	aac	tta	gat	tac	atc	144
Arg	Val	Arg	Ile	Glu	Glu	Ser	Leu	Tyr	Arg	Leu	Asn	Leu	Asp	Tyr	Ile	
		35					40					45				
gat	ctc	ctc	ttg	att	cac	tgg	cct	aat	ccc	agc	aag	gat	ctc	tac	gtc	192
Asp	Leu	Leu	Leu	Ile	His	Trp	Pro	Asn	Pro	Ser	Lys	Asp	Leu	Tyr	Val	
	50					55					60					
gag	gcg	tgg	gaa	acg	ctg	att	gaa	gtc	cgc	gat	gct	ggc	ctg	gtc	aag	240
Glu	Ala	Trp	Glu	Thr	Leu	Ile	Glu	Val	Arg	Asp	Ala	Gly	Leu	Val	Lys	
65					70				75						80	
cac	atc	gga	gtg	tct	aac	ttc	ctt	cca	aat	cac	att	gat	cgc	ctg	cgc	288
His	Ile	Gly	Val	Ser	Asn	Phe	Leu	Pro	Asn	His	Ile	Asp	Arg	Leu	Arg	
				85					90					95		
cgc	gaa	acc	ggt	gaa	ctg	ccg	gcc	gtt	aac	cag	atc	gag	ttg	cac	ccc	336
Arg	Glu	Thr	Gly	Glu	Leu	Pro	Ala	Val	Asn	Gln	Ile	Glu	Leu	His	Pro	
			100					105					110			
tat	ttc	ccg	cag	gtg	gag	cag	gta	gat	ttc	cac	gat	gag	ctg	ggc	atc	384
Tyr	Phe	Pro	Gln	Val	Glu	Gln	Val	Asp	Phe	His	Asp	Glu	Leu	Gly	Ile	
		115					120					125				
att	acc	gag	gcc	tgg	agc	ccg	ctc	agc	aac	ggt	cgc	gga	ctc	gtc	gaa	432
Ile	Thr	Glu	Ala	Trp	Ser	Pro	Leu	Ser	Asn	Gly	Arg	Gly	Leu	Val	Glu	
	130					135					140					
gag	cca	ttg	ctc	aag	gaa	atc	ggc	gag	cgc	tac	ggg	gtc	ggc	agc	ggc	480
Glu	Pro	Leu	Leu	Lys	Glu	Ile	Gly	Glu	Arg	Tyr	Gly	Val	Gly	Ser	Gly	
145					150				155						160	
gaa	atc	gcc	ctc	gct	tgg	cat	cac	gcc	agg	gga	atc	gtt	ccg	att	cca	528
Glu	Ile	Ala	Leu	Ala	Trp	His	His	Ala	Arg	Gly	Ile	Val	Pro	Ile	Pro	
				165					170					175		
cgc	tcc	acc	aac	ccg	gcc	agg	cag	cgc	agc	aac	ttg	gag	gcg	gta	aag	576
Arg	Ser	Thr	Asn	Pro	Ala	Arg	Gln	Arg	Ser	Asn	Leu	Glu	Ala	Val	Lys	
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 <213> Corynebacterium glutamicum

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 Asp Leu Leu Leu Ile His Trp Pro Asn Pro Ser Lys Asp Leu Tyr Val
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 Glu Ala Trp Glu Thr Leu Ile Glu Val Arg Asp Ala Gly Leu Val Lys
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 His Ile Gly Val Ser Asn Phe Leu Pro Asn His Ile Asp Arg Leu Arg
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 Arg Glu Thr Gly Glu Leu Pro Ala Val Asn Gln Ile Glu Leu His Pro
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 Tyr Phe Pro Gln Val Glu Gln Val Asp Phe His Asp Glu Leu Gly Ile
 115 120 125
 Ile Thr Glu Ala Trp Ser Pro Leu Ser Asn Gly Arg Gly Leu Val Glu
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 Glu Pro Leu Leu Lys Glu Ile Gly Glu Arg Tyr Gly Val Gly Ser Gly
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 Glu Ile Ala Leu Ala Trp His His Ala Arg Gly Ile Val Pro Ile Pro
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 Arg Ser Thr Asn Pro Ala Arg Gln Arg Ser Asn Leu Glu Ala Val Lys
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 Lys Asn Gly Arg Ile Lys Asp Gln Asp Pro Ala Val Tyr Glu Glu Phe
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<223> RXA02373

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Gln Ser Leu Met Asp Gln Lys Asn Lys Leu Ser Lys Ser Glu Gly Ile
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Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr Ala Ala Ile Tyr Gly
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Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn Asp Arg His Leu Asp
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Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys Leu Gly Leu Asp Tyr
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Val Ala Ala Trp Lys Gly Leu Glu Lys Leu Gly Asp Arg Ala Arg Ser
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Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu Glu Lys Leu Leu Ala
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Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile Glu Leu His Pro Ala
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 Lys Thr Val Thr Lys Ser Arg Met Val Glu Asn Ile Asp Val Phe Asp
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 Phe Glu Leu Ser Asp Glu Glu Met Ala Ala Ile Thr Ala Leu Glu Arg
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 Pro Gln Leu Gly Phe Gly Val Phe Lys Val Asp Pro Asp Glu Ala Glu
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 Arg Val Val Thr Glu Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr
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 Ala Ala Ile Tyr Gly Asn Glu Glu Gly Val Gly Arg Ala Ile Ala Lys
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 Ser Gly Ile Pro Arg Glu Glu Leu Phe Ile Thr Thr Lys Leu Trp Asn
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 Asp Arg His Leu Asp Val Glu Ala Ala Phe Glu Glu Ser Leu Gln Lys
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 Asp Arg Ala Arg Ser Ile Gly Val Cys Asn Phe Leu Pro Glu His Leu
 165 170 175
 Glu Lys Leu Leu Ala Glu Ala Thr Thr Val Pro Ala Ile Asn Gln Ile
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 Glu Leu His Pro Ala Leu Gln Gln Arg Asp Ala Val Glu Ala Ser Leu
 195 200 205
 Ala Ala Gly Ile Thr Val Glu Ser Trp Gly Pro Leu Gly Gln Gly Arg
 210 215 220
 Phe Asp Leu Gly Ala Glu Glu Pro Ile Ala Ala Ala Lys Asn His
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 Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys
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 Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn
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Ser	Ala	Lys	Arg	Ala	Phe	Glu	Ser	Tyr	Arg	Leu	Thr	Thr	Pro	Glu	Val	
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Arg	Ala	Asp	Phe	Leu	Asp	Ser	Ile	Ala	Asp	Asn	Ile	Asp	Ala	Leu	Ser	
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Gly	Glu	Ile	Val	Gln	Arg	Ala	Ser	Leu	Glu	Thr	Gly	Leu	Gly	Thr	Thr	
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Arg	Leu	Thr	Gly	Glu	Val	Ala	Arg	Thr	Ser	Asn	Gln	Leu	Arg	Leu	Phe	
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Gly	Pro	Arg	Ile	Asp	Leu	Arg	Gln	Arg	Gln	Val	Pro	Leu	Gly	Pro	Val	
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gcg	gta	ttc	ggg	gca	agc	aac	ttc	ccc	gtc	gct	ttc	tct	act	gct	ggg	595
Ala	Val	Phe	Gly	Ala	Ser	Asn	Phe	Pro	Val	Ala	Phe	Ser	Thr	Ala	Gly	
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Gly	Asp	Thr	Ala	Ser	Ala	Leu	Ala	Ala	Gly	Cys	Pro	Val	Val	Phe	Lys	
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gcg	cat	aat	gcg	cac	cct	gga	aca	gct	gag	ctc	gtc	ggg	caa	gcg	gtg	691
Ala	His	Asn	Ala	His	Pro	Gly	Thr	Ala	Glu	Leu	Val	Gly	Gln	Ala	Val	
			185					190					195			
cgg	gga	gcc	gtc	gaa	aag	cat	gag	ttt	gat	gct	ggg	gtg	ttt	aac	ctt	739
Arg	Gly	Ala	Val	Glu	Lys	His	Glu	Phe	Asp	Ala	Gly	Val	Phe	Asn	Leu	
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Val	Tyr	Gly	Arg	Gly	Val	Glu	Ile	Gly	Gln	Glu	Leu	Ala	Ala	Asp	Pro	
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Asn	Ile	Thr	Ala	Ile	Gly	Phe	Thr	Gly	Ser	Arg	Gln	Gly	Gly	Leu	Ala	
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Leu	Ser	Gln	Thr	Ala	Phe	Ser	Arg	Pro	Val	Pro	Val	Pro	Val	Phe	Ala	
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Glu	Met	Ser	Ala	Thr	Asn	Pro	Val	Phe	Val	Phe	Pro	Gly	Ala	Leu	Ala	
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Asp	Leu	Asp	Ala	Ser	Ser	Ser	Leu	Ala	Glu	Ala	Phe	Thr	Ala	Ser	Val	

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Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln Glu Val Ser Lys Leu 425 430 435		
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1651

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Ile Asp Arg
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<210> 862

<211> 520

<212> PRT

<213> Corynebacterium glutamicum

<400> 862

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35 40 45

Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu
50 55 60

Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn
65 70 75 80

Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr
85 90 95

Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn
100 105 110

Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg
115 120 125

Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val
130 135 140

Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala
145 150 155 160

Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys
165 170 175

Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu
180 185 190

Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala
195 200 205

Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu
 210 215 220
 Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg
 225 230 235 240
 Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro
 245 250 255
 Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe
 260 265 270
 Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala
 275 280 285
 Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro
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 325 330 335
 Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala
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 Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu
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 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu
 405 410 415
 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln
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 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val
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 Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile
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 His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val
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 Gly Thr Leu Ala Ile Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr
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 <223> RXS00419

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 Met Leu Asn Ala Val
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ggc aaa gcc caa aac att ctc ctt ctt ggt gga acc tct gag atc ggt 163
 Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly Thr Ser Glu Ile Gly
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 Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly Pro Ser His Val Thr
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 Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp Ala Ala Val Ala Glu
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ggc gac gtt gac gta gca atc gtg gct ttc ggc atc ctc ggc gac aac 403
 Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly Ile Leu Gly Asp Asn
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 Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val Glu Ala Thr Thr Val
 105 110 115

aac tac acc gcc ggc gtt tcc gta ggt gta ctg ctg ggc cag aaa ttt 499
 Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu Leu Gly Gln Lys Phe
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 Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu Ser Ser Val Ala Gly
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 Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly Ser Ala Lys Ala Gly
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 Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala Leu Arg Gly Ser Gly
 170 175 180

gcc aac gta ttg gtg gtt cgc cca ggc cag gta cgc acc aag atg tcc 691
 Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys Met Ser
 185 190 195

gca gat ggt ggc gaa gcc cca ctg acc gtc aac cgc gaa gac gtg gca 739
 Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp Val Ala
 200 205 210

gat gct gtt tat gat gca gtg gtg aac aag aag gac atc atc ttt gtc 787
 Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys Asp Ile Ile Phe Val
 215 220 225

cac cca ctg ttc cag tac gtc tct ttt gcg ttc caa ttc att ccg cga 835
 His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile Pro Arg
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gca atc ttc cgc aag ctg ccg ttc taacggaagt tacggaagtt acg 882
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<210> 864

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 864

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Pro Ser His Val Thr Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp
 35 40 45

Ala Ala Val Ala Glu Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val
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Val Asp Phe Asp Ala Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp
 65 70 75 80

Ala Ala Phe Glu Asn Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly
 85 90 95

Ile Leu Gly Asp Asn Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val
 100 105 110

Glu Ala Thr Thr Val Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu
 115 120 125

Leu Gly Gln Lys Phe Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu
 130 135 140

Ser Ser Val Ala Gly Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly
 145 150 155 160

Ser Ala Lys Ala Gly Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala
 165 170 175

Leu Arg Gly Ser Gly Ala Asn Val Leu Val Val Arg Pro Gly Gln Val
 180 185 190

Arg Thr Lys Met Ser Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn
 195 200 205

Arg Glu Asp Val Ala Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys
 210 215 220

Asp Ile Ile Phe Val His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe
 225 230 235 240

Gln Phe Ile Pro Arg Ala Ile Phe Arg Lys Leu Pro Phe
 245 250

<210> 865

<211> 1673

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1650)

<223> RXC00416

<400> 865

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Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp	
20 25 30	
cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc	144
Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly	
35 40 45	
ttg tcg gac atg aac tac atc gat atg cct acc ttc tac cct gct gga	192
Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly	
50 55 60	
tgg ttc tgg ctc ggt ggt cgc ttg gcc aat ctt ttg ggg ctg ccc ggt	240
Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly	
65 70 75 80	
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Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala	
85 90 95	
tct gtg tta gtt cca gtg tgg cag cgc atc acc ggt tcc ctg ccg gtg	336
Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val	
100 105 110	
gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat	384
Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn	
115 120 125	
tcc gaa gag ccc tac gct gca atc gtt gcg atg ggt att cca gcg atg	432
Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met	

130	135	140	
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ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe 165 170 175			528
acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala 180 185 190			576
gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu 195 200 205			624
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agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val 260 265 270			816
cgt ttc cac aac aat gag gtg cgc gcg atg tgg gtc ggc atc gca gtg Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val 275 280 285			864
ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn 290 295 300			912
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1152
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370 375 380

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Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala
385 390 395 400

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1248
Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu
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Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr
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1344
Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro
435 440 445

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1392
Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile
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cga agc tgg gat gag ttg gct gat cct caa caa ttc agc gac gcc ttg
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Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu
465 470 475 480

aac acc tct cca tgg acg atc cct gag gtg ttc atc ttc cgt ggc tcc
1488
Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser
485 490 495

atc gat gat cct gac gcc ggt tgg aaa tac gac gtg gct gaa gat ctg
1536
Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu
500 505 510

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1584
Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
515 520 525

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1632
Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
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1673
Val Val Thr His Asn Glu
545 550

<210> 866
 <211> 550
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 866

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Gln	Gly	Phe	Arg	Thr	Gln	Phe	Leu	Thr	Arg	Met	Ala	Asp	Asp	Ile	Gly
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Leu	Ser	Asp	Met	Asn	Tyr	Ile	Asp	Met	Pro	Thr	Phe	Tyr	Pro	Ala	Gly
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Trp	Phe	Trp	Leu	Gly	Gly	Arg	Leu	Ala	Asn	Leu	Leu	Gly	Leu	Pro	Gly
65					70					75					80
Trp	Glu	Ala	Phe	Gln	Pro	Trp	Ala	Ile	Val	Ser	Met	Ala	Val	Ala	Ala
				85					90					95	
Ser	Val	Leu	Val	Pro	Val	Trp	Gln	Arg	Ile	Thr	Gly	Ser	Leu	Pro	Val
			100					105					110		
Ala	Thr	Gly	Ile	Ala	Leu	Val	Thr	Thr	Cys	Ile	Ile	Leu	Ala	Met	Asn
		115					120					125			
Ser	Glu	Glu	Pro	Tyr	Ala	Ala	Ile	Val	Ala	Met	Gly	Ile	Pro	Ala	Met
	130					135					140				
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Gly	Gly	Ile	Ile	Tyr	Leu	Gly	Val	Ser	Ala	Thr	Phe	Tyr	Thr	Leu	Phe
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Thr	Gly	Ala	Ile	Ala	Leu	Ser	Ala	Val	Ala	Val	Cys	Ile	Val	Val	Ala
			180					185					190		
Ala	Ile	Val	Gln	Arg	Ser	Ile	Lys	Pro	Leu	Leu	Trp	Leu	Ala	Val	Leu
		195					200					205			
Gly	Gly	Gly	Ser	Ile	Val	Ile	Ala	Leu	Ile	Ser	Trp	Gly	Pro	Tyr	Leu
	210					215					220				
Leu	Ala	Ser	Ile	Asn	Gly	Ala	Glu	Arg	Ser	Gly	Asp	Ser	Ala	Thr	His
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Tyr	Leu	Pro	Leu	Glu	Gly	Thr	Gln	Phe	Pro	Val	Pro	Phe	Leu	Ala	Ser
				245					250					255	
Ser	Val	Val	Gly	Leu	Leu	Cys	Leu	Val	Gly	Leu	Ile	Tyr	Leu	Val	Val
			260					265					270		
Arg	Phe	His	Asn	Asn	Glu	Val	Arg	Ala	Met	Trp	Val	Gly	Ile	Ala	Val
		275					280					285			
Phe	Tyr	Ala	Trp	Met	Gly	Met	Ser	Met	Ala	Ile	Thr	Leu	Leu	Gly	Asn

290	295	300
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala 305 310 315 320		
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr 325 330 335		
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr 340 345 350		
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln 355 360 365		
Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp 370 375 380		
Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala 385 390 395 400		
Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu 405 410 415		
Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr 420 425 430		
Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro 435 440 445		
Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile 450 455 460		
Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu 465 470 475 480		
Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser 485 490 495		
Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu 500 505 510		
Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro 515 520 525		
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101) .. (1036)
 <223> RXC02206

<400> 867

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Met Val Gly Ser Ser
1 5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
10 15 20

ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn
25 30 35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val
40 45 50

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Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser
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Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu
70 75 80 85

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90 95 100

gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg 451
Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val
105 110 115

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Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu
120 125 130

gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga 547
Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly
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Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala
150 155 160 165

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Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu
170 175 180

ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta 691
Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu
185 190 195

ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act 739
Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr
200 205 210

gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca 787
Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr

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215	220	225	
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Gly Arg Asp Ala Glu Val	Gln Ser Tyr Leu Asp	Asn Arg Gly Arg Ile	
230	235	240 245	
att gtc gat gct ctt gat	act gca gcc aaa gga	tta ggc att agc ccc	883
Ile Val Asp Ala Leu Asp	Thr Ala Ala Lys Gly	Leu Gly Ile Ser Pro	
	250	255 260	
gct gtc aca gcc acc acc	tgg gtg cgt gat cgt	ccc gga gtg aca gct	931
Ala Val Thr Ala Thr Thr	Trp Val Arg Asp Arg	Pro Gly Val Thr Ala	
	265	270 275	
gtc atc gtg ggc gct cgc	aca cat gaa cag ctg	tca cat ctt ctc aag	979
Val Ile Val Gly Ala Arg	Thr His Glu Gln Leu	Ser His Leu Leu Lys	
	280	285 290	
gcg gaa tcg gtg act ttg	cca aca cca atc aca	caa gcc ctt gat gat	
1027			
Ala Glu Ser Val Thr Leu	Pro Thr Pro Ile Thr	Gln Ala Leu Asp Asp	
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1059			
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<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 868

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Lys Ala Phe Ile Asn Ser	Gly Gly Thr Leu Ile	Asp Val Ser Pro Asn
	35	40 45
Tyr Thr Thr Gly Val Ala	Glu Glu Met Leu Gly	Thr Met Leu Asp Ala
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Glu Val Ser Arg Ser Ala	Val Val Ile Ser Ser	Ser Ala Gly Val Asn
	65	70 75 80
Pro Ala Leu Pro Leu Gly	Arg Arg Val Asp Cys	Ser Arg Arg Asn Leu
	85	90 95
Ile Ala Gln Leu Asp Val	Thr Leu Arg Ala Leu	Asn Thr Asp Tyr Leu
	100	105 110
Asp Leu Trp Ser Val Gly	Tyr Trp Asp Glu Gly	Thr Pro Pro His Glu
	115	120 125
Val Ala Asp Thr Leu Asp	Tyr Ala Val Arg Thr	Gly Arg Val Arg Tyr
	130	135 140

Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala
145 150 155 160

Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln
165 170 175

Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro
180 185 190

Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly
195 200 205

Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser
210 215 220

Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
225 230 235 240

Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
245 250 255

Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg
260 265 270

Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu
275 280 285

Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr
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Gln Ala Leu Asp Asp Val Ser Leu
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<210> 869

<211> 621

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(598)

<223> RXS03074

<400> 869

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Met Thr Gln Ser Ala
1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
25 30 35

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Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
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 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165
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<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 870

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 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr

	100		105		110
Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr					
	115		120		125
Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe					
	130		135		140
Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr					
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					160
Glu Ala Pro Ile Lys Gln					
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<210> 871

<211> 621

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(598)

<223> FRXA02906

<400> 871

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	Met Thr Gln Ser Ala	
	1 5	

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac	163
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn	
	10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa	211
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu	
	25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc	259
Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu	
	40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc	307
Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile	
	55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca	355
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala	
	70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca	403
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala	
	90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc	451
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala	
	105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga	499
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Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130

gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165

cag taatttggtt tgacgacgca gta 621
 Gln

<210> 872
 <211> 166
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 872
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Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160

Glu Ala Pro Ile Lys Gln
 165

<210> 873
 <211> 1752
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1729)

<223> RXA02315

<400> 873

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				Met	Ser	Ser	Thr	Pro	
				1				5	

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Ala	Gln	Asp	Leu	Ala	Arg	Ala	Val	Ile	Asp	Ser	Leu	Ala	Pro	His	Val	
			10					15						20		

act	gac	gtg	gtg	tta	tgc	cca	gga	tcc	agg	aac	tca	ccg	ttg	tcg	ctt	211
Thr	Asp	Val	Val	Leu	Cys	Pro	Gly	Ser	Arg	Asn	Ser	Pro	Leu	Ser	Leu	
			25					30					35			

gag	ttg	ctg	gcg	cgg	cag	gat	ctg	cgt	gtc	cat	gtg	cgt	atc	gac	gag	259
Glu	Leu	Leu	Ala	Arg	Gln	Asp	Leu	Arg	Val	His	Val	Arg	Ile	Asp	Glu	
		40					45					50				

cgc	agc	gcc	tca	ttt	ttg	gcg	ctg	tcc	cta	gcg	cgt	acc	cag	gcc	cgg	307
Arg	Ser	Ala	Ser	Phe	Leu	Ala	Leu	Ser	Leu	Ala	Arg	Thr	Gln	Ala	Arg	
	55					60					65					

ccg	gtg	gct	gtg	gtg	atg	acc	tcc	ggc	acg	gct	gta	gct	aac	tgc	ctg	355
Pro	Val	Ala	Val	Val	Met	Thr	Ser	Gly	Thr	Ala	Val	Ala	Asn	Cys	Leu	
70					75					80					85	

cct	gct	gtt	gct	gaa	gct	gcg	cat	gcc	cat	atc	ccg	ttg	att	gtg	ctc	403
Pro	Ala	Val	Ala	Glu	Ala	Ala	His	Ala	His	Ile	Pro	Leu	Ile	Val	Leu	
				90					95					100		

tct	gct	gac	cgt	cct	gca	cat	ttg	gtg	gga	acg	ggg	gcg	agc	caa	acg	451
Ser	Ala	Asp	Arg	Pro	Ala	His	Leu	Val	Gly	Thr	Gly	Ala	Ser	Gln	Thr	
			105					110					115			

att	aac	cag	acc	ggc	att	ttt	ggc	gat	ctt	gca	ccg	acg	gtc	ggc	atc	499
Ile	Asn	Gln	Thr	Gly	Ile	Phe	Gly	Asp	Leu	Ala	Pro	Thr	Val	Gly	Ile	
		120					125					130				

act	gag	ctg	gat	cag	gta	gcg	cag	att	gct	gaa	agc	ctt	gct	cag	ggg	547
Thr	Glu	Leu	Asp	Gln	Val	Ala	Gln	Ile	Ala	Glu	Ser	Leu	Ala	Gln	Gly	
	135					140					145					

gct	tcc	cag	att	ccg	cgt	cat	ttc	aat	ctt	gca	ctt	gat	gtt	cct	ttg	595
Ala	Ser	Gln	Ile	Pro	Arg	His	Phe	Asn	Leu	Ala	Leu	Asp	Val	Pro	Leu	
150					155					160					165	

gtt	gct	cct	gaa	ctg	cca	gag	ctt	cat	ggc	gag	gca	gtt	gga	gca	tca	643
Val	Ala	Pro	Glu	Leu	Pro	Glu	Leu	His	Gly	Glu	Ala	Val	Gly	Ala	Ser	
			170					175						180		

tgg	acg	cat	cgc	tgg	atc	aac	cac	ggc	gag	gtg	acc	gtg	gac	ctg	ggg	691
Trp	Thr	His	Arg	Trp	Ile	Asn	His	Gly	Glu	Val	Thr	Val	Asp	Leu	Gly	
			185					190					195			

gag	cac	acc	ctc	gtg	att	gcc	ggc	gat	gaa	gca	tgg	gaa	gtg	gaa	ggg	739
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Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	Trp	Glu	Val	Glu	Gly		
		200					205					210					
ctg	gaa	gat	gtg	ccc	acc	atc	gct	gaa	cct	act	gca	cca	aag	cct	tat	787	
Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	Ala	Pro	Lys	Pro	Tyr		
	215					220					225						
aat	ccg	gtg	cac	cca	ctg	gct	gct	gaa	atc	ttg	ctg	aag	gag	cag	gtc	835	
Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu	Leu	Lys	Glu	Gln	Val		
230					235					240					245		
tcc	gcg	gaa	ggc	tat	gtg	gta	aac	acc	agg	cct	gat	cat	gtg	atc	gtg	883	
Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro	Asp	His	Val	Ile	Val		
				250					255					260			
gtg	gga	cac	ccc	acg	ctg	cac	cgc	gga	gtg	ttg	aag	ttg	atg	tca	gat	931	
Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	Lys	Leu	Met	Ser	Asp		
			265					270					275				
cct	ggc	att	aaa	tta	act	gtg	ctt	tca	cgc	acc	gat	atc	atc	act	gat	979	
Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	Asp	Ile	Ile	Thr	Asp		
		280					285					290					
ccc	ggc	cgc	cat	gcc	gat	cag	gtg	ggc	agc	aca	gtg	aaa	gtc	acc	ggc		
1027																	
Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr	Val	Lys	Val	Thr	Gly		
	295					300					305						
acc	cag	gaa	aag	cag	tgg	cta	aag	atc	tgt	tcg	gca	gca	tca	gaa	ctt		
1075																	
Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser	Ala	Ala	Ser	Glu	Leu		
310					315					320					325		
gcg	gcc	gat	ggt	gtg	cgt	gac	gtc	ctg	gac	aac	caa	gaa	ttc	ggt	ttc		
1123																	
Ala	Ala	Asp	Gly	Val	Arg	Asp	Val	Leu	Asp	Asn	Gln	Glu	Phe	Gly	Phe		
				330					335					340			
acc	ggc	ctc	cat	gtt	gcc	gca	gcc	gtg	gcg	gat	acc	tta	ggc	acc	ggc		
1171																	
Thr	Gly	Leu	His	Val	Ala	Ala	Ala	Val	Ala	Asp	Thr	Leu	Gly	Thr	Gly		
			345					350					355				
gat	act	ctc	ttt	gct	gca	gca	tcc	aac	tca	atc	cgt	gac	ctc	tcc	ctg		
1219																	
Asp	Thr	Leu	Phe	Ala	Ala	Ala	Ser	Asn	Ser	Ile	Arg	Asp	Leu	Ser	Leu		
		360					365					370					
gtg	ggt	atg	cct	ttt	gat	ggc	gtg	gat	acc	ttc	tcc	cca	cga	ggt	gtc		
1267																	
Val	Gly	Met	Pro	Phe	Asp	Gly	Val	Asp	Thr	Phe	Ser	Pro	Arg	Gly	Val		
	375					380					385						
gca	ggc	att	gat	ggt	tct	gtt	gct	caa	gca	atc	ggc	act	tca	ctt	gct		
1315																	
Ala	Gly	Ile	Asp	Gly	Ser	Val	Ala	Gln	Ala	Ile	Gly	Thr	Ser	Leu	Ala		
390					395					400					405		
gtg	cag	tcc	cgc	cac	ccc	gat	gaa	atc	cgc	gcg	cca	cgc	act	gtg	gcc		
1363																	
Val	Gln	Ser	Arg	His	Pro	Asp	Glu	Ile	Arg	Ala	Pro	Arg	Thr	Val	Ala		

410	415	420
ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc 1411		
Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile 425 430 435		
ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac 1459		
Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn 440 445 450		
gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt 1507		
Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly 455 460 465		
ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc 1555		
Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser 470 475 480 485		
atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac 1603		
Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp 490 495 500		
aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc 1651		
Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser 505 510 515		
gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca 1699		
Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala 520 525 530		
caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt 1749		
Gln Gln Gln Ala Leu Met Asp Thr Val His 535 540		

gcg
1752

<210> 874
 <211> 543
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 874
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 Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn
 20 25 30
 Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His
 35 40 45

Val	Arg	Ile	Asp	Glu	Arg	Ser	Ala	Ser	Phe	Leu	Ala	Leu	Ser	Leu	Ala
	50					55					60				
Arg	Thr	Gln	Ala	Arg	Pro	Val	Ala	Val	Val	Met	Thr	Ser	Gly	Thr	Ala
	65				70					75					80
Val	Ala	Asn	Cys	Leu	Pro	Ala	Val	Ala	Glu	Ala	Ala	His	Ala	His	Ile
				85					90					95	
Pro	Leu	Ile	Val	Leu	Ser	Ala	Asp	Arg	Pro	Ala	His	Leu	Val	Gly	Thr
			100					105					110		
Gly	Ala	Ser	Gln	Thr	Ile	Asn	Gln	Thr	Gly	Ile	Phe	Gly	Asp	Leu	Ala
		115					120					125			
Pro	Thr	Val	Gly	Ile	Thr	Glu	Leu	Asp	Gln	Val	Ala	Gln	Ile	Ala	Glu
	130					135					140				
Ser	Leu	Ala	Gln	Gly	Ala	Ser	Gln	Ile	Pro	Arg	His	Phe	Asn	Leu	Ala
145					150					155					160
Leu	Asp	Val	Pro	Leu	Val	Ala	Pro	Glu	Leu	Pro	Glu	Leu	His	Gly	Glu
				165					170					175	
Ala	Val	Gly	Ala	Ser	Trp	Thr	His	Arg	Trp	Ile	Asn	His	Gly	Glu	Val
			180					185					190		
Thr	Val	Asp	Leu	Gly	Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala
		195					200					205			
Trp	Glu	Val	Glu	Gly	Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr
	210					215					220				
Ala	Pro	Lys	Pro	Tyr	Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu
225					230					235					240
Leu	Lys	Glu	Gln	Val	Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro
				245					250					255	
Asp	His	Val	Ile	Val	Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu
			260					265					270		
Lys	Leu	Met	Ser	Asp	Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr
		275					280					285			
Asp	Ile	Ile	Thr	Asp	Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr
	290					295					300				
Val	Lys	Val	Thr	Gly	Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser
305					310					315					320
Ala	Ala	Ser	Glu	Leu	Ala	Ala	Asp	Gly	Val	Arg	Asp	Val	Leu	Asp	Asn
				325					330					335	
Gln	Glu	Phe	Gly	Phe	Thr	Gly	Leu	His	Val	Ala	Ala	Ala	Val	Ala	Asp
			340					345					350		
Thr	Leu	Gly	Thr	Gly	Asp	Thr	Leu	Phe	Ala	Ala	Ala	Ser	Asn	Ser	Ile
		355					360					365			
Arg	Asp	Leu	Ser	Leu	Val	Gly	Met	Pro	Phe	Asp	Gly	Val	Asp	Thr	Phe

370	375	380
Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile 385 390 395 400		
Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala 405 410 415		
Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile 420 425 430		
Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr 435 440 445		
Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu 450 455 460		
Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr 465 470 475 480		
Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu 485 490 495		
His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp 500 505 510		
Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg 515 520 525		
Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His 530 535 540		

<210> 875

<211> 1080

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1057)

<223> RXA02319

<400> 875

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agaccttggc catttcggca gaggcttaag gttaaagatt atg agc aac tac agc	115
Met Ser Asn Tyr Ser	5
1	

acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt	163
Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe	
10 15 20	

gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc	211
Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg	
25 30 35	

gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat	259
Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn	
40 45 50	

gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His 55 60 65	307
gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly 70 75 80 85	355
ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln 90 95 100	403
cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg 105 110 115	451
gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys 120 125 130	499
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg 135 140 145	547
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly 150 155 160 165	595
ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg 170 175 180	643
caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp 185 190 195	691
gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn 200 205 210	739
gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met 215 220 225	787
caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu 230 235 240 245	835
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr 250 255 260	883
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu 265 270 275	931
atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met 280 285 290	979

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa
 1027
 Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu
 295 300 305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atgggggtcct
 1077
 Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
 310 315

aaa
 1080

<210> 876
 <211> 319
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 876
 Met Ser Asn Tyr Ser Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala
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Thr Val Pro Gly Phe Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His
 20 25 30

Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg
 35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr
 50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu
 65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys
 85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala
 100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp
 115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val
 130 135 140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn
 145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu
 165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp
 180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met
 195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr
 210 215 220

Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp
 225 230 235 240
 His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn
 245 250 255
 Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu
 260 265 270
 Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr
 275 280 285
 Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe
 290 295 300
 Leu Glu Lys Arg Glu Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
 305 310 315

<210> 877

<211> 1017

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(994)

<223> RXS00393

<400> 877

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 Met Ser His Thr Glu
 1 5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
 10 15 20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
 25 30 35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
 40 45 50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
 Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
 55 60 65

tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
 70 75 80 85

cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
 90 95 100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
105 110 115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
120 125 130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
135 140 145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
150 155 160 165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
170 175 180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
185 190 195

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
200 205 210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
215 220 225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
230 235 240 245

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
250 255 260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc 931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile
265 270 275

ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg 979
Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu
280 285 290

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1017
Ala Leu Ala Phe Ser
295

<210> 878

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 878

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Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp	35	40	45
Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val	50	55	60
Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp	65	70	75
Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys	85	90	95
Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala	100	105	110
Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly	115	120	125
Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro	130	135	140
Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly	145	150	155
Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser	165	170	175
Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly	180	185	190
Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr	195	200	205
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys	210	215	220
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu	225	230	235
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu	245	250	255
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp	260	265	270
Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala	275	280	285
Val Leu Thr Gly Leu Ala Leu Ala Phe Ser	290	295	

<210> 879

<211> 1005

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(982)

<223> FRXA00393

<400> 879

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				Met	Ser	His	Thr	Glu	
				1				5	

ccc	cag	ccg	aat	tct	gta	act	ttg	tcc	gat	tgg	att	caa	ggc	gca	cgc	163
Pro	Gln	Pro	Asn	Ser	Val	Thr	Leu	Ser	Asp	Trp	Ile	Gln	Gly	Ala	Arg	
			10					15						20		

ccg	cgt	acc	tgg	gca	aat	gcg	ttc	gcg	cct	gtc	att	gcc	ggg	tca	ggg	211
Pro	Arg	Thr	Trp	Ala	Asn	Ala	Phe	Ala	Pro	Val	Ile	Ala	Gly	Ser	Gly	
			25					30					35			

gtc	gcc	gct	ttt	cat	gat	ggg	ttt	gtg	tgg	tgg	aag	gcc	ttg	ctg	gcg	259
Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp	Lys	Ala	Leu	Leu	Ala	
		40					45					50				

ctt	gtc	gtg	gcg	tgg	gct	ttg	atc	atc	ggg	gtg	aat	tac	gcc	aat	gat	307
Leu	Val	Val	Ala	Trp	Ala	Leu	Ile	Ile	Gly	Val	Asn	Tyr	Ala	Asn	Asp	
		55				60					65					

tac	tct	gat	ggc	att	cgt	ggc	acc	gat	gaa	gac	cgc	acc	ggg	cct	ctg	355
Tyr	Ser	Asp	Gly	Ile	Arg	Gly	Thr	Asp	Glu	Asp	Arg	Thr	Gly	Pro	Leu	
70					75				80						85	

cga	ctc	act	ggg	tct	ggg	ttg	gct	gag	ccg	aag	aaa	gtg	aaa	gct	gcg	403
Arg	Leu	Thr	Gly	Ser	Gly	Leu	Ala	Glu	Pro	Lys	Lys	Val	Lys	Ala	Ala	
				90					95					100		

gcg	ttt	att	tct	ttc	ggg	atc	gca	ggg	gtc	gcc	ggc	acc	gcg	ctg	agc	451
Ala	Phe	Ile	Ser	Phe	Gly	Ile	Ala	Gly	Val	Ala	Gly	Thr	Ala	Leu	Ser	
			105					110					115			

ctg	ttg	agc	gcg	tgg	tgg	ctg	atc	ctc	atc	ggc	atc	ctg	tgt	gtg	ctg	499
Leu	Leu	Ser	Ala	Trp	Trp	Leu	Ile	Leu	Ile	Gly	Ile	Leu	Cys	Val	Leu	
		120				125						130				

ggc	gcg	tgg	ttc	tac	acc	ggc	ggg	aaa	aat	cct	tat	ggg	tac	cgc	ggg	547
Gly	Ala	Trp	Phe	Tyr	Thr	Gly	Gly	Lys	Asn	Pro	Tyr	Gly	Tyr	Arg	Gly	
		135				140					145					

ctc	ggc	gag	att	gct	gtg	ttc	atc	ttc	ttc	ggc	ctc	gtc	gcg	gtc	atg	595
Leu	Gly	Glu	Ile	Ala	Val	Phe	Ile	Phe	Phe	Gly	Leu	Val	Ala	Val	Met	
150					155					160					165	

gga	acg	cag	ttc	acc	caa	acc	ggg	tcc	gtc	agc	tgg	gcc	ggg	ttg	gcc	643
Gly	Thr	Gln	Phe	Thr	Gln	Thr	Gly	Ser	Val	Ser	Trp	Ala	Gly	Leu	Ala	
				170				175						180		

gcc	gca	gtt	ggc	gtg	ggg	tcg	atg	tct	gct	ggc	gtg	aac	ttg	gcc	aac	691
Ala	Ala	Val	Gly	Val	Gly	Ser	Met	Ser	Ala	Gly	Val	Asn	Leu	Ala	Asn	
			185					190					195			

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
 200 205 210
 gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
 215 220 225
 att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
 230 235 240 245
 cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
 250 255 260
 ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser
 265 270 275
 gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979
 Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro Cys Ser Arg Ala Trp
 280 285 290

cat tagcggttag ctaaaacgct ttt
 1005
 His

<210> 880
 <211> 294
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 880
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 Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
 20 25 30
 Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
 35 40 45
 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
 50 55 60
 Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
 65 70 75 80
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
 85 90 95
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
 100 105 110
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
 115 120 125
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro

130	135	140
Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly 145 150 155 160		
Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser 165 170 175		
Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly 180 185 190		
Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr 195 200 205		
Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys 210 215 220		
Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu 225 230 235 240		
Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu 245 250 255		
Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp 260 265 270		
Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro 275 280 285		
Cys Ser Arg Ala Trp His 290		

<210> 881
 <211> 843
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(820)
 <223> RXA00391

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 tttcctcccc atccctgtac aagataaaac ccgtgcacag ttg ctg cgc gat tct 115
 Leu Leu Arg Asp Ser
 1 5
 caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc 163
 Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala
 10 15 20
 act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg 211
 Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu
 25 30 35
 aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa 259
 Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu
 40 45 50

ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag 307
 Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln
 55 60 65

gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat 355
 Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp
 70 75 80 85

ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa 403
 Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu
 90 95 100

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln
 105 110 115

tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu
 120 125 130

ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg
 135 140 145

att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser
 150 155 160 165

tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly
 170 175 180

gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met
 185 190 195

att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn
 200 205 210

gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile
 215 220 225

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
 230 235 240

tgc 843

<210> 882

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 882

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile
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Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala
 20 25 30
 Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln
 35 40 45
 Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His
 50 55 60
 Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu
 65 70 75 80
 Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala
 85 90 95
 Gly Ala Ala Ala Glu Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser
 100 105 110
 Leu Thr Pro Met Gln Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile
 115 120 125
 Glu Ala Leu Lys Leu Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu
 130 135 140
 Ser Lys Gln Ala Arg Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val
 145 150 155 160
 Thr Thr Tyr Gly Ser Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly
 165 170 175
 Lys Pro Ile Pro Gly Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu
 180 185 190
 Leu Gly Gly Pro Met Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His
 195 200 205
 Pro Asp Phe Ala Asn Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu
 210 215 220
 Leu His Asp Gly Ile Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
 225 230 235 240

<210> 883

<211> 384

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(361)

<223> RXS02908

<400> 883

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 gtgactggtc gcgtggatac ccgtcattga ttccgggtgga ttg aag ttg cac cca 115
 Leu Lys Leu His Pro

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<220>
<221> CDS
<222> (101)..(682)
<223> RXA00997
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<400> 885

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gcaccatgggt gctgaacaag tagccctata ctcggggcacc atg act aca tgg aaa 115
                                   Met Thr Thr Trp Lys
                                   1 5

gag ctc aca gat aac aac cca gcg cac tca gaa aac tac gcg cag cgc 163
Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu Asn Tyr Ala Gln Arg
                                   10 15 20

tgg cga aac ctc gcc gca gca ggc aat gat att tac ggc gaa gcc cgc 211
Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile Tyr Gly Glu Ala Arg
                                   25 30 35

ctc att gat gcc atg gca ccc agg gga gcg aaa atc ttg gat gct ggc 259
Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys Ile Leu Asp Ala Gly
                                   40 45 50

tgc ggc cag gga cgc atc ggt ggc tac ctg tcc aag caa ggc cac gat 307
Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser Lys Gln Gly His Asp
                                   55 60 65

gtt cta ggc aca gac ctt gat ccc atc ctg att gat tac gcc aag cag 355
Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile Asp Tyr Ala Lys Gln
                                   70 75 80 85

gac ttt cca gaa gct cgc tgg gtg gtg gga gat ctc tct gtt gat cag 403
Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp Leu Ser Val Asp Gln
                                   90 95 100

atc tca gag act gat ttt gat ctc att gtc tcc gcc ggc aac gtc atg 451
Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser Ala Gly Asn Val Met
                                   105 110 115

ggc ttt ctc gct gag gat ggt cgc gaa cct gca cta gcc aac att cac 499
Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala Leu Ala Asn Ile His
                                   120 125 130

cgc gca ctg ggc gcc gat ggc cgc gct gtc atc ggt ttc ggc gca gga 547
Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile Gly Phe Gly Ala Gly
                                   135 140 145

cgt gga tgg gtc ttt gga gac ttc ctc gaa gtc gca gaa cgc gtg ggc 595
Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val Ala Glu Arg Val Gly
                                   150 155 160 165

ctc gag ttg gaa aat gct ttt gag tct tgg gat ctt aag cct ttt gtc 643
Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp Leu Lys Pro Phe Val
                                   170 175 180

caa ggc tct gag ttc tta gtg gcg gta ttt acc aag aag taacacctct 692
Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr Lys Lys
                                   185 190

atcttgcacc tga 705

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<210> 886

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 886

Met Thr Thr Trp Lys Glu Leu Thr Asp Asn Asn Pro Ala His Ser Glu
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Asn Tyr Ala Gln Arg Trp Arg Asn Leu Ala Ala Ala Gly Asn Asp Ile
 20 25 30

Tyr Gly Glu Ala Arg Leu Ile Asp Ala Met Ala Pro Arg Gly Ala Lys
 35 40 45

Ile Leu Asp Ala Gly Cys Gly Gln Gly Arg Ile Gly Gly Tyr Leu Ser
 50 55 60

Lys Gln Gly His Asp Val Leu Gly Thr Asp Leu Asp Pro Ile Leu Ile
 65 70 75 80

Asp Tyr Ala Lys Gln Asp Phe Pro Glu Ala Arg Trp Val Val Gly Asp
 85 90 95

Leu Ser Val Asp Gln Ile Ser Glu Thr Asp Phe Asp Leu Ile Val Ser
 100 105 110

Ala Gly Asn Val Met Gly Phe Leu Ala Glu Asp Gly Arg Glu Pro Ala
 115 120 125

Leu Ala Asn Ile His Arg Ala Leu Gly Ala Asp Gly Arg Ala Val Ile
 130 135 140

Gly Phe Gly Ala Gly Arg Gly Trp Val Phe Gly Asp Phe Leu Glu Val
 145 150 155 160

Ala Glu Arg Val Gly Leu Glu Leu Glu Asn Ala Phe Glu Ser Trp Asp
 165 170 175

Leu Lys Pro Phe Val Gln Gly Ser Glu Phe Leu Val Ala Val Phe Thr
 180 185 190

Lys Lys

<210> 887

<211> 861

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(838)

<223> RXA02189

<400> 887

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attgagccag ttctctcaag caaacgata ctggtgggat gtg gac gcg gcc gac 115
 Val Asp Ala Ala Asp
 1 5

tat cac gaa cgc cac cct tct tat tta ggc acg gat tcc gct cac ggc	163
Tyr His Glu Arg His Pro Ser Tyr Leu Gly Thr Asp Ser Ala His Gly	
10 15 20	
gag ttc tac tgg tgc ccc gag atg ctg cat gaa aaa gat gta cgt ctt	211
Glu Phe Tyr Trp Cys Pro Glu Met Leu His Glu Lys Asp Val Arg Leu	
25 30 35	
ctt ggc act ccc gca gca ctc tcc ggc aag aaa att tta gag atc ggt	259
Leu Gly Thr Pro Ala Ala Leu Ser Gly Lys Lys Ile Leu Glu Ile Gly	
40 45 50	
tgc ggc tcg gca ccg tgt gct cgg tgg ctg gcc aat gat gtt ccg aat	307
Cys Gly Ser Ala Pro Cys Ala Arg Trp Leu Ala Asn Asp Val Pro Asn	
55 60 65	
gcc ttt gtc acc gct ttc gac att tct tca caa atg ctc aaa tac gca	355
Ala Phe Val Thr Ala Phe Asp Ile Ser Ser Gln Met Leu Lys Tyr Ala	
70 75 80 85	
ggt cac gac cat aac gta cac ctc gta cag gcc gat gca atg tca ctc	403
Gly His Asp His Asn Val His Leu Val Gln Ala Asp Ala Met Ser Leu	
90 95 100	
ccc tac gcc gac agt tcc ttt gac gtg gtc ttt tcc gtt ttc ggc gcc	451
Pro Tyr Ala Asp Ser Ser Phe Asp Val Val Phe Ser Val Phe Gly Ala	
105 110 115	
atc ccc ttt gtg gag gat tcc gcc gca ctc atg aag gaa atc gcg cgc	499
Ile Pro Phe Val Glu Asp Ser Ala Ala Leu Met Lys Glu Ile Ala Arg	
120 125 130	
gtc ctc aaa ccc ggc gga cgc ctc att ttc tcc atc acc cac ccg atg	547
Val Leu Lys Pro Gly Gly Arg Leu Ile Phe Ser Ile Thr His Pro Met	
135 140 145	
cgc tgg att ttc ctc gac gat ccc ggc ccc gca ggc ctc acc gcg atc	595
Arg Trp Ile Phe Leu Asp Asp Pro Gly Pro Ala Gly Leu Thr Ala Ile	
150 155 160 165	
acc agc tac ttc gac cag cgc ggc tac gtc gaa gaa gac gag gaa acc	643
Thr Ser Tyr Phe Asp Gln Arg Gly Tyr Val Glu Glu Asp Glu Glu Thr	
170 175 180	
ggt gct tta agc tat gcg gaa cag cac cgc acc atg ggc gcg cgg atc	691
Gly Ala Leu Ser Tyr Ala Glu Gln His Arg Thr Met Gly Ala Arg Ile	
185 190 195	
aat gag ctt atc gac gcc tcc ctc cac tta gat cac ctc atc gaa cca	739
Asn Glu Leu Ile Asp Ala Ser Leu His Leu Asp His Leu Ile Glu Pro	
200 205 210	
gaa tgg cca gat gag ttg gaa gaa aac tgg ggc caa tgg tca cca ctt	787
Glu Trp Pro Asp Glu Leu Glu Glu Asn Trp Gly Gln Trp Ser Pro Leu	
215 220 225	
cga gga aag ctc ttc ccc ggg aca gca atc ttc ctc gcc acg tac cgc	835
Arg Gly Lys Leu Phe Pro Gly Thr Ala Ile Phe Leu Ala Thr Tyr Arg	
230 235 240 245	
ccc taaaaaacca acggcgctca ttt	861

Pro

<210> 888

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 888

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Asp	Ser	Ala	His	Gly	Glu	Phe	Tyr	Trp	Cys	Pro	Glu	Met	Leu	His	Glu
			20					25					30		

Lys	Asp	Val	Arg	Leu	Leu	Gly	Thr	Pro	Ala	Ala	Leu	Ser	Gly	Lys	Lys
		35					40					45			

Ile	Leu	Glu	Ile	Gly	Cys	Gly	Ser	Ala	Pro	Cys	Ala	Arg	Trp	Leu	Ala
	50					55					60				

Asn	Asp	Val	Pro	Asn	Ala	Phe	Val	Thr	Ala	Phe	Asp	Ile	Ser	Ser	Gln
65					70					75					80

Met	Leu	Lys	Tyr	Ala	Gly	His	Asp	His	Asn	Val	His	Leu	Val	Gln	Ala
				85					90					95	

Asp	Ala	Met	Ser	Leu	Pro	Tyr	Ala	Asp	Ser	Ser	Phe	Asp	Val	Val	Phe
			100					105					110		

Ser	Val	Phe	Gly	Ala	Ile	Pro	Phe	Val	Glu	Asp	Ser	Ala	Ala	Leu	Met
		115					120					125			

Lys	Glu	Ile	Ala	Arg	Val	Leu	Lys	Pro	Gly	Gly	Arg	Leu	Ile	Phe	Ser
	130					135					140				

Ile	Thr	His	Pro	Met	Arg	Trp	Ile	Phe	Leu	Asp	Asp	Pro	Gly	Pro	Ala
145					150					155					160

Gly	Leu	Thr	Ala	Ile	Thr	Ser	Tyr	Phe	Asp	Gln	Arg	Gly	Tyr	Val	Glu
				165					170					175	

Glu	Asp	Glu	Glu	Thr	Gly	Ala	Leu	Ser	Tyr	Ala	Glu	Gln	His	Arg	Thr
			180					185					190		

Met	Gly	Ala	Arg	Ile	Asn	Glu	Leu	Ile	Asp	Ala	Ser	Leu	His	Leu	Asp
		195					200					205			

His	Leu	Ile	Glu	Pro	Glu	Trp	Pro	Asp	Glu	Leu	Glu	Glu	Asn	Trp	Gly
	210					215					220				

Gln	Trp	Ser	Pro	Leu	Arg	Gly	Lys	Leu	Phe	Pro	Gly	Thr	Ala	Ile	Phe
225					230					235					240

Leu	Ala	Thr	Tyr	Arg	Pro
				245	

<210> 889

<211> 813

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(790)

<223> RXA02311

<400> 889

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                               Val Ala Lys Ala Asp
                               1 5

tta gac aag gac ccc ttc gac gta gcg tca atg ttc gat gac gtc gga 163
Leu Asp Lys Asp Pro Phe Asp Val Ala Ser Met Phe Asp Asp Val Gly
                               10 15 20

aag aac tac gat ctc acc aat acc gtg ctt tct ttt ggt cag gac cgt 211
Lys Asn Tyr Asp Leu Thr Asn Thr Val Leu Ser Phe Gly Gln Asp Arg
                               25 30 35

gtg tgg cga aag cgc act agg cag cgc ctg gac ctc aag cca ggg gag 259
Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp Leu Lys Pro Gly Glu
                               40 45 50

aag gtg ctt gat cta gct gca gga aca gcc gtt tcc acc gtg gag ttg 307
Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val Ser Thr Val Glu Leu
                               55 60 65

gca aaa tcc ggc gcg ttt tgt gtg gcg tgt gat ttc tcc cag ggc atg 355
Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp Phe Ser Gln Gly Met
70 75 80 85

ctc gcc gca ggt aaa gac cgc gat gtg tcc aag gtt gtg ggc gat ggc 403
Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys Val Val Gly Asp Gly
90 95 100

atg cag ttg ccg ttt gca gac aac agc ttt gat gct gtg acc att tct 451
Met Gln Leu Pro Phe Ala Asp Asn Ser Phe Asp Ala Val Thr Ile Ser
105 110 115

tat ggt ctg cgc aat att cac gat ttc cgc gct ggc ctg aaa gaa atg 499
Tyr Gly Leu Arg Asn Ile His Asp Phe Arg Ala Gly Leu Lys Glu Met
120 125 130

gcc cgc gtg act aaa cct ggt gga cgc ctc acc gtg gcg gag ttc tcc 547
Ala Arg Val Thr Lys Pro Gly Gly Arg Leu Thr Val Ala Glu Phe Ser
135 140 145

acc ccc gtg atc cct gtg ttc ggc acc gtg tac aag gag tac ctc atg 595
Thr Pro Val Ile Pro Val Phe Gly Thr Val Tyr Lys Glu Tyr Leu Met
150 155 160 165

cgc ctg ctg ccc cag gcg gcg cgc gca gta tcg tcc aac ccg gag gcc 643
Arg Leu Leu Pro Gln Ala Ala Arg Ala Val Ser Ser Asn Pro Glu Ala
170 175 180

tac att tac ctg gct gat tcc atc cgc gca tgg cct agc cag gcg gaa 691
Tyr Ile Tyr Leu Ala Asp Ser Ile Arg Ala Trp Pro Ser Gln Ala Glu

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185	190	195	
cta gca cgg gag atc aac cag aat ggt tgg tca gat tgc ggt tgg cag			739
Leu Ala Arg Glu Ile Asn Gln Asn Gly Trp Ser Asp Cys Gly Trp Gln			
200	205	210	
aac ctg acc ttc ggc atc gtc gcg ctg cac tcg gcg att aaa cca gag			787
Asn Leu Thr Phe Gly Ile Val Ala Leu His Ser Ala Ile Lys Pro Glu			
215	220	225	
aac tagtcgagtc ccacagaggg gag			813
Asn			
230			
<210> 890			
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<213> Corynebacterium glutamicum			
<400> 890			
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Phe Asp Asp Val Gly Lys Asn Tyr Asp Leu Thr Asn Thr Val Leu Ser			
20	25	30	
Phe Gly Gln Asp Arg Val Trp Arg Lys Arg Thr Arg Gln Arg Leu Asp			
35	40	45	
Leu Lys Pro Gly Glu Lys Val Leu Asp Leu Ala Ala Gly Thr Ala Val			
50	55	60	
Ser Thr Val Glu Leu Ala Lys Ser Gly Ala Phe Cys Val Ala Cys Asp			
65	70	75	80
Phe Ser Gln Gly Met Leu Ala Ala Gly Lys Asp Arg Asp Val Ser Lys			
85	90	95	
Val Val Gly Asp Gly Met Gln Leu Pro Phe Ala Asp Asn Ser Phe Asp			
100	105	110	
Ala Val Thr Ile Ser Tyr Gly Leu Arg Asn Ile His Asp Phe Arg Ala			
115	120	125	
Gly Leu Lys Glu Met Ala Arg Val Thr Lys Pro Gly Gly Arg Leu Thr			
130	135	140	
Val Ala Glu Phe Ser Thr Pro Val Ile Pro Val Phe Gly Thr Val Tyr			
145	150	155	160
Lys Glu Tyr Leu Met Arg Leu Leu Pro Gln Ala Ala Arg Ala Val Ser			
165	170	175	
Ser Asn Pro Glu Ala Tyr Ile Tyr Leu Ala Asp Ser Ile Arg Ala Trp			
180	185	190	
Pro Ser Gln Ala Glu Leu Ala Arg Glu Ile Asn Gln Asn Gly Trp Ser			
195	200	205	
Asp Cys Gly Trp Gln Asn Leu Thr Phe Gly Ile Val Ala Leu His Ser			

210	215	220
Ala Ile Lys Pro Glu Asn		
225	230	
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<223> RXN02912		
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gatattgaaa tgacgtattc ctgattgggc tgaaaaaatct gtg aca tca cct gaa 115		
Val Thr Ser Pro Glu 1 5		
tta caa aac atc ctt aac aat tat tgg agc ggc agg gca gag gct tac 163		
Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly Arg Ala Glu Ala Tyr 10 15 20		
cac ctc aac caa acc caa agc gag cgt gca caa ttt gaa cgc ccc atc 211		
His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln Phe Glu Arg Pro Ile 25 30 35		
tgg gaa aag gtg tgg tcg aag gct ttg cct atc gtg tcg gaa gaa gcg 259		
Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile Val Ser Glu Glu Ala 40 45 50		
gta aag gtt ctc gat ctt ggc tgt ggc gct ggt tat gtc acc cac ctt 307		
Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly Tyr Val Thr His Leu 55 60 65		
cta agc gat tgc gga tac gaa aca atc ggc gtt gat ggt tct gag gaa 355		
Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val Asp Gly Ser Glu Glu 70 75 80 85		
atg atc aat caa gct acg cag gag aat ggt ctt cgc agg tcg acg ggt 403		
Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu Arg Arg Ser Thr Gly 90 95 100		
cgg gcg act gcc att ttt cag gtc ggg gat gcg cat gat ccc gag ttc 451		
Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala His Asp Pro Glu Phe 105 110 115		
cgg gaa ggc tct ttt gat gcg ata acc agc cgg tat gtg ttg tgg act 499		
Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg Tyr Val Leu Trp Thr 120 125 130		
ctg ctg gat ccc cag gca gcg att aat cgt tgg gtg tct ttg cta aaa 547		
Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp Val Ser Leu Leu Lys 135 140 145		
cct ggt ggg gtt att gcg tgc gta gat gcg gct tgg tat ccg aag ggc 595		
Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala Trp Tyr Pro Lys Gly		

150	155	160	165	
att gat gct ggc acg gaa gta gat tca gtg gat ggt ccg agt gct ttc				643
Ile Asp Ala Gly Thr Glu Val Asp Ser Val Asp Gly Pro Ser Ala Phe				
	170	175	180	
gta gag acc tat acc ccg gaa ctt ttg agg aat ctt ccc atg tca acg				691
Val Glu Thr Tyr Thr Pro Glu Leu Leu Arg Asn Leu Pro Met Ser Thr				
	185	190	195	
acc tcc act ggc cac aat ttc gca gag ctt ttc cac aac gct ggc ctc				739
Thr Ser Thr Gly His Asn Phe Ala Glu Leu Phe His Asn Ala Gly Leu				
	200	205	210	
aaa gaa gtc aca ttg aca ccc att gag ggg ctg gct gaa ctt gac cag				787
Lys Glu Val Thr Leu Thr Pro Ile Glu Gly Leu Ala Glu Leu Asp Gln				
	215	220	225	
cga ttt ggc ctc tca cca ggg cat gag tcg act ccg cag ttc cta ttc				835
Arg Phe Gly Leu Ser Pro Gly His Glu Ser Thr Pro Gln Phe Leu Phe				
	230	235	240	245
agg gga att aaa tcc agt tagtgctggt ttaagcggtc gag				876
Arg Gly Ile Lys Ser Ser				
	250			

<210> 892

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 892

Val Thr Ser Pro Glu Leu Gln Asn Ile Leu Asn Asn Tyr Trp Ser Gly				
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Arg Ala Glu Ala Tyr His Leu Asn Gln Thr Gln Ser Glu Arg Ala Gln				
	20	25	30	
Phe Glu Arg Pro Ile Trp Glu Lys Val Trp Ser Lys Ala Leu Pro Ile				
	35	40	45	
Val Ser Glu Glu Ala Val Lys Val Leu Asp Leu Gly Cys Gly Ala Gly				
	50	55	60	
Tyr Val Thr His Leu Leu Ser Asp Cys Gly Tyr Glu Thr Ile Gly Val				
	65	70	75	80
Asp Gly Ser Glu Glu Met Ile Asn Gln Ala Thr Gln Glu Asn Gly Leu				
	85	90	95	
Arg Arg Ser Thr Gly Arg Ala Thr Ala Ile Phe Gln Val Gly Asp Ala				
	100	105	110	
His Asp Pro Glu Phe Arg Glu Gly Ser Phe Asp Ala Ile Thr Ser Arg				
	115	120	125	
Tyr Val Leu Trp Thr Leu Leu Asp Pro Gln Ala Ala Ile Asn Arg Trp				
	130	135	140	
Val Ser Leu Leu Lys Pro Gly Gly Val Ile Ala Cys Val Asp Ala Ala				

145		150		155		160
Trp Tyr Pro Lys Gly Ile Asp Ala Gly Thr Glu Val Asp Ser Val Asp						
		165		170		175
Gly Pro Ser Ala Phe Val Glu Thr Tyr Thr Pro Glu Leu Leu Arg Asn						
		180		185		190
Leu Pro Met Ser Thr Thr Ser Thr Gly His Asn Phe Ala Glu Leu Phe						
		195		200		205
His Asn Ala Gly Leu Lys Glu Val Thr Leu Thr Pro Ile Glu Gly Leu						
		210		215		220
Ala Glu Leu Asp Gln Arg Phe Gly Leu Ser Pro Gly His Glu Ser Thr						
		225		230		235
Pro Gln Phe Leu Phe Arg Gly Ile Lys Ser Ser						
		245		250		

<210> 893

<211> 585

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(562)

<223> RXS00998

<400> 893

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tgaaaatcca accatttttag gccgactaga gtaattaatt	atg act tcc cgc gat	115
	Met Thr Ser Arg Asp	
	1 5	

gat caa ccc caa gat ctg ctt tcg ctt gca gaa ctt gcc gcc acc aga	163
Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu Leu Ala Ala Thr Arg	
	10 15 20

gct tta acc aca gac gaa ctt gaa gca ctc aac aac gcc aat tat ggc	211
Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn Asn Ala Asn Tyr Gly	
	25 30 35

ctc gac cgc aat ctg ggg ctg cgc tac acc acc atc gag ccc ggc cgg	259
Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr Ile Glu Pro Gly Arg	
	40 45 50

gtg gtc agc gaa ctt cac gtg gca tcc aag cac ctg caa gtg gtg ggc	307
Val Val Ser Glu Leu His Val Ala Ser Lys His Leu Gln Val Val Gly	
	55 60 65

ttg gtc aac ggt ggt gtc tac gcc gcc atc gcc gaa tcc act gga tca	355
Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala Glu Ser Thr Gly Ser	
	70 75 80 85

gtc gcc agc atg att tcc gcc cct gga aaa atg gtc gtc ggc atc aac	403
Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met Val Val Gly Ile Asn	
	90 95 100

aac aac acc gac ttc att tct gct gtg agc tcc ggt gtc atc gtg gcc 451
 Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser Gly Val Ile Val Ala
 105 110 115

gaa gca acg ccg att cag cta ggt ggc cgc acc cat ctg tgg cag atc 499
 Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr His Leu Trp Gln Ile
 120 125 130

gaa tgc acc cac cgc gga gaa gtc gtc gca cga acc aca ctg cgc acc 547
 Glu Cys Thr His Arg Gly Glu Val Val Ala Arg Thr Thr Leu Arg Thr
 135 140 145

atg gtg ctg aac aag tagccctata ctcgggcacc atg 585
 Met Val Leu Asn Lys
 150

<210> 894

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 894

Met Thr Ser Arg Asp Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu
 1 5 10 15

Leu Ala Ala Thr Arg Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn
 20 25 30

Asn Ala Asn Tyr Gly Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr
 35 40 45

Ile Glu Pro Gly Arg Val Val Ser Glu Leu His Val Ala Ser Lys His
 50 55 60

Leu Gln Val Val Gly Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala
 65 70 75 80

Glu Ser Thr Gly Ser Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met
 85 90 95

Val Val Gly Ile Asn Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser
 100 105 110

Gly Val Ile Val Ala Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr
 115 120 125

His Leu Trp Gln Ile Glu Cys Thr His Arg Gly Glu Val Val Ala Arg
 130 135 140

Thr Thr Leu Arg Thr Met Val Leu Asn Lys
 145 150

<210> 895

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1075)

<223> RXA01215

<400> 895

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cccaaaacgt ccacaaccag gaaggctaag caggatcctc atg act gct cac tgg 115
 Met Thr Ala His Trp
 1 5

aaa caa aac caa aag aac ctc atg ctg ttt tcg ggt cgt gcg cac cca 163
 Lys Gln Asn Gln Lys Asn Leu Met Leu Phe Ser Gly Arg Ala His Pro
 10 15 20

gaa ctg gca gaa gct gta gct aaa gag ctc gac gtc aac gtc acc cca 211
 Glu Leu Ala Glu Ala Val Ala Lys Glu Leu Asp Val Asn Val Thr Pro
 25 30 35

atg acg gca cgc gat ttc gcc aac ggt gaa atc tac gtc cgc ttc gag 259
 Met Thr Ala Arg Asp Phe Ala Asn Gly Glu Ile Tyr Val Arg Phe Glu
 40 45 50

gaa tca gtt cgt ggc tcc gac tgc ttc gtc ctg cag tcc cac acc cag 307
 Glu Ser Val Arg Gly Ser Asp Cys Phe Val Leu Gln Ser His Thr Gln
 55 60 65

cct ctc aac aag tgg ctc atg gaa cag ctg ctg atg atc gac gct ttg 355
 Pro Leu Asn Lys Trp Leu Met Glu Gln Leu Leu Met Ile Asp Ala Leu
 70 75 80 85

aag cgt ggt tcc gca aag cgc atc acc gcg atc ctg ccg ttc tac cca 403
 Lys Arg Gly Ser Ala Lys Arg Ile Thr Ala Ile Leu Pro Phe Tyr Pro
 90 95 100

tat gcc cgc cag gac aag aag cac cgc ggc cgc gag cca att tct gct 451
 Tyr Ala Arg Gln Asp Lys Lys His Arg Gly Arg Glu Pro Ile Ser Ala
 105 110 115

cgc ctc atc gcc gac ctc atg ctc acc gct ggc gcg gac cgt atc gtg 499
 Arg Leu Ile Ala Asp Leu Met Leu Thr Ala Gly Ala Asp Arg Ile Val
 120 125 130

tcc gtg gac ttg cac acc gat cag atc cag ggc ttc ttc gac ggc cca 547
 Ser Val Asp Leu His Thr Asp Gln Ile Gln Gly Phe Phe Asp Gly Pro
 135 140 145

gtc gat cac atg cac gcc atg ccg atc ctc acc gat cac atc aag gaa 595
 Val Asp His Met His Ala Met Pro Ile Leu Thr Asp His Ile Lys Glu
 150 155 160 165

aac tac aac ctg gac aac atc tgc gtg gtc tcc cct gac gca ggt cgc 643
 Asn Tyr Asn Leu Asp Asn Ile Cys Val Val Ser Pro Asp Ala Gly Arg
 170 175 180

gtg aag gtt gca gag aag tgg gct aac acc ttg ggc gat gcc cca atg 691
 Val Lys Val Ala Glu Lys Trp Ala Asn Thr Leu Gly Asp Ala Pro Met
 185 190 195

gcg ttc gtg cac aag acc cgc tcc acc gag gta gca aac cag gtt gtc 739
 Ala Phe Val His Lys Thr Arg Ser Thr Glu Val Ala Asn Gln Val Val

200	205	210	
gcc aac cgc gtc gtc ggt gac gtc gac ggc aag gac tgc gtg ctt ctc			787
Ala Asn Arg Val Val Gly Asp Val Asp Gly Lys Asp Cys Val Leu Leu			
215	220	225	
gac gac atg atc gac act ggc ggc acc atc gcc ggc gct gtg ggc gtc			835
Asp Asp Met Ile Asp Thr Gly Gly Thr Ile Ala Gly Ala Val Gly Val			
230	235	240	245
ctg aag aag gct ggc gca aag tca gtc gtc atc gcc tgc acc cac ggt			883
Leu Lys Lys Ala Gly Ala Lys Ser Val Val Ile Ala Cys Thr His Gly			
250	255	260	
gtg ttc tct gac cca gcc cgc gag cgc ctg tct gca tgc ggt gct gaa			931
Val Phe Ser Asp Pro Ala Arg Glu Arg Leu Ser Ala Cys Gly Ala Glu			
265	270	275	
gaa gtc atc acc acc gac acc ctg cca cag tcc acc gag ggc tgg agc			979
Glu Val Ile Thr Thr Asp Thr Leu Pro Gln Ser Thr Glu Gly Trp Ser			
280	285	290	
aac ctg acc gtt ttg tcg atc gca ccg ctg ctg gct cgc acc atc aac			
1027			
Asn Leu Thr Val Leu Ser Ile Ala Pro Leu Leu Ala Arg Thr Ile Asn			
295	300	305	
gag atc ttc gaa aac ggt tcc gtc acc acc ctc ttc gag ggc gag gcc			
1075			
Glu Ile Phe Glu Asn Gly Ser Val Thr Thr Leu Phe Glu Gly Glu Ala			
310	315	320	325
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1098			

<210> 896

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 896

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			20					25					30		

Val	Asn	Val	Thr	Pro	Met	Thr	Ala	Arg	Asp	Phe	Ala	Asn	Gly	Glu	Ile
		35					40					45			

Tyr	Val	Arg	Phe	Glu	Glu	Ser	Val	Arg	Gly	Ser	Asp	Cys	Phe	Val	Leu
	50					55					60				

Gln	Ser	His	Thr	Gln	Pro	Leu	Asn	Lys	Trp	Leu	Met	Glu	Gln	Leu	Leu
65					70					75					80

Met	Ile	Asp	Ala	Leu	Lys	Arg	Gly	Ser	Ala	Lys	Arg	Ile	Thr	Ala	Ile
				85					90					95	

Leu	Pro	Phe	Tyr	Pro	Tyr	Ala	Arg	Gln	Asp	Lys	Lys	His	Arg	Gly	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100					105					110						
Glu	Pro	Ile	Ser	Ala	Arg	Leu	Ile	Ala	Asp	Leu	Met	Leu	Thr	Ala	Gly	
115					120					125						
Ala	Asp	Arg	Ile	Val	Ser	Val	Asp	Leu	His	Thr	Asp	Gln	Ile	Gln	Gly	
130					135					140						
Phe	Phe	Asp	Gly	Pro	Val	Asp	His	Met	His	Ala	Met	Pro	Ile	Leu	Thr	
145					150					155					160	
Asp	His	Ile	Lys	Glu	Asn	Tyr	Asn	Leu	Asp	Asn	Ile	Cys	Val	Val	Ser	
165					170					175						
Pro	Asp	Ala	Gly	Arg	Val	Lys	Val	Ala	Glu	Lys	Trp	Ala	Asn	Thr	Leu	
180					185					190						
Gly	Asp	Ala	Pro	Met	Ala	Phe	Val	His	Lys	Thr	Arg	Ser	Thr	Glu	Val	
195					200					205						
Ala	Asn	Gln	Val	Val	Ala	Asn	Arg	Val	Val	Gly	Asp	Val	Asp	Gly	Lys	
210					215					220						
Asp	Cys	Val	Leu	Leu	Asp	Asp	Met	Ile	Asp	Thr	Gly	Gly	Thr	Ile	Ala	
225					230					235					240	
Gly	Ala	Val	Gly	Val	Leu	Lys	Lys	Ala	Gly	Ala	Lys	Ser	Val	Val	Ile	
245					250					255						
Ala	Cys	Thr	His	Gly	Val	Phe	Ser	Asp	Pro	Ala	Arg	Glu	Arg	Leu	Ser	
260					265					270						
Ala	Cys	Gly	Ala	Glu	Glu	Val	Ile	Thr	Thr	Asp	Thr	Leu	Pro	Gln	Ser	
275					280					285						
Thr	Glu	Gly	Trp	Ser	Asn	Leu	Thr	Val	Leu	Ser	Ile	Ala	Pro	Leu	Leu	
290					295					300						
Ala	Arg	Thr	Ile	Asn	Glu	Ile	Phe	Glu	Asn	Gly	Ser	Val	Thr	Thr	Leu	
305					310					315					320	
Phe	Glu	Gly	Glu	Ala												
325																

<210> 897

<211> 1470

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1447)

<223> RXN00558

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Val Val Lys Lys Pro

1

5

gcg ggc atc gca gta ggc gat ggc gaa cag atc ctg gtt ttc aaa gat	163
Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile Leu Val Phe Lys Asp	
10 15 20	
ttg ggc cta gtc tcc caa gtt ttc gac caa cca att ctg gaa tcc ctc	211
Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro Ile Leu Glu Ser Leu	
25 30 35	
cgc gga aac atc gcc atc gga cac acc cga tac acc acc gcc ggc gga	259
Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr Thr Thr Ala Gly Gly	
40 45 50	
aac acc tgg gaa aat gcc cag cct atg ttc cgc atg gca cca gat ggc	307
Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg Met Ala Pro Asp Gly	
55 60 65	
acc gat atc gcc ctt gga cac aac ggc aac ctg att aat tac atc gag	355
Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu Ile Asn Tyr Ile Glu	
70 75 80 85	
ttg ttg gac aaa gcc acc gaa ctt ggc ctc gtc gat ccc gcc aag aag	403
Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val Asp Pro Ala Lys Lys	
90 95 100	
cca tca gat acc gat gtg ctc act gga ctg ctc gca agc ggc gtc cat	451
Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu Ala Ser Gly Val His	
105 110 115	
gac gga aat aat ctc ttt gat tcc gcc aag gaa ctc ctc ccc agc gtc	499
Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu Leu Leu Pro Ser Val	
120 125 130	
aag gga gcc tac tgc ctc acc ttc acc gac gga cac acc ctg tac gca	547
Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly His Thr Leu Tyr Ala	
135 140 145	
gcg cgt gat cca ttc ggc atc cgc cca ctg tcc atc ggc cgc ctc gag	595
Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser Ile Gly Arg Leu Glu	
150 155 160 165	
cgc ggc tgg gta gtc gca tct gaa acc gca gcg ctc gac atc gta ggt	643
Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala Leu Asp Ile Val Gly	
170 175 180	
gcc tcg cat gtg cgc gag gtc gaa cca ggc gaa ctg att gct atc gac	691
Ala Ser His Val Arg Glu Val Glu Pro Gly Glu Leu Ile Ala Ile Asp	
185 190 195	
gaa tcc ggc ctc aag tcc gca cga ttc gcc gag aca acc cgc aaa ggt	739
Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu Thr Thr Arg Lys Gly	
200 205 210	
tgc gtc ttc gaa tac gtt tac ctg gct cgt cca gac tcc gtg atc aag	787
Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro Asp Ser Val Ile Lys	
215 220 225	
gga aga aac gtc aac gaa gcc cga ctt gaa atc ggc cgc aag ctc gct	835
Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile Gly Arg Lys Leu Ala	
230 235 240 245	

gca gaa gca cca gca gtc ggc gat cta gtc atc cca acc cca gaa tca 883
 Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile Pro Thr Pro Glu Ser
 250 255 260

ggc acc cca gca gca gtt gga ttc gcc caa gca tct ggc atc cca ttc 931
 Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala Ser Gly Ile Pro Phe
 265 270 275

ggc caa ggc atg gtc aaa aac gcc tac gtt ggc cga acc ttc atc cag 979
 Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly Arg Thr Phe Ile Gln
 280 285 290

cct tcc gac act ctc cgc caa ctg gga atc cgc ctc aag ctg aac cca
 1027
 Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg Leu Lys Leu Asn Pro
 295 300 305

ttg cgc gag gtt atc gcc gga aag cgc ctt gtg gtt gtg gat gat tcc
 1075
 Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val Val Val Asp Asp Ser
 310 315 320 325

atc gtc cgc ggt aac acc caa cgc gcc gtg atc cgc atg ttg cgc gaa
 1123
 Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile Arg Met Leu Arg Glu
 330 335 340

gcc ggt gca gct gag gtt cac gta cgc atc gcc tca cca ccc gtg aaa
 1171
 Ala Gly Ala Ala Glu Val His Val Arg Ile Ala Ser Pro Pro Val Lys
 345 350 355

tgg cca tgc ttc tac ggc atc gat ttt gcc acc cca ggc gaa ctc att
 1219
 Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr Pro Gly Glu Leu Ile
 360 365 370

gcc aac gct gtc acc agt gac aac gaa gca gaa atg gta gaa gca gtc
 1267
 Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu Met Val Glu Ala Val
 375 380 385

cgc tcc gca atc ggc gca gac acc ctc ggc tac gtc tcc atc gac tcc
 1315
 Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr Val Ser Ile Asp Ser
 390 395 400 405

atg gtt gca gca acc gag caa cca gcc aac gaa ctc tgc atc gcc tgc
 1363
 Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu Leu Cys Ile Ala Cys
 410 415 420

ttc gac ggc aaa tac ccc atg ggt ctg cca cag gga aac agc aac gca
 1411
 Phe Asp Gly Lys Tyr Pro Met Gly Leu Pro Gln Gly Asn Ser Asn Ala
 425 430 435

gac cta gtc cgc aag atg caa gca acc gcc tca agt taagatcggt
 1457
 Asp Leu Val Arg Lys Met Gln Ala Thr Ala Ser Ser
 440 445

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1470

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<210> 898
<211> 449
<212> PRT
<213> Corynebacterium glutamicum
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          20          25          30
Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr
          35          40          45
Thr Thr Ala Gly Gly Asn Thr Trp Glu Asn Ala Gln Pro Met Phe Arg
 50          55          60
Met Ala Pro Asp Gly Thr Asp Ile Ala Leu Gly His Asn Gly Asn Leu
 65          70          75          80
Ile Asn Tyr Ile Glu Leu Leu Asp Lys Ala Thr Glu Leu Gly Leu Val
          85          90          95
Asp Pro Ala Lys Lys Pro Ser Asp Thr Asp Val Leu Thr Gly Leu Leu
          100          105          110
Ala Ser Gly Val His Asp Gly Asn Asn Leu Phe Asp Ser Ala Lys Glu
          115          120          125
Leu Leu Pro Ser Val Lys Gly Ala Tyr Cys Leu Thr Phe Thr Asp Gly
 130          135          140
His Thr Leu Tyr Ala Ala Arg Asp Pro Phe Gly Ile Arg Pro Leu Ser
 145          150          155          160
Ile Gly Arg Leu Glu Arg Gly Trp Val Val Ala Ser Glu Thr Ala Ala
          165          170          175
Leu Asp Ile Val Gly Ala Ser His Val Arg Glu Val Glu Pro Gly Glu
          180          185          190
Leu Ile Ala Ile Asp Glu Ser Gly Leu Lys Ser Ala Arg Phe Ala Glu
          195          200          205
Thr Thr Arg Lys Gly Cys Val Phe Glu Tyr Val Tyr Leu Ala Arg Pro
 210          215          220
Asp Ser Val Ile Lys Gly Arg Asn Val Asn Glu Ala Arg Leu Glu Ile
 225          230          235          240
Gly Arg Lys Leu Ala Ala Glu Ala Pro Ala Val Gly Asp Leu Val Ile
          245          250          255
Pro Thr Pro Glu Ser Gly Thr Pro Ala Ala Val Gly Phe Ala Gln Ala
          260          265          270

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Ser Gly Ile Pro Phe Gly Gln Gly Met Val Lys Asn Ala Tyr Val Gly
 275 280 285

Arg Thr Phe Ile Gln Pro Ser Asp Thr Leu Arg Gln Leu Gly Ile Arg
 290 295 300

Leu Lys Leu Asn Pro Leu Arg Glu Val Ile Ala Gly Lys Arg Leu Val
 305 310 315 320

Val Val Asp Asp Ser Ile Val Arg Gly Asn Thr Gln Arg Ala Val Ile
 325 330 335

Arg Met Leu Arg Glu Ala Gly Ala Ala Glu Val His Val Arg Ile Ala
 340 345 350

Ser Pro Pro Val Lys Trp Pro Cys Phe Tyr Gly Ile Asp Phe Ala Thr
 355 360 365

Pro Gly Glu Leu Ile Ala Asn Ala Val Thr Ser Asp Asn Glu Ala Glu
 370 375 380

Met Val Glu Ala Val Arg Ser Ala Ile Gly Ala Asp Thr Leu Gly Tyr
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Val Ser Ile Asp Ser Met Val Ala Ala Thr Glu Gln Pro Ala Asn Glu
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 Val Val Lys Lys Pro Ala Gly Ile Ala Val Gly Asp Gly Glu Gln Ile
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 Leu Val Phe Lys Asp Leu Gly Leu Val Ser Gln Val Phe Asp Gln Pro
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 Ile Leu Glu Ser Leu Arg Gly Asn Ile Ala Ile Gly His Thr Arg Tyr

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Thr	Thr	Ala	Gly	Gly	Asn	Thr	Trp	Glu	Asn	Ala	Gln	Pro	Met	Phe	Arg		
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Met	Ala	Pro	Asp	Gly	Thr	Asp	Ile	Ala	Leu	Gly	His	Asn	Gly	Asn	Leu		
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Ile	Asn	Tyr	Ile	Glu	Leu	Leu	Asp	Lys	Ala	Thr	Glu	Leu	Gly	Leu	Val		
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Asp	Pro	Ala	Lys	Lys	Pro	Ser	Asp	Thr	Asp	Val	Leu	Thr	Gly	Leu	Leu		
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Ala	Ser	Gly	Val	His	Asp	Gly	Asn	Asn	Leu	Phe	Asp	Ser	Ala	Lys	Glu		
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Leu	Leu	Pro	Ser	Val	Lys	Gly	Ala	Tyr	Cys	Leu	Thr	Phe	Thr	Asp	Gly		
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<212> PRT

<213> Corynebacterium glutamicum

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Asp	Pro	Ala	Lys	Lys	Pro	Ser	Asp	Thr	Asp	Val	Leu	Thr	Gly	Leu	Leu
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Ala	Ser	Gly	Val	His	Asp	Gly	Asn	Asn	Leu	Phe	Asp	Ser	Ala	Lys	Glu
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His Thr Leu
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 Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr
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 gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt 211
 Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu
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 gga tcg atc gca act gtc cac cct ggc atc aag gct gat gat cca gag 259
 Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu
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 gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc 307
 Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile
 55 60 65
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 Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala Asp Ala Leu Arg Ala
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 Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp Ala Ala Arg Ile Glu
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 Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala Ala Gln Gly Val Arg
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 Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala Ser Ser Glu Asp Ile
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 Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp Val Val Lys Asp Asp
 135 140 145
 ggt ttg tct gcg ggc aag ggt gtt gtg gtt acc ccc gat cgt gca gca 595

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Ala	Arg	Ala	His	Val 170	Asp	Ala	Val	Leu	Glu 175	Gly	Gly	Asn	Pro	Val 180	Leu	
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Leu	Glu	Ser	Phe 185	Leu	Asp	Gly	Pro	Glu 190	Val	Ser	Leu	Phe	Cys 195	Leu	Val	
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Asp	Gly	Glu 200	Thr	Val	Val	Pro	Leu 205	Leu	Pro	Ala	Gln	Asp 210	His	Lys	Arg	
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Ala	Tyr 215	Asp	Asn	Asp	Glu	Gly 220	Pro	Asn	Thr	Gly	Gly 225	Met	Gly	Ala	Tyr	
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Ala	Pro	Leu	Pro	Trp 235	Leu	Pro	Glu	Asp	Gly	Val 240	Gln	Arg	Ile	Val 245	Asp	
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Glu	Val	Cys	Val 250	Pro	Val	Ala	Arg	Glu	Met 255	Val	Ala	Arg	Gly	Cys 260	Ala	
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Tyr	Ser	Gly	Leu 265	Leu	Tyr	Ala	Gly	Ile 270	Ala	Trp	Gly	Ala	Glu 275	Gly	Pro	
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Ala	Val 280	Val	Glu	Phe	Asn	Cys	Arg 285	Phe	Gly	Asp	Pro	Glu 290	Thr	Gln	Ala	
gta	ctg	gca	cta	ctg	aag	act	cct	cta	gca	gta	ctg	ctc	aac	gca	ggt	
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1171	Arg	Thr	Gly	Asp	Val	Ile	Arg	Asn	Ala	Asp	Ala	Asp	Asn	Val	Leu	His
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gct	ggt	acc	gca	ctc	aac	gct	gaa	ggc	gag	ctg	gtc	tct	gcg	ggc	ggt	
1219	Ala	Gly	Thr	Ala	Leu	Asn	Ala	Glu	Gly	Glu	Leu	Val	Ser	Ala	Gly	Gly
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 Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu Glu Ala Ala Arg
 375 380 385

gat aac gcg tac acc acc atc aag gac att gaa ctt gag gga agc cac
 1315
 Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu Glu Gly Ser His
 390 395 400 405

tac cgc agc gat atc gca ttg gct gca tta gag ggt cgt atc tcg atc
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 1386

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 <213> Corynebacterium glutamicum

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Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys
 35 40 45

Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser
 50 55 60

Asp Leu Val Val Ile Gly Pro Glu Ile Pro Leu Val Ala Gly Val Ala
 65 70 75 80

Asp Ala Leu Arg Ala Ala Gly Ile Ala Val Phe Gly Pro Asn Lys Asp
 85 90 95

Ala Ala Arg Ile Glu Gly Ser Lys Ala Phe Ala Lys Asp Val Met Ala
 100 105 110

Ala Gln Gly Val Arg Thr Ala His Ala Glu Thr Ile Thr Pro Gly Ala
 115 120 125

Ser Ser Glu Asp Ile Asp Ala Ala Ile Asp Arg Phe Gly Pro Thr Trp
 130 135 140

Val Val Lys Asp Asp Gly Leu Ser Ala Gly Lys Gly Val Val Val Thr
 145 150 155 160

Pro Asp Arg Ala Ala Ala Arg Ala His Val Asp Ala Val Leu Glu Gly
 165 170 175

Gly Asn Pro Val Leu Leu Glu Ser Phe Leu Asp Gly Pro Glu Val Ser
 180 185 190

Leu Phe Cys Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala
 195 200 205
 Gln Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly
 210 215 220
 Gly Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val
 225 230 235 240
 Gln Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val
 245 250 255
 Ala Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp
 260 265 270
 Gly Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp
 275 280 285
 Pro Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val
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 Glu Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn
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 Tyr Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala
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 Asp Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu
 355 360 365
 Val Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr
 370 375 380
 Leu Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu
 385 390 395 400
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 405 410 415
 Gly Arg Ile Ser Ile
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 Met Arg Ile Leu Val

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Ile Gly Ser Gly Ala Arg Glu His Ala Leu Leu Arg Gly Leu Ser Thr			
	10	15	20
gac cct gca acc act gaa ctc cac gtt gcc cca ggt aac gct ggt ctt			211
Asp Pro Ala Thr Thr Glu Leu His Val Ala Pro Gly Asn Ala Gly Leu			
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gga tcg atc gca act gtc cac cct ggc atc aag gct gat gat cca gag			259
Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys Ala Asp Asp Pro Glu			
	40	45	50
gct gtc act gcg ttg gct aaa gaa ctg aac tct gat ctg gtt gtt atc			307
Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser Asp Leu Val Val Ile			
	55	60	65
ggc cca gag atc cct ttg gtt gcg ggt gtt gct gat gca ctt cgc gcg			355
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gcg ggt atc			364
Ala Gly Ile			

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<400> 904

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Gly Asn Ala Gly Leu Gly Ser Ile Ala Thr Val His Pro Gly Ile Lys			
35	40	45	

Ala Asp Asp Pro Glu Ala Val Thr Ala Leu Ala Lys Glu Leu Asn Ser			
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<212> DNA

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<223> FRXA00626

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Arg	Ile	Val	Asp	Glu	Val	Cys	Val	Pro	Val	Ala	Arg	Glu	Met	Val	Ala	
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Ala	Glu	Gly	Pro	Ala	Val	Val	Glu	Phe	Asn	Cys	Arg	Phe	Gly	Asp	Pro	
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gaa	acc	cag	gct	gta	ctg	gca	cta	ctg	aag	act	cct	cta	gca	gta	ctg	432
Glu	Thr	Gln	Ala	Val	Leu	Ala	Leu	Leu	Lys	Thr	Pro	Leu	Ala	Val	Leu	
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Leu	Asn	Ala	Val	Ala	Thr	Gly	Thr	Leu	Ala	Glu	Gln	Pro	Ala	Leu	Glu	
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Trp	Glu	Asp	Ala	Tyr	Ala	Leu	Thr	Val	Val	Leu	Ala	Ser	Tyr	Asn	Tyr	
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cca	gag	gca	cct	cgt	act	ggt	gat	gtc	atc	cgc	aac	gct	gat	gca	gat	576
Pro	Glu	Ala	Pro	Arg	Thr	Gly	Asp	Val	Ile	Arg	Asn	Ala	Asp	Ala	Asp	
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Asn	Val	Leu	His	Ala	Gly	Thr	Ala	Leu	Asn	Ala	Glu	Gly	Glu	Leu	Val	
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Ser	Ala	Gly	Gly	Arg	Val	Leu	Asn	Val	Ile	Gly	Val	Gly	Glu	Thr	Leu	
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<210> 906

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 906

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Phe Phe Leu Val Asp Gly Glu Thr Val Val Pro Leu Leu Pro Ala Gln
 35 40 45

Asp His Lys Arg Ala Tyr Asp Asn Asp Glu Gly Pro Asn Thr Gly Gly
 50 55 60

Met Gly Ala Tyr Ala Pro Leu Pro Trp Leu Pro Glu Asp Gly Val Gln
 65 70 75 80

Arg Ile Val Asp Glu Val Cys Val Pro Val Ala Arg Glu Met Val Ala
 85 90 95

Arg Gly Cys Ala Tyr Ser Gly Leu Leu Tyr Ala Gly Ile Ala Trp Gly
 100 105 110

Ala Glu Gly Pro Ala Val Val Glu Phe Asn Cys Arg Phe Gly Asp Pro
 115 120 125

Glu Thr Gln Ala Val Leu Ala Leu Leu Lys Thr Pro Leu Ala Val Leu
 130 135 140

Leu Asn Ala Val Ala Thr Gly Thr Leu Ala Glu Gln Pro Ala Leu Glu
 145 150 155 160

Trp Glu Asp Ala Tyr Ala Leu Thr Val Val Leu Ala Ser Tyr Asn Tyr
 165 170 175

Pro Glu Ala Pro Arg Thr Gly Asp Val Ile Arg Asn Ala Asp Ala Asp
 180 185 190

Asn Val Leu His Ala Gly Thr Ala Leu Asn Ala Glu Gly Glu Leu Val
 195 200 205

Ser Ala Gly Gly Arg Val Leu Asn Val Ile Gly Val Gly Glu Thr Leu
 210 215 220

Glu Ala Ala Arg Asp Asn Ala Tyr Thr Thr Ile Lys Asp Ile Glu Leu
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245 250 255

Arg Ile Ser Ile
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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101) . . (691)

<223> RXA02623

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Val Asn Ser Asp Ser
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Thr Thr Thr Ile Val Val Leu Ala Ser Gly Thr Gly Thr Leu Leu Gln
10 15 20

tca ctc att gaa gcg caa ggt acc tat tcg atc gtg ggc gtt gtc tct 211
Ser Leu Ile Glu Ala Gln Gly Thr Tyr Ser Ile Val Gly Val Val Ser
25 30 35

gac gtc gaa tgc cct gca ctt tcc aga gcc gca gat gca ggt att gat 259
Asp Val Glu Cys Pro Ala Leu Ser Arg Ala Ala Asp Ala Gly Ile Asp
40 45 50

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Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala Gln Trp Asn His Glu
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ctt gca gac gca gtt gca gta agc gac cca gat ttg gtg gtc tct gcg 355
Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp Leu Val Val Ser Ala
70 75 80 85

gga ttc atg aaa att ttg ggc gaa ggt ttc ctc tca agg ttc ccg tcc 403
Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu Ser Arg Phe Pro Ser
90 95 100

cgc atc atc aac acc cac cca gct tta ttg cct tct ttc cct ggt gcc 451
 Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro Ser Phe Pro Gly Ala
 105 110 115

cac gcg gtt cgc gat gct ttg gca tac ggt gtg aaa gtg tca ggt tcg 499
His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val Lys Val Ser Gly Ser
120 125 130

aca gtt cac ctt gtc gat gct ggt gtg gat acc ggc cca att att gct 547
Thr Val His Leu Val Asp Ala Gly Val Asp Thr Gly Pro Ile Ile Ala
135 140 145

caa cga gca gtg ccg gta gaa gtg aat gat gat gaa tcc agc ctg cat 595

Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp Glu Ser Ser Leu His
 150 155 160 165

gaa aga atc aag cag gtt gag cgt aaa ctc att gta gaa gtc ctg aac 643
 Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile Val Glu Val Leu Asn
 170 175 180

agc gtg gaa ttt tcg cgt cag ggt ggc gta caa ctc aac tgg aga ggc 691
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 35 40 45

Asp Ala Gly Ile Asp Thr Ala Val Val Pro Leu Gly Lys Asp Arg Ala
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Gln Trp Asn His Glu Leu Ala Asp Ala Val Ala Val Ser Asp Pro Asp
 65 70 75 80

Leu Val Val Ser Ala Gly Phe Met Lys Ile Leu Gly Glu Gly Phe Leu
 85 90 95

Ser Arg Phe Pro Ser Arg Ile Ile Asn Thr His Pro Ala Leu Leu Pro
 100 105 110

Ser Phe Pro Gly Ala His Ala Val Arg Asp Ala Leu Ala Tyr Gly Val
 115 120 125

Lys Val Ser Gly Ser Thr Val His Leu Val Asp Ala Gly Val Asp Thr
 130 135 140

Gly Pro Ile Ile Ala Gln Arg Ala Val Pro Val Glu Val Asn Asp Asp
 145 150 155 160

Glu Ser Ser Leu His Glu Arg Ile Lys Gln Val Glu Arg Lys Leu Ile
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Val Glu Val Leu Asn Ser Val Glu Phe Ser Arg Gln Gly Gly Val Gln
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Leu Asn Trp Arg Gly
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 Met Tyr Ile Pro Glu
 1 5

tcg atc ggc acc cct ttg acc ccc aat gcc acg aaa gtg atg ctg ctg 163
 Ser Ile Gly Thr Pro Leu Thr Pro Asn Ala Thr Lys Val Met Leu Leu
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gga tca gga gaa tta ggc aaa gaa gta gcc atc gct ttc cag cgt ctc 211
 Gly Ser Gly Glu Leu Gly Lys Glu Val Ala Ile Ala Phe Gln Arg Leu
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ggc ctg gaa gtc cat gca gtt gat cgc tac gaa cat gcc cca gcc cac 259
 Gly Leu Glu Val His Ala Val Asp Arg Tyr Glu His Ala Pro Ala His
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cag gtc gct cac ttc tcc tat gtc atc gac atg aca gat gca gcc cag 307
 Gln Val Ala His Phe Ser Tyr Val Ile Asp Met Thr Asp Ala Ala Gln
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gtg cgg gaa ttg gtg gag cgt gtg cgc cca gat ttt gtc att cct gaa 355
 Val Arg Glu Leu Val Glu Arg Val Arg Pro Asp Phe Val Ile Pro Glu
 70 75 80 85

atc gaa gca ctg gca acc gat gaa ctg gtg aag atc gaa gaa gag ggg 403
 Ile Glu Ala Leu Ala Thr Asp Glu Leu Val Lys Ile Glu Glu Glu Gly
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cta gct acc atc gtg ccc act gca cgt gca gcc aag ctg acc atg aac 451
 Leu Ala Thr Ile Val Pro Thr Ala Arg Ala Ala Lys Leu Thr Met Asn
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cgc gaa ggc atc cgc aag ctg gcg gca gag gaa ctg ggt ctt cca acc 499
 Arg Glu Gly Ile Arg Lys Leu Ala Ala Glu Glu Leu Gly Leu Pro Thr
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tcc aac tat gag ttc tgc tcc act ttc gag gaa ttc tcc gca gct gct 547
 Ser Asn Tyr Glu Phe Cys Ser Thr Phe Glu Glu Phe Ser Ala Ala Ala
 135 140 145

gaa aag ctt ggt tac ccc aac gtg gtg aaa cca gtg atg agt tct tcc 595
 Glu Lys Leu Gly Tyr Pro Asn Val Val Lys Pro Val Met Ser Ser Ser
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ggc aag ggc caa tct gtt ttg cgt agt tca gac gat ctg cag gca gca 643
 Gly Lys Gly Gln Ser Val Leu Arg Ser Ser Asp Asp Leu Gln Ala Ala
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tgg gat tat gcg atg agc ggt gca cgc gtg gcc aac tcc cgc gtc atc 691

Trp	Asp	Tyr	Ala	Met	Ser	Gly	Ala	Arg	Val	Ala	Asn	Ser	Arg	Val	Ile	
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Val	Glu	Ala	Phe	Val	Glu	Phe	Asp	Tyr	Glu	Ile	Thr	Leu	Leu	Thr	Val	
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Arg	Ser	Ile	Asp	Pro	Thr	Thr	Ser	Lys	Pro	Ala	Thr	Trp	Phe	Cys	Glu	
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ccc	att	ggg	cac	cgc	caa	gaa	gac	ggc	gac	tac	gtg	gaa	tcc	tgg	cag	835
Pro	Ile	Gly	His	Arg	Gln	Glu	Asp	Gly	Asp	Tyr	Val	Glu	Ser	Trp	Gln	
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Pro	Met	Glu	Met	Thr	Pro	Arg	Ala	Leu	Glu	Asn	Ala	Arg	Ser	Val	Ala	
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Ala	Arg	Ile	Thr	Asn	Ala	Leu	Gly	Gly	Arg	Gly	Val	Phe	Gly	Val	Glu	
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Leu	Phe	Val	Ser	Gly	Asp	Asp	Val	Tyr	Phe	Ser	Glu	Val	Ser	Pro	Arg	
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1027																
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310					315				320						325	
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1123																
Leu	Ile	Ser	Pro	Gly	Ala	Ser	Ala	Val	Ile	Tyr	Gly	Gly	Ile	Glu	Ser	
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gaa	ggc	gtg	agc	tac	acc	ggg	ttg	gct	gaa	gcg	ctg	gca	gtg	gct	gaa	
1171																
Glu	Gly	Val	Ser	Tyr	Thr	Gly	Leu	Ala	Glu	Ala	Leu	Ala	Val	Ala	Glu	
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act	gat	ctt	cgt	atc	ttt	gcc	aag	cca	gag	gcc	ttc	acc	aag	cgt	cgc	
1219																
Thr	Asp	Leu	Arg	Ile	Phe	Ala	Lys	Pro	Glu	Ala	Phe	Thr	Lys	Arg	Arg	
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Met	Gly	Val	Ala	Val	Ser	Thr	Ala	Glu	Asp	Val	Ala	Ala	Ala	Arg	Asp	
	375					380					385					
cgc	gcc	act	ttg	gct	gcc	gcg	gcg	atc	aag	gtt	cat	cca	gga	aat	tcc	
1315																
Arg	Ala	Thr	Leu	Ala	Ala	Ala	Ala	Ile	Lys	Val	His	Pro	Gly	Asn	Ser	
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1347

Ala Glu Ala

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<212> PRT

<213> Corynebacterium glutamicum

<400> 910

Met Tyr Ile Pro Glu Ser Ile Gly Thr Pro Leu Thr Pro Asn Ala Thr
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Lys Val Met Leu Leu Gly Ser Gly Glu Leu Gly Lys Glu Val Ala Ile
20 25 30

Ala Phe Gln Arg Leu Gly Leu Glu Val His Ala Val Asp Arg Tyr Glu
35 40 45

His Ala Pro Ala His Gln Val Ala His Phe Ser Tyr Val Ile Asp Met
50 55 60

Thr Asp Ala Ala Gln Val Arg Glu Leu Val Glu Arg Val Arg Pro Asp
65 70 75 80

Phe Val Ile Pro Glu Ile Glu Ala Leu Ala Thr Asp Glu Leu Val Lys
85 90 95

Ile Glu Glu Glu Gly Leu Ala Thr Ile Val Pro Thr Ala Arg Ala Ala
100 105 110

Lys Leu Thr Met Asn Arg Glu Gly Ile Arg Lys Leu Ala Ala Glu Glu
115 120 125

Leu Gly Leu Pro Thr Ser Asn Tyr Glu Phe Cys Ser Thr Phe Glu Glu
130 135 140

Phe Ser Ala Ala Ala Glu Lys Leu Gly Tyr Pro Asn Val Val Lys Pro
145 150 155 160

Val Met Ser Ser Ser Gly Lys Gly Gln Ser Val Leu Arg Ser Ser Asp
165 170 175

Asp Leu Gln Ala Ala Trp Asp Tyr Ala Met Ser Gly Ala Arg Val Ala
180 185 190

Asn Ser Arg Val Ile Val Glu Ala Phe Val Glu Phe Asp Tyr Glu Ile
195 200 205

Thr Leu Leu Thr Val Arg Ser Ile Asp Pro Thr Thr Ser Lys Pro Ala
210 215 220

Thr Trp Phe Cys Glu Pro Ile Gly His Arg Gln Glu Asp Gly Asp Tyr
225 230 235 240

Val Glu Ser Trp Gln Pro Met Glu Met Thr Pro Arg Ala Leu Glu Asn
245 250 255

Ala Arg Ser Val Ala Ala Arg Ile Thr Asn Ala Leu Gly Gly Arg Gly
 260 265 270

Val Phe Gly Val Glu Leu Phe Val Ser Gly Asp Asp Val Tyr Phe Ser
 275 280 285

Glu Val Ser Pro Arg Pro His Asp Thr Gly Leu Val Thr Leu Ala Thr
 290 295 300

Gln Arg Phe Ser Glu Phe Glu Leu His Ala Lys Ala Ile Leu Gly Leu
 305 310 315 320

Pro Val Asp Val Thr Leu Ile Ser Pro Gly Ala Ser Ala Val Ile Tyr
 325 330 335

Gly Gly Ile Glu Ser Glu Gly Val Ser Tyr Thr Gly Leu Ala Glu Ala
 340 345 350

Leu Ala Val Ala Glu Thr Asp Leu Arg Ile Phe Ala Lys Pro Glu Ala
 355 360 365

Phe Thr Lys Arg Arg Met Gly Val Ala Val Ser Thr Ala Glu Asp Val
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Ala Ala Ala Arg Asp Arg Ala Thr Leu Ala Ala Ala Ala Ile Lys Val
 385 390 395 400

His Pro Gly Asn Ser Ala Glu Ala
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 Met Ser Thr Phe Val
 1 5

aat gac acc gtc gaa gac gca atc aag acc cct gag ctg gat cag cca 163
 Asn Asp Thr Val Glu Asp Ala Ile Lys Thr Pro Glu Leu Asp Gln Pro
 10 15 20

ttt gag gct ctt ggt ctg aaa gac gac gag tac gcg cgc atc aag gaa 211
 Phe Glu Ala Leu Gly Leu Lys Asp Asp Glu Tyr Ala Arg Ile Lys Glu
 25 30 35

atc ctt ggc cgc cgc cca acc gac gcc gag ctg acc gtt tac tcc gtc 259
 Ile Leu Gly Arg Arg Pro Thr Asp Ala Glu Leu Thr Val Tyr Ser Val
 40 45 50

atg tgg tcg gag cac tgc tcc tac aag tcc tcc aag gtt cac ctg cgt 307

Met	Trp	Ser	Glu	His	Cys	Ser	Tyr	Lys	Ser	Ser	Lys	Val	His	Leu	Arg	
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Tyr	Phe	Gly	Glu	Thr	Thr	Thr	Glu	Glu	Met	Ala	Ser	Lys	Ile	Leu	Ala	
70					75					80					85	
ggc	atc	ggc	gag	aac	gct	ggt	gtg	gtc	gac	atc	gga	gac	ggc	aac	gcc	403
Gly	Ile	Gly	Glu	Asn	Ala	Gly	Val	Val	Asp	Ile	Gly	Asp	Gly	Asn	Ala	
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gtg	acc	ttc	cgc	gtg	gag	tcc	cac	aac	cac	cca	tcc	ttc	gta	gag	cca	451
Val	Thr	Phe	Arg	Val	Glu	Ser	His	Asn	His	Pro	Ser	Phe	Val	Glu	Pro	
			105					110					115			
cac	cag	ggc	gct	gcg	acc	ggc	gtc	ggc	ggc	atc	gtc	cgc	gac	att	atg	499
His	Gln	Gly	Ala	Ala	Thr	Gly	Val	Gly	Gly	Ile	Val	Arg	Asp	Ile	Met	
		120					125					130				
gct	atg	ggc	gca	cgc	cca	atc	gct	gtg	atg	gat	cag	ctg	cgt	ttc	ggt	547
Ala	Met	Gly	Ala	Arg	Pro	Ile	Ala	Val	Met	Asp	Gln	Leu	Arg	Phe	Gly	
	135					140					145					
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Ala	Leu	Asp	Asn	Pro	Asp	Thr	Gln	Arg	Val	Phe	Pro	Gly	Val	Val	Asp	
	150				155					160					165	
ggc	att	tcc	cat	tac	ggc	aac	tgc	ctc	ggc	ctg	cca	aac	atc	ggt	ggc	643
Gly	Ile	Ser	His	Tyr	Gly	Asn	Cys	Leu	Gly	Leu	Pro	Asn	Ile	Gly	Gly	
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gaa	acc	gtc	ttc	gac	gat	tcc	tac	gca	ggt	aac	cca	ctg	gtc	aac	gca	691
Glu	Thr	Val	Phe	Asp	Asp	Ser	Tyr	Ala	Gly	Asn	Pro	Leu	Val	Asn	Ala	
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Leu	Cys	Val	Gly	Thr	Leu	Lys	Val	Glu	Asp	Leu	Lys	Leu	Ala	Phe	Ala	
		200					205					210				
tcc	ggc	acc	ggc	aac	aag	gtg	atc	ctg	ttc	ggt	tcc	cgc	acc	ggc	ctt	787
Ser	Gly	Thr	Gly	Asn	Lys	Val	Ile	Leu	Phe	Gly	Ser	Arg	Thr	Gly	Leu	
	215					220					225					
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Asp	Gly	Ile	Gly	Gly	Val	Ser	Val	Leu	Gly	Ser	Ala	Ser	Phe	Glu	Glu	
	230				235					240				245		
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Gly	Glu	Glu	Arg	Lys	Leu	Pro	Ala	Val	Gln	Val	Gly	Asp	Pro	Phe	Ala	
				250					255					260		
gag	aag	gta	ctc	atc	gag	tgc	tgc	ctc	gag	ctg	tac	aag	gct	ggc	gtc	931
Glu	Lys	Val	Leu	Ile	Glu	Cys	Cys	Leu	Glu	Leu	Tyr	Lys	Ala	Gly	Val	
			265					270					275			
gtg	gtc	ggt	att	cag	gac	ctc	ggt	ggc	ggc	gga	ctt	gcg	tgt	gca	acc	979
Val	Val	Gly	Ile	Gln	Asp	Leu	Gly	Gly	Gly	Gly	Leu	Ala	Cys	Ala	Thr	
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1027																

Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met Arg Val Asn Leu Asp
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 aac gtc cca ctg cgc gca gag aac atg tct gca gct gaa atc ctg gct
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 Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala Ala Glu Ile Leu Ala
 310 315 320 325
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 1123
 Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val Thr Pro Glu Asn Val
 330 335 340
 gag cgt ttc ctc gag atc tgt gca aag tgg gat gtc acc tgc gca gaa
 1171
 Glu Arg Phe Leu Glu Ile Cys Ala Lys Trp Asp Val Thr Cys Ala Glu
 345 350 355
 atc ggc gaa gtt acc gac gag aag gac cgc tac gtt gtg gtc cac aac
 1219
 Ile Gly Glu Val Thr Asp Glu Lys Asp Arg Tyr Val Val Val His Asn
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 ggt gaa gtt gtt atc gac gca cct cca tca acc atc gat gaa ggc cct
 1267
 Gly Glu Val Val Ile Asp Ala Pro Pro Ser Thr Ile Asp Glu Gly Pro
 375 380 385
 gtc tac aac cgc cca gtt gct cgc cct gag aac cag gac gaa ctg cag
 1315
 Val Tyr Asn Arg Pro Val Ala Arg Pro Glu Asn Gln Asp Glu Leu Gln
 390 395 400 405
 ctc gaa ggc gag atc gct cgc cca gtc gac gtt gaa gag atc aag gct
 1363
 Leu Glu Gly Glu Ile Ala Arg Pro Val Asp Val Glu Glu Ile Lys Ala
 410 415 420
 gct tgg ctg aag ctt gtc gct tca cca gca ctt gca tcc cgc gcg ttt
 1411
 Ala Trp Leu Lys Leu Val Ala Ser Pro Ala Leu Ala Ser Arg Ala Phe
 425 430 435
 atc acc gag cag tac gac cgc tac gtc cgc ggc aac acc gtt cag gca
 1459
 Ile Thr Glu Gln Tyr Asp Arg Tyr Val Arg Gly Asn Thr Val Gln Ala
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 aag aac gcc aat gct ggc gtc ttg cgt atc gac gaa gag acc aac cgt
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 Lys Asn Ala Asn Ala Gly Val Leu Arg Ile Asp Glu Glu Thr Asn Arg
 455 460 465
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 1555
 Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys Leu Glu
 470 475 480 485
 cca aac act ggc gcg cag ctt gca ctg gct gag gct tac cgc aac gtg
 1603
 Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg Asn Val

490								495					500					
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1843																		
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Ile	Gly	Asn	Val	Leu	Pro	Ser	Glu	Asp	Asn	Asp	Leu	Tyr	Leu	Leu	Gly			
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Ala	Gly	Leu	Asn	Gly	Leu	Pro	Pro	Val	Val	Asp	Leu	Leu	Asn	Glu	Gln			
	615					620				625								
cgt	ctt	gca	gac	ctg	ttc	gtc	ggt	tct	gat	ctg	ttt	gct	gca	tcc	cac			
2035																		
Arg	Leu	Ala	Asp	Leu	Phe	Val	Gly	Ser	Asp	Leu	Phe	Ala	Ala	Ser	His			
630					635					640					645			
gat	ctg	tct	gag	ggc	ggc	ctt	ggc	cag	acc	ctc	gca	gag	ctt	gcg	atc			
2083																		
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cac	cag	aaa	aag	gga	atg	gat	gtt	gat	ctc	tcc	cag	atc	cac	cca	tcc			
2131																		
His	Gln	Lys	Lys	Gly	Met	Asp	Val	Asp	Leu	Ser	Gln	Ile	His	Pro	Ser			
			665				670					675						
ctg	ttc	acc	tca	ctg	ttt	gct	gag	tcc	gct	tcc	cgc	atc	gtg	gtt	gca			
2179																		
Leu	Phe	Thr	Ser	Leu	Phe	Ala	Glu	Ser	Ala	Ser	Arg	Ile	Val	Val	Ala			
		680					685					690						

acc aac cgc ggc gaa gag ttg gaa aag cgc gca gca gag ctg ggt gtt
2227

Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala Ala Glu Leu Gly Val
695 700 705

cca gtg ttc aag ctg ggc tgc acc aac gat tca gcc gtc atc gct gtc
2275

Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser Ala Val Ile Ala Val
710 715 720 725

aag ggc gca gac gtt gag ttc act gtt tcc gtg gag gaa ctc cgc gaa
2323

Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val Glu Glu Leu Arg Glu
730 735 740

gca tgg acc aac act ttg cct gag gcc ttc ggt cac gca gtt gga gct
2371

Ala Trp Thr Asn Thr Leu Pro Glu Ala Phe Gly His Ala Val Gly Ala
745 750 755

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<210> 912

<211> 762

<212> PRT

<213> Corynebacterium glutamicum

<400> 912

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35 40 45

Thr Val Tyr Ser Val Met Trp Ser Glu His Cys Ser Tyr Lys Ser Ser
50 55 60

Lys Val His Leu Arg Tyr Phe Gly Glu Thr Thr Thr Glu Glu Met Ala
65 70 75 80

Ser Lys Ile Leu Ala Gly Ile Gly Glu Asn Ala Gly Val Val Asp Ile
85 90 95

Gly Asp Gly Asn Ala Val Thr Phe Arg Val Glu Ser His Asn His Pro
100 105 110

Ser Phe Val Glu Pro His Gln Gly Ala Ala Thr Gly Val Gly Gly Ile
115 120 125

Val Arg Asp Ile Met Ala Met Gly Ala Arg Pro Ile Ala Val Met Asp
130 135 140

Gln Leu Arg Phe Gly Ala Leu Asp Asn Pro Asp Thr Gln Arg Val Phe

145					150					155				160	
Pro	Gly	Val	Val	Asp	Gly	Ile	Ser	His	Tyr	Gly	Asn	Cys	Leu	Gly	Leu
				165					170					175	
Pro	Asn	Ile	Gly	Gly	Glu	Thr	Val	Phe	Asp	Asp	Ser	Tyr	Ala	Gly	Asn
			180					185					190		
Pro	Leu	Val	Asn	Ala	Leu	Cys	Val	Gly	Thr	Leu	Lys	Val	Glu	Asp	Leu
		195					200					205			
Lys	Leu	Ala	Phe	Ala	Ser	Gly	Thr	Gly	Asn	Lys	Val	Ile	Leu	Phe	Gly
	210					215					220				
Ser	Arg	Thr	Gly	Leu	Asp	Gly	Ile	Gly	Gly	Val	Ser	Val	Leu	Gly	Ser
225					230					235					240
Ala	Ser	Phe	Glu	Glu	Gly	Glu	Glu	Arg	Lys	Leu	Pro	Ala	Val	Gln	Val
				245					250					255	
Gly	Asp	Pro	Phe	Ala	Glu	Lys	Val	Leu	Ile	Glu	Cys	Cys	Leu	Glu	Leu
			260					265					270		
Tyr	Lys	Ala	Gly	Val	Val	Val	Gly	Ile	Gln	Asp	Leu	Gly	Gly	Gly	Gly
		275					280					285			
Leu	Ala	Cys	Ala	Thr	Ser	Glu	Leu	Ala	Ala	Ala	Gly	Asp	Gly	Gly	Met
	290					295					300				
Arg	Val	Asn	Leu	Asp	Asn	Val	Pro	Leu	Arg	Ala	Glu	Asn	Met	Ser	Ala
305					310					315					320
Ala	Glu	Ile	Leu	Ala	Ser	Glu	Ser	Gln	Glu	Arg	Met	Cys	Ala	Val	Val
				325					330					335	
Thr	Pro	Glu	Asn	Val	Glu	Arg	Phe	Leu	Glu	Ile	Cys	Ala	Lys	Trp	Asp
			340					345					350		
Val	Thr	Cys	Ala	Glu	Ile	Gly	Glu	Val	Thr	Asp	Glu	Lys	Asp	Arg	Tyr
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Val	Val	Val	His	Asn	Gly	Glu	Val	Val	Ile	Asp	Ala	Pro	Pro	Ser	Thr
						375					380				
Ile	Asp	Glu	Gly	Pro	Val	Tyr	Asn	Arg	Pro	Val	Ala	Arg	Pro	Glu	Asn
385					390					395					400
Gln	Asp	Glu	Leu	Gln	Leu	Glu	Gly	Glu	Ile	Ala	Arg	Pro	Val	Asp	Val
				405					410					415	
Glu	Glu	Ile	Lys	Ala	Ala	Trp	Leu	Lys	Leu	Val	Ala	Ser	Pro	Ala	Leu
			420					425					430		
Ala	Ser	Arg	Ala	Phe	Ile	Thr	Glu	Gln	Tyr	Asp	Arg	Tyr	Val	Arg	Gly
		435					440					445			
Asn	Thr	Val	Gln	Ala	Lys	Asn	Ala	Asn	Ala	Gly	Val	Leu	Arg	Ile	Asp
						455					460				
Glu	Glu	Thr	Asn	Arg	Gly	Val	Ala	Ile	Ser	Ala	Asp	Ala	Ser	Gly	Arg
465					470					475					480

Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu
 485 490 495
 Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr
 500 505 510
 Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln
 515 520 525
 Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly
 530 535 540
 Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp
 545 550 555 560
 Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp
 565 570 575
 Asn Val Glu Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp
 580 585 590
 Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp
 595 600 605
 Gln Gln Val Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp
 610 615 620
 Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu
 625 630 635 640
 Phe Ala Ala Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu
 645 650 655
 Ala Glu Leu Ala Ile His Gln Lys Lys Gly Met Asp Val Asp Leu Ser
 660 665 670
 Gln Ile His Pro Ser Leu Phe Thr Ser Leu Phe Ala Glu Ser Ala Ser
 675 680 685
 Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu Lys Arg Ala
 690 695 700
 Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr Asn Asp Ser
 705 710 715 720
 Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr Val Ser Val
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 His Ala Val Gly Ala Asn Ala Val Val Ala
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<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (54) .. (638)

<223> FRXA02805

<400> 913

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 Val Phe
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 Pro Gly Val Val Asp Gly Ile Ser His Tyr Gly Asn Cys Leu Gly Leu
 5 10 15

cca aac atc ggt ggc gaa acc gtc ttc gac gat tcc tac gca ggt aac 155
 Pro Asn Ile Gly Gly Glu Thr Val Phe Asp Asp Ser Tyr Ala Gly Asn
 20 25 30

cca ctg gtc aac gca ctg tgc gtg ggt acc ctc aag gtg gaa gac ctc 203
 Pro Leu Val Asn Ala Leu Cys Val Gly Thr Leu Lys Val Glu Asp Leu
 35 40 45 50

aag ctt gca ttc gca tcc ggc acc ggc aac aag gtg atc ctg ttc ggt 251
 Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu Phe Gly
 55 60 65

tcc cgc acc ggc ctt gat ggc atc ggt ggc gtg tcc gtc ctg ggt tcc 299
 Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu Gly Ser
 70 75 80

gca tcc ttc gaa gaa ggc gaa gag cgc aag ctc cca gct gtt cag gtt 347
 Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val Gln Val
 85 90 95

ggc gat cct ttc gca gag aag gta ctc atc gag tgc tgc ctc gag ctg 395
 Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu Glu Leu
 100 105 110

tac aag gct ggc gtc gtg gtc ggt att cag gac ctc ggt ggc ggc gga 443
 Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly Gly Gly
 115 120 125 130

ctt gcg tgt gca acc tct gag ctg gca gcc gca ggc gac ggc ggc atg 491
 Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly Gly Met
 135 140 145

cgc gtc aac cta gac aac gtc cca ctg cgc gca gag aac atg tct gca 539
 Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met Ser Ala
 150 155 160

gct gaa atc ctg gct tcc gag tcc cag gag cgc atg tgt gct gtt gtc 587
 Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala Val Val
 165 170 175

acc cct gaa aac gtt gag cgt ttc ctc gag atc tgt gca aag tgg gat 635
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gtc 638
 Val
 195

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 35 40 45
 Asp Leu Lys Leu Ala Phe Ala Ser Gly Thr Gly Asn Lys Val Ile Leu
 50 55 60
 Phe Gly Ser Arg Thr Gly Leu Asp Gly Ile Gly Gly Val Ser Val Leu
 65 70 75 80
 Gly Ser Ala Ser Phe Glu Glu Gly Glu Glu Arg Lys Leu Pro Ala Val
 85 90 95
 Gln Val Gly Asp Pro Phe Ala Glu Lys Val Leu Ile Glu Cys Cys Leu
 100 105 110
 Glu Leu Tyr Lys Ala Gly Val Val Val Gly Ile Gln Asp Leu Gly Gly
 115 120 125
 Gly Gly Leu Ala Cys Ala Thr Ser Glu Leu Ala Ala Ala Gly Asp Gly
 130 135 140
 Gly Met Arg Val Asn Leu Asp Asn Val Pro Leu Arg Ala Glu Asn Met
 145 150 155 160
 Ser Ala Ala Glu Ile Leu Ala Ser Glu Ser Gln Glu Arg Met Cys Ala
 165 170 175
 Val Val Thr Pro Glu Asn Val Glu Arg Phe Leu Glu Ile Cys Ala Lys
 180 185 190
 Trp Asp Val
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 <222> (23)..(697)
 <223> FRXA00537

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tcc gcg gca aca ccg ttc aag caa aag aac gcc aat gct ggc gtc ttg	15			20			25			100
Ser Ala Ala Thr Pro Phe Lys Gln Lys Asn Ala Asn Ala Gly Val Leu										
cgt atc gac gaa gag acc anc cgt ggc gtt gcg atc tcc gcc gac gca	30			35			40			148
Arg Ile Asp Glu Glu Thr Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala										
tcc ggc cgt tac acc aag ctc gag cca aac act ggc gcg cag ctt gca	45			50			55			196
Ser Gly Arg Tyr Thr Lys Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala										
ctg gct gag gct tac cgc aac gtg gtc tcc acc ggt gca cgc cca gtg	60			65			70			244
Leu Ala Glu Ala Tyr Arg Asn Val Val Ser Thr Gly Ala Arg Pro Val										
gct gtc acc aac tgc ctg aac ttc ggt tcc cca gaa aac gct ggt gtt	75			80			85			292
Ala Val Thr Asn Cys Leu Asn Phe Gly Ser Pro Glu Asn Ala Gly Val										
atg tgg cag ttc aag gaa gca gtc cac ggt ctg gca gac gga tcc aag	95			100			105			340
Met Trp Gln Phe Lys Glu Ala Val His Gly Leu Ala Asp Gly Ser Lys										
ctt ttg ggc att cca gtg tcc ggc ggt aac gtc tcc ttc tac aac cag	110			115			120			388
Leu Leu Gly Ile Pro Val Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln										
act ggt gac gag ccc atc ctg cca acc cca gtc gtg ggt gtt ttg gga	125			130			135			436
Thr Gly Asp Glu Pro Ile Leu Pro Thr Pro Val Val Gly Val Leu Gly										
gtc ttg gac aac gtc gag cag agc atc ggc aac gtc ctc cca tcc gag	140			145			150			484
Val Leu Asp Asn Val Glu Gln Ser Ile Gly Asn Val Leu Pro Ser Glu										
gac aac gat ctc tac ctc ctg ggt gag acc ttc gat gag ttc ggt ggc	155			160			165			532
Asp Asn Asp Leu Tyr Leu Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly										
tcc atc tgg cag cag gtt tct ggc gct ggc ctc aac ggt ctg cca cca	175			180			185			580
Ser Ile Trp Gln Gln Val Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro										
gta gtt gac ctg ctc aac gag cag cgt ctt gca gac ctg ttc gtc ggt	190			195			200			628
Val Val Asp Leu Leu Asn Glu Gln Arg Leu Ala Asp Leu Phe Val Gly										
tct gat ctg ttt gct gca tcc cac gat ctg tct gag ggc ggc ctt ggc	205			210			215			676
Ser Asp Leu Phe Ala Ala Ser His Asp Leu Ser Glu Gly Gly Leu Gly										
cag acc ctc gca gag ctt gcg	220			225						697
Gln Thr Leu Ala Glu Leu Ala										

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<213> Corynebacterium glutamicum

<400> 916

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 20 25 30
 Xaa Arg Gly Val Ala Ile Ser Ala Asp Ala Ser Gly Arg Tyr Thr Lys
 35 40 45
 Leu Glu Pro Asn Thr Gly Ala Gln Leu Ala Leu Ala Glu Ala Tyr Arg
 50 55 60
 Asn Val Val Ser Thr Gly Ala Arg Pro Val Ala Val Thr Asn Cys Leu
 65 70 75 80
 Asn Phe Gly Ser Pro Glu Asn Ala Gly Val Met Trp Gln Phe Lys Glu
 85 90 95
 Ala Val His Gly Leu Ala Asp Gly Ser Lys Leu Leu Gly Ile Pro Val
 100 105 110
 Ser Gly Gly Asn Val Ser Phe Tyr Asn Gln Thr Gly Asp Glu Pro Ile
 115 120 125
 Leu Pro Thr Pro Val Val Gly Val Leu Gly Val Leu Asp Asn Val Glu
 130 135 140
 Gln Ser Ile Gly Asn Val Leu Pro Ser Glu Asp Asn Asp Leu Tyr Leu
 145 150 155 160
 Leu Gly Glu Thr Phe Asp Glu Phe Gly Gly Ser Ile Trp Gln Gln Val
 165 170 175
 Ser Gly Ala Gly Leu Asn Gly Leu Pro Pro Val Val Asp Leu Leu Asn
 180 185 190
 Glu Gln Arg Leu Ala Asp Leu Phe Val Gly Ser Asp Leu Phe Ala Ala
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 Ser His Asp Leu Ser Glu Gly Gly Leu Gly Gln Thr Leu Ala Glu Leu
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Ala
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<211> 302

<212> DNA

<213> Corynebacterium glutamicum

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<223> FRXA00561

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  1                    5                    10                    15

ccc gct tcc cgc atc gtg gtt gca acc aac cgc ggc gaa gag ttg gaa 96
Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu
                    20                    25                    30

aag cgc gca gca gag ctg ggt gtt cca gtg ttc aag ctg ggc tgc acc 144
Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr
                    35                    40                    45

aac gat tca gcc gtc atc gct gtc aag ggc gca gac gtt gag ttc act 192
Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr
                    50                    55                    60

gtt tcc gtg gag gaa ctc cgc gaa gca tgg acc aac act ttg cct gag 240
Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu
  65                    70                    75                    80

gcc ttc ggt cac gca gtt gga gct aac gca gta gtt gca taattttctg 289
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Pro Ala Ser Arg Ile Val Val Ala Thr Asn Arg Gly Glu Glu Leu Glu
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Lys Arg Ala Ala Glu Leu Gly Val Pro Val Phe Lys Leu Gly Cys Thr
                    35                    40                    45

Asn Asp Ser Ala Val Ile Ala Val Lys Gly Ala Asp Val Glu Phe Thr
                    50                    55                    60

Val Ser Val Glu Glu Leu Arg Glu Ala Trp Thr Asn Thr Leu Pro Glu
  65                    70                    75                    80

Ala Phe Gly His Ala Val Gly Ala Asn Ala Val Val Ala
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(769)
 <223> RXA00541

<400> 919

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Val Ser Ala Lys Ile
1 5

ggt gtc att acc ttc cca ggc acc ctt gac gat gta gat gca gca cgc 163
Gly Val Ile Thr Phe Pro Gly Thr Leu Asp Asp Val Asp Ala Ala Arg
10 15 20

gct gct cgc atc gca ggt gca gaa gta atc agc ctg tgg cac gct gac 211
Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser Leu Trp His Ala Asp
25 30 35

gag gat ctc aag ggc gtc gac gca gtt gtc gtt ccc ggt gga ttc tcc 259
Glu Asp Leu Lys Gly Val Asp Ala Val Val Val Pro Gly Gly Phe Ser
40 45 50

tac ggc gat tac ctg cgc acc ggt gca atc tct gca ctg gcg cca gta 307
Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser Ala Leu Ala Pro Val
55 60 65

atg cag tcc gtg att gag cag gcc ggt aag ggt atg cca gtc ttg ggc 355
Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly Met Pro Val Leu Gly
70 75 80 85

att tgc aac ggc ttc cag atc ctc acc gaa gca cgc ctg ctt cca ggc 403
Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala Arg Leu Leu Pro Gly
90 95 100

gcg ctg acc cgc aac aag ggt ctg cac ttt cac tgt gta gac gca cac 451
Ala Leu Thr Arg Asn Lys Gly Leu His Phe His Cys Val Asp Ala His
105 110 115

ctc gtt gta gag aac aac acc act gca tgg acc aac act ttg gaa aag 499
Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr Asn Thr Leu Glu Lys
120 125 130

ggt cag cag atc ctt att cct gca aag cac ggt gaa ggt cgc ttc cag 547
Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly Glu Gly Arg Phe Gln
135 140 145

gca gac gca gag acc atc gcc cag ctt gag ggt gaa ggc cgc gtg gtg 595
Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly Glu Gly Arg Val Val
150 155 160 165

ttc cgt tac acc gat aac ttc aac ggt tcc gtc aac gat atc gcc ggt 643
Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val Asn Asp Ile Ala Gly
170 175 180

atc act aat gaa act ggt cgc atc gtc ggt ctc atg ccg cac ccg gaa 691
Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu Met Pro His Pro Glu
185 190 195

cat gcc gtc gaa aag cta acc ggc cca tct att gat ggc ctg gag ctg 739
His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile Asp Gly Leu Glu Leu
200 205 210

ttc ctg tcc gcc gtt ggc acc atc gcg gct taagaggagt aaatatgagc 789

Phe Leu Ser Ala Val Gly Thr Ile Ala Ala
215 220

act

792

<210> 920
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<212> PRT
<213> Corynebacterium glutamicum

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Val Asp Ala Ala Arg Ala Ala Arg Ile Ala Gly Ala Glu Val Ile Ser
20 25 30
Leu Trp His Ala Asp Glu Asp Leu Lys Gly Val Asp Ala Val Val Val
35 40 45
Pro Gly Gly Phe Ser Tyr Gly Asp Tyr Leu Arg Thr Gly Ala Ile Ser
50 55 60
Ala Leu Ala Pro Val Met Gln Ser Val Ile Glu Gln Ala Gly Lys Gly
65 70 75 80
Met Pro Val Leu Gly Ile Cys Asn Gly Phe Gln Ile Leu Thr Glu Ala
85 90 95
Arg Leu Leu Pro Gly Ala Leu Thr Arg Asn Lys Gly Leu His Phe His
100 105 110
Cys Val Asp Ala His Leu Val Val Glu Asn Asn Thr Thr Ala Trp Thr
115 120 125
Asn Thr Leu Glu Lys Gly Gln Gln Ile Leu Ile Pro Ala Lys His Gly
130 135 140
Glu Gly Arg Phe Gln Ala Asp Ala Glu Thr Ile Ala Gln Leu Glu Gly
145 150 155 160
Glu Gly Arg Val Val Phe Arg Tyr Thr Asp Asn Phe Asn Gly Ser Val
165 170 175
Asn Asp Ile Ala Gly Ile Thr Asn Glu Thr Gly Arg Ile Val Gly Leu
180 185 190
Met Pro His Pro Glu His Ala Val Glu Lys Leu Thr Gly Pro Ser Ile
195 200 205
Asp Gly Leu Glu Leu Phe Leu Ser Ala Val Gly Thr Ile Ala Ala
210 215 220

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<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(991)

<223> RXA00620

<400> 921

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 Met Arg Pro Glu Leu
 1 5

tcc cag tac aag cac ctg tcg gca ggc aag gtc cgt gag atc tac gag 163
 Ser Gln Tyr Lys His Leu Ser Ala Gly Lys Val Arg Glu Ile Tyr Glu
 10 15 20

atc gac gac aag cac atc ctc atg gtg gct tcc gat cgt atc tct gca 211
 Ile Asp Asp Lys His Ile Leu Met Val Ala Ser Asp Arg Ile Ser Ala
 25 30 35

tac gat ttc atc ctc gat acc gaa att cca gac aag ggt cga gtg ctc 259
 Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp Lys Gly Arg Val Leu
 40 45 50

act gcg atg agc cag ttc ttc ttc gac acc atc gat ttt cct aat cac 307
 Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile Asp Phe Pro Asn His
 55 60 65

ctt gca ggt ccc gct gat gat cca cgt atc cca gaa gaa gtt ttg gga 355
 Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro Glu Glu Val Leu Gly
 70 75 80 85

cga gca atg gtg tgc aag aag ctc aac atg ctt cct ttt gaa tgc gtg 403
 Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu Pro Phe Glu Cys Val
 90 95 100

gtt cgt gga tac ctc act ggc tct gga ctt gtt gaa tac aag cag acc 451
 Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val Glu Tyr Lys Gln Thr
 105 110 115

agc tcc gtg tgt gga gtt gag ctc cca gaa ggc ctc gtt gaa tct tct 499
 Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly Leu Val Glu Ser Ser
 120 125 130

cag ctg cct gag cca atc ttt acc cca gcc acc aag gct gac atc ggc 547
 Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr Lys Ala Asp Ile Gly
 135 140 145

gac cac gac atc aat gtc tcc ttt gac gtt gtt gaa gaa cgt ctc ggc 595
 Asp His Asp Ile Asn Val Ser Phe Asp Val Val Glu Glu Arg Leu Gly
 150 155 160 165

gaa gct cgt gcg aac cag ttg cgc gat gcc tct att gct att tac aag 643
 Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser Ile Ala Ile Tyr Lys
 170 175 180

gct gct gct gag atc gcc cgt gac cgt ggc gtc atc ctt gcc gac acc 691
 Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val Ile Leu Ala Asp Thr
 185 190 195

aaa ttt gag ttc ggc atc gat gaa gat ggc acc ctc gtg ctt ggt gat 739
 Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr Leu Val Leu Gly Asp

200	205	210	
gaa gtc ctt acc cca gat tcc tcc cgc tac tgg cct ttg gaa ggc tat			787
Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp Pro Leu Glu Gly Tyr			
215	220	225	
gaa gca gga tct gtg caa cca agc ttt gat aag caa ttc gtg cgc aac			835
Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys Gln Phe Val Arg Asn			
230	235	240	245
tgg ctc acc ggc cct aaa tct ggc tgg gac aag gat tcc ggc ttg gag			883
Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys Asp Ser Gly Leu Glu			
	250	255	260
cca cca gct ctg cca ggt tcc gtt gtt gag gca acc cgc gag cgc tac			931
Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala Thr Arg Glu Arg Tyr			
	265	270	275
atc gag gcc tac gag ctg att tct ggt cag aag ttc tgc cag tgg att			979
Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys Phe Cys Gln Trp Ile			
	280	285	290

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 1014
 Gly Ser Cys Val
 295

<210> 922
 <211> 297
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 <213> Corynebacterium glutamicum

<400> 922
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 20 25 30
 Asp Arg Ile Ser Ala Tyr Asp Phe Ile Leu Asp Thr Glu Ile Pro Asp
 35 40 45
 Lys Gly Arg Val Leu Thr Ala Met Ser Gln Phe Phe Phe Asp Thr Ile
 50 55 60
 Asp Phe Pro Asn His Leu Ala Gly Pro Ala Asp Asp Pro Arg Ile Pro
 65 70 75 80
 Glu Glu Val Leu Gly Arg Ala Met Val Cys Lys Lys Leu Asn Met Leu
 85 90 95
 Pro Phe Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Leu Val
 100 105 110
 Glu Tyr Lys Gln Thr Ser Ser Val Cys Gly Val Glu Leu Pro Glu Gly
 115 120 125
 Leu Val Glu Ser Ser Gln Leu Pro Glu Pro Ile Phe Thr Pro Ala Thr
 130 135 140

Lys Ala Asp Ile Gly Asp His Asp Ile Asn Val Ser Phe Asp Val Val
 145 150 155 160
 Glu Glu Arg Leu Gly Glu Ala Arg Ala Asn Gln Leu Arg Asp Ala Ser
 165 170 175
 Ile Ala Ile Tyr Lys Ala Ala Ala Glu Ile Ala Arg Asp Arg Gly Val
 180 185 190
 Ile Leu Ala Asp Thr Lys Phe Glu Phe Gly Ile Asp Glu Asp Gly Thr
 195 200 205
 Leu Val Leu Gly Asp Glu Val Leu Thr Pro Asp Ser Ser Arg Tyr Trp
 210 215 220
 Pro Leu Glu Gly Tyr Glu Ala Gly Ser Val Gln Pro Ser Phe Asp Lys
 225 230 235 240
 Gln Phe Val Arg Asn Trp Leu Thr Gly Pro Lys Ser Gly Trp Asp Lys
 245 250 255
 Asp Ser Gly Leu Glu Pro Pro Ala Leu Pro Gly Ser Val Val Glu Ala
 260 265 270
 Thr Arg Glu Arg Tyr Ile Glu Ala Tyr Glu Leu Ile Ser Gly Gln Lys
 275 280 285
 Phe Cys Gln Trp Ile Gly Ser Cys Val
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1270)
 <223> RXN00770

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 Leu Leu Ser Pro Tyr
 1 5
 gcg tgg ggg ttg tcc cgc gca ctt tta gac agt tat gtt cct aat aag 163
 Ala Trp Gly Leu Ser Arg Ala Leu Leu Asp Ser Tyr Val Pro Asn Lys
 10 15 20
 ttc caa acc cca gca gga gaa gcg aag tac acg atg agt gat cac cag 211
 Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr Met Ser Asp His Gln
 25 30 35
 gac acc acc gcc gaa ggc gtt tca tac gca gca gca gga gtc gac atc 259
 Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala Ala Gly Val Asp Ile
 40 45 50
 gaa gcc ggc gat cgt gcc gtc gaa ctc ttt gca cca atg gcc aag cgc 307

Glu	Ala	Gly	Asp	Arg	Ala	Val	Glu	Leu	Phe	Ala	Pro	Met	Ala	Lys	Arg	
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gcc	acc	cgc	cca	gag	gtt	ctt	ggc	aac	ctc	gga	ggc	ttc	gca	gga	ctc	355
Ala	Thr	Arg	Pro	Glu	Val	Leu	Gly	Asn	Leu	Gly	Gly	Phe	Ala	Gly	Leu	
70					75					80					85	
ttt	gag	ctc	gga	aaa	tac	aag	aag	cca	atc	ctc	gca	gca	gga	tct	gac	403
Phe	Glu	Leu	Gly	Lys	Tyr	Lys	Lys	Pro	Ile	Leu	Ala	Ala	Gly	Ser	Asp	
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gga	gtc	ggc	acc	aag	ctt	gtc	atc	gcc	cag	atg	atg	gac	aag	cac	gac	451
Gly	Val	Gly	Thr	Lys	Leu	Val	Ile	Ala	Gln	Met	Met	Asp	Lys	His	Asp	
			105					110					115			
acc	atc	ggc	atc	gac	ctt	gtt	gca	atg	tgt	gtg	gat	gac	ctc	gtt	gtc	499
Thr	Ile	Gly	Ile	Asp	Leu	Val	Ala	Met	Cys	Val	Asp	Asp	Leu	Val	Val	
		120					125					130				
acc	ggc	gca	gag	cca	ctg	ttc	ctc	cag	gac	tac	atc	gcc	atc	ggc	aag	547
Thr	Gly	Ala	Glu	Pro	Leu	Phe	Leu	Gln	Asp	Tyr	Ile	Ala	Ile	Gly	Lys	
	135					140					145					
gtt	gtc	cca	gag	cac	gtt	gct	gag	atc	gtc	tcc	ggt	atc	gca	gaa	ggc	595
Val	Val	Pro	Glu	His	Val	Ala	Glu	Ile	Val	Ser	Gly	Ile	Ala	Glu	Gly	
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Cys	Val	Gln	Ala	Gly	Cys	Ala	Leu	Leu	Gly	Gly	Glu	Thr	Ala	Glu	His	
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cca	ggt	gtt	atg	gaa	cca	gac	cac	tac	gat	gtc	tcc	gca	act	gca	gtc	691
Pro	Gly	Val	Met	Glu	Pro	Asp	His	Tyr	Asp	Val	Ser	Ala	Thr	Ala	Val	
			185					190					195			
ggc	gtt	gtc	gaa	gca	gat	gaa	ctg	cta	gga	cca	gac	cgc	gtc	cgc	gca	739
Gly	Val	Val	Glu	Ala	Asp	Glu	Leu	Leu	Gly	Pro	Asp	Arg	Val	Arg	Ala	
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ggc	gac	gtc	ctc	atc	ggc	atg	gct	tcc	tcc	ggt	ctg	cac	tcc	aac	ggt	787
Gly	Asp	Val	Leu	Ile	Gly	Met	Ala	Ser	Ser	Gly	Leu	His	Ser	Asn	Gly	
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tac	tcc	ctg	gct	cgc	cac	gtc	ctc	ctg	gaa	aag	gca	ggc	ctg	gcg	ctt	835
Tyr	Ser	Leu	Ala	Arg	His	Val	Leu	Leu	Glu	Lys	Ala	Gly	Leu	Ala	Leu	
230					235					240					245	
gac	gga	cac	atc	gaa	gaa	ctc	gga	cgc	acc	ctc	ggt	gaa	gaa	ctt	ctc	883
Asp	Gly	His	Ile	Glu	Glu	Leu	Gly	Arg	Thr	Leu	Gly	Glu	Glu	Leu	Leu	
				250					255					260		
gag	cca	acc	cgc	atc	tac	gcc	aag	gac	tgc	ctg	gca	ctg	atc	gca	gag	931
Glu	Pro	Thr	Arg	Ile	Tyr	Ala	Lys	Asp	Cys	Leu	Ala	Leu	Ile	Ala	Glu	
			265					270					275			
tgc	gaa	gtt	cac	acc	ttc	tgc	cac	gtc	acc	ggc	ggc	ggc	ctc	gca	ggc	979
Cys	Glu	Val	His	Thr	Phe	Cys	His	Val	Thr	Gly	Gly	Gly	Leu	Ala	Gly	
		280					285					290				
aac	ctc	gag	cgg	gtt	gtc	cca	gaa	ggg	ctc	gtc	gca	gaa	atg	tcc	cga	1027

Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val Ala Glu Met Ser Arg
 295 300 305

gca act tgg acc cca ggc caa atc ttc cgc acc atc tcc tct gtg ggc
 1075

Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr Ile Ser Ser Val Gly
 310 315 320 325

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 1123

Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe Asn Met Gly Val Gly
 330 335 340

atg gtt gca gtc gtt gct gaa aag gac cgc gac cgc gcc ctg gca atg
 1171

Met Val Ala Val Val Ala Glu Lys Asp Arg Asp Arg Ala Leu Ala Met
 345 350 355

ctc acc gca cgt cac att gac tgc tgg gaa atc gga acc gta cgc aac
 1219

Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile Gly Thr Val Arg Asn
 360 365 370

ggt gaa gag gga gag cct cgc gtg atc ctc aac ggc gag cac cct ggc
 1267

Gly Glu Glu Gly Glu Pro Arg Val Ile Leu Asn Gly Glu His Pro Gly
 375 380 385

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 1293

Tyr
 390

<210> 924

<211> 390

<212> PRT

<213> Corynebacterium glutamicum

<400> 924

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 20 25 30

Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala
 35 40 45

Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala
 50 55 60

Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly
 65 70 75 80

Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu
 85 90 95

Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met
 100 105 110


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Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val
    115                                120                                125

Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr
    130                                135                                140

Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser
    145                                150                                155                                160

Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly
                                165                                170                                175

Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val
                                180                                185                                190

Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro
                                195                                200                                205

Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly
    210                                215                                220

Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys
    225                                230                                235                                240

Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Leu
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Gly Glu Glu Leu Leu Glu Pro Thr Arg Ile Tyr Ala Lys Asp Cys Leu
                                260                                265                                270

Ala Leu Ile Ala Glu Cys Glu Val His Thr Phe Cys His Val Thr Gly
                                275                                280                                285

Gly Gly Leu Ala Gly Asn Leu Glu Arg Val Val Pro Glu Gly Leu Val
    290                                295                                300

Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile Phe Arg Thr
    305                                310                                315                                320

Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu Lys Thr Phe
                                325                                330                                335

Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys Asp Arg Asp
                                340                                345                                350

Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys Trp Glu Ile
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Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val Ile Leu Asn
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Gly Glu His Pro Gly Tyr
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<212> DNA

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<220>

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<222> (15)..(818)

<223> FRXA00557

<400> 925

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ctt tta gac agt tat gtt cct aat aag ttc caa acc cca gca gga gaa	98
Leu Leu Asp Ser Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu	
15 20 25	
gcg aag tac acg atg agt gat cac cag gac acc acc gcc gaa ggc gtt	146
Ala Lys Tyr Thr Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val	
30 35 40	
tca tac gca gca gca gga gtc gac atc gaa gcc ggc gat cgt gcc gtc	194
Ser Tyr Ala Ala Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val	
45 50 55 60	
gaa ctc ttt gca cca atg gcc aag cgc gcc acc cgc cca gag gtt ctt	242
Glu Leu Phe Ala Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu	
65 70 75	
ggc aac ctc gga ggc ttc gca gga ctc ttt gag ctc gga aaa tac aag	290
Gly Asn Leu Gly Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys	
80 85 90	
aag cca atc ctc gca gca gga tct gac gga gtc ggc acc aag ctt gtc	338
Lys Pro Ile Leu Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val	
95 100 105	
atc gcc cag atg atg gac aag cac gac acc atc ggc atc gac ctt gtt	386
Ile Ala Gln Met Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val	
110 115 120	
gca atg tgt gtg gat gac ctc gtt gtc acc ggc gca gag cca ctg ttc	434
Ala Met Cys Val Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe	
125 130 135 140	
ctc cag gac tac atc gcc atc ggc aag gtt gtc cca gag cac gtt gct	482
Leu Gln Asp Tyr Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala	
145 150 155	
gag atc gtc tcc ggt atc gca gaa ggc tgt gtc cag gca ggc tgt gct	530
Glu Ile Val Ser Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala	
160 165 170	
ctg ctc ggt ggc gaa acc gca gaa cac cca ggt gtt atg gaa cca gac	578
Leu Leu Gly Gly Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp	
175 180 185	
cac tac gat gtc tcc gca act gca gtc ggc gtt gtc gaa gca gat gaa	626
His Tyr Asp Val Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu	
190 195 200	
ctg cta gga cca gac cgc gtc cgc gca ggc gac gtc ctc atc ggc atg	674
Leu Leu Gly Pro Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met	
205 210 215 220	

gct tcc tcc ggt ctg cac tcc aac ggt tac tcc ctg gct cgc cac gtc 722
 Ala Ser Ser Gly Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val
 225 230 235

ctc ctg gaa aag gca ggc ctg gcg ctt gac gga cac atc gaa gaa ctc 770
 Leu Leu Glu Lys Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu
 240 245 250

gga cgc acc ccc ggt gaa gaa ctt ctc gag cca acc cgc atg tac gcc 818
 Gly Arg Thr Pro Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala
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<210> 926

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 926

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Tyr Val Pro Asn Lys Phe Gln Thr Pro Ala Gly Glu Ala Lys Tyr Thr
 20 25 30

Met Ser Asp His Gln Asp Thr Thr Ala Glu Gly Val Ser Tyr Ala Ala
 35 40 45

Ala Gly Val Asp Ile Glu Ala Gly Asp Arg Ala Val Glu Leu Phe Ala
 50 55 60

Pro Met Ala Lys Arg Ala Thr Arg Pro Glu Val Leu Gly Asn Leu Gly
 65 70 75 80

Gly Phe Ala Gly Leu Phe Glu Leu Gly Lys Tyr Lys Lys Pro Ile Leu
 85 90 95

Ala Ala Gly Ser Asp Gly Val Gly Thr Lys Leu Val Ile Ala Gln Met
 100 105 110

Met Asp Lys His Asp Thr Ile Gly Ile Asp Leu Val Ala Met Cys Val
 115 120 125

Asp Asp Leu Val Val Thr Gly Ala Glu Pro Leu Phe Leu Gln Asp Tyr
 130 135 140

Ile Ala Ile Gly Lys Val Val Pro Glu His Val Ala Glu Ile Val Ser
 145 150 155 160

Gly Ile Ala Glu Gly Cys Val Gln Ala Gly Cys Ala Leu Leu Gly Gly
 165 170 175

Glu Thr Ala Glu His Pro Gly Val Met Glu Pro Asp His Tyr Asp Val
 180 185 190

Ser Ala Thr Ala Val Gly Val Val Glu Ala Asp Glu Leu Leu Gly Pro
 195 200 205

Asp Arg Val Arg Ala Gly Asp Val Leu Ile Gly Met Ala Ser Ser Gly
 210 215 220

Leu His Ser Asn Gly Tyr Ser Leu Ala Arg His Val Leu Leu Glu Lys
 225 230 235 240

Ala Gly Leu Ala Leu Asp Gly His Ile Glu Glu Leu Gly Arg Thr Pro
 245 250 255

Gly Glu Glu Leu Leu Glu Pro Thr Arg Met Tyr Ala
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<210> 927

<211> 338

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(315)

<223> FRXA00770

<400> 927

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ggg ctc gtc gca gaa atg tcc cga gca act tgg acc cca ggc caa atc 96
 Gly Leu Val Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile
 20 25 30

ttc cgc acc atc tcc tct gtg ggc aag gtt tcc cgc gaa gaa atg gaa 144
 Phe Arg Thr Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu
 35 40 45

aag acc ttc aac atg ggt gtc ggc atg gtt gca gtc gtt gct gaa aag 192
 Lys Thr Phe Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys
 50 55 60

gac cgc gac cgc gcc ctg gca atg ctc acc gca cgt cac att gac tgc 240
 Asp Arg Asp Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys
 65 70 75 80

tgg gaa atc gga acc gta cgc aac ggt gaa gag gga gag cct cgc gtg 288
 Trp Glu Ile Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val
 85 90 95

atc ctc aac ggc gag cac cct ggc tac taagcccaac tgtctgctct 335
 Ile Leu Asn Gly Glu His Pro Gly Tyr
 100 105

aag 338

<210> 928

<211> 105

<212> PRT

<213> Corynebacterium glutamicum

<400> 928

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Gly Leu Val Ala Glu Met Ser Arg Ala Thr Trp Thr Pro Gly Gln Ile
 20 25 30

Phe Arg Thr Ile Ser Ser Val Gly Lys Val Ser Arg Glu Glu Met Glu
 35 40 45

Lys Thr Phe Asn Met Gly Val Gly Met Val Ala Val Val Ala Glu Lys
 50 55 60

Asp Arg Asp Arg Ala Leu Ala Met Leu Thr Ala Arg His Ile Asp Cys
 65 70 75 80

Trp Glu Ile Gly Thr Val Arg Asn Gly Glu Glu Gly Glu Pro Arg Val
 85 90 95

Ile Leu Asn Gly Glu His Pro Gly Tyr
 100 105

<210> 929

<211> 1320

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1297)

<223> RXN02345

<400> 929

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 Val Thr Ser Thr Gly 5
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aac caa gcc cac gct cca gga atg ccc atc gtc gca gta att ggt gac 163
 Asn Gln Ala His Ala Pro Gly Met Pro Ile Val Ala Val Ile Gly Asp 20
 10 15

ggc caa tta gcc cgc atg atg cag acc tcc gcc atc gaa ctc gga caa 211
 Gly Gln Leu Ala Arg Met Met Gln Thr Ser Ala Ile Glu Leu Gly Gln 35
 25 30

tca ctg cga gtt cta gct gga gcg ccg gat tcc tcc gca gct caa gta 259
 Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser Ser Ala Ala Gln Val 50
 40 45

gct gct gat gtt gtt ctc ggc gat tac acc aac att gat gat ctg cgc 307
 Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn Ile Asp Asp Leu Arg 65
 55 60 65

gtc gcc atc gaa ggc gcc gat gtg atg acc ttc gac cac gag cac gtc 355
 Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe Asp His Glu His Val 85
 70 75 80

ccc aac gaa cac ctg cac caa ctc atc gca gaa ggc gtc aac gtt cag 403
 Pro Asn Glu His Leu His Gln Leu Ile Ala Glu Gly Val Asn Val Gln 100
 90 95 100

cca cgc cca gaa gcg ctg gtc aac gca caa gac aaa ctt gtc atg cgc 451

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Lys	Arg	Leu	Arg	Glu	Leu	Gly	Ala	Pro	Val	Pro	Pro	Phe	Ala	Ala	Ile		
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Asp	Gly	Gly	Thr	Pro	Leu	Met	Ala	Glu	Lys	Lys	Val	Ala	Leu	Asn	Arg		
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gaa	ctg	tcc	gcc	atg	gtt	gcc	cgc	acc	cca	agt	gga	gaa	acc	aaa	gcg	739	
Glu	Leu	Ser	Ala	Met	Val	Ala	Arg	Thr	Pro	Ser	Gly	Glu	Thr	Lys	Ala		
		200					205					210					
tgg	cca	gtc	gta	gaa	tca	gtg	cag	aag	aac	ggg	gtg	tgt	gca	gaa	gca	787	
Trp	Pro	Val	Val	Glu	Ser	Val	Gln	Lys	Asn	Gly	Val	Cys	Ala	Glu	Ala		
	215					220					225						
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Ile	Ala	Pro	Ala	Pro	Glu	Leu	Ser	Ala	Glu	Leu	Gln	Glu	Ser	Thr	Arg		
230					235					240					245		
gga	ttg	gcc	cag	aag	atc	gcc	acg	gaa	ctc	ggc	gtc	act	ggg	gtc	ttg	883	
Gly	Leu	Ala	Gln	Lys	Ile	Ala	Thr	Glu	Leu	Gly	Val	Thr	Gly	Val	Leu		
				250				255						260			
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Ala	Val	Glu	Leu	Phe	Glu	Thr	Leu	Asp	Gln	Asn	Gly	Gln	Pro	Glu	Ile		
			265					270					275				
ttt	gtc	aac	gag	ctc	gcc	atg	cgt	tca	cac	aac	acc	ggc	cac	tgg	act	979	
Phe	Val	Asn	Glu	Leu	Ala	Met	Arg	Ser	His	Asn	Thr	Gly	His	Trp	Thr		
		280					285					290					
caa	gat	ggc	tgc	gtg	acc	agc	caa	ttc	gag	cag	cac	ctc	cgc	gca	gtc		
1027																	
Gln	Asp	Gly	Cys	Val	Thr	Ser	Gln	Phe	Glu	Gln	His	Leu	Arg	Ala	Val		
	295					300					305						
ctc	gac	tac	cca	ctg	ggg	gct	acc	gac	act	ttg	gct	gat	tac	acc	gtg		
1075																	
Leu	Asp	Tyr	Pro	Leu	Gly	Ala	Thr	Asp	Thr	Leu	Ala	Asp	Tyr	Thr	Val		
310					315					320					325		
atg	gcc	aac	gtg	ctc	ggg	gcc	gac	acc	gac	cca	gag	atg	ccc	atg	gca		
1123																	
Met	Ala	Asn	Val	Leu	Gly	Ala	Asp	Thr	Asp	Pro	Glu	Met	Pro	Met	Ala		
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acc cgc atg gtg gaa gtg ggg cgc aag tac cca gat gcc aag att cac
1171

Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp Ala Lys Ile His
345 350 355

ctc tac ggc aag gga cat cgc ccg gga cga aag att ggc cac gtc aac
1219

Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile Gly His Val Asn
360 365 370

atg gtg gga tcc gac ctt gaa aag acc cga gcc gaa gcc ctg gcc tgc
1267

Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu Ala Leu Ala Cys
375 380 385

gca tac ttc ctt gtc aac gct cgc tgg gat taggtctttt ctgagcgccta
1317

Ala Tyr Phe Leu Val Asn Ala Arg Trp Asp
390 395

gca
1320

<210> 930

<211> 399

<212> PRT

<213> Corynebacterium glutamicum

<400> 930

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20 25 30

Ile Glu Leu Gly Gln Ser Leu Arg Val Leu Ala Gly Ala Pro Asp Ser
35 40 45

Ser Ala Ala Gln Val Ala Ala Asp Val Val Leu Gly Asp Tyr Thr Asn
50 55 60

Ile Asp Asp Leu Arg Val Ala Ile Glu Gly Ala Asp Val Met Thr Phe
65 70 75 80

Asp His Glu His Val Pro Asn Glu His Leu His Gln Leu Ile Ala Glu
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Gly Val Asn Val Gln Pro Arg Pro Glu Ala Leu Val Asn Ala Gln Asp
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Lys Leu Val Met Arg Lys Arg Leu Arg Glu Leu Gly Ala Pro Val Pro
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Pro Phe Ala Ala Ile Glu Ser Val Glu Asp Ala Val Gly Phe Phe Glu
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Gly Lys Gly Val Trp Phe Pro Ala Asp Val Ala Glu Leu Gln Ser Leu
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 Val Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys
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 Val Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser
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 Gly Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly
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 Val Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu
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 Gln Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly
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 Val Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn
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 Gly Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn
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 Thr Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln
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 Asp Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys
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Ala Glu Leu Leu Asp Gly Gly Thr Pro Leu Met Ala Glu Lys Lys Val	
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Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly	
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Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val	
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Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln	
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Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val	
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Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly	
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Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr	
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Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala	
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Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu	
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Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp	
210 215 220	
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Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile	
225 230 235 240	
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Gly His Val Asn Met Val Gly Ser Asp Leu Glu Lys Thr Arg Ala Glu	
245 250 255	
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Ala Leu Asn Arg Glu Leu Ser Ala Met Val Ala Arg Thr Pro Ser Gly
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Glu Thr Lys Ala Trp Pro Val Val Glu Ser Val Gln Lys Asn Gly Val
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Cys Ala Glu Ala Ile Ala Pro Ala Pro Glu Leu Ser Ala Glu Leu Gln
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Glu Ser Thr Arg Gly Leu Ala Gln Lys Ile Ala Thr Glu Leu Gly Val
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Thr Gly Val Leu Ala Val Glu Leu Phe Glu Thr Leu Asp Gln Asn Gly
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Gln Pro Glu Ile Phe Val Asn Glu Leu Ala Met Arg Ser His Asn Thr
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Gly His Trp Thr Gln Asp Gly Cys Val Thr Ser Gln Phe Glu Gln His
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Leu Arg Ala Val Leu Asp Tyr Pro Leu Gly Ala Thr Asp Thr Leu Ala
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Asp Tyr Thr Val Met Ala Asn Val Leu Gly Ala Asp Thr Asp Pro Glu
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Met Pro Met Ala Thr Arg Met Val Glu Val Gly Arg Lys Tyr Pro Asp
 210 215 220

Ala Lys Ile His Leu Tyr Gly Lys Gly His Arg Pro Gly Arg Lys Ile
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 Val Gly Pro Leu Val 5
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 Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala 20
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gca gag gta ctc gct gag ttt ggc att cct ttt gaa gtc gga gtt gtc 211
 Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val 35
 25 30

tct gca cac cgc acc cca gag aag atg ctc aac tac gca aag act gca 259
 Ser Ala His Arg Thr Pro Glu Lys Met Leu Asn Tyr Ala Lys Thr Ala 50
 40 45

cat gag cgc ggc atc aag acg atc atc gcg tgt gct ggc ggc gct gca 307
 His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys Ala Gly Gly Ala Ala 65
 55 60

cac ctg cca ggc atg gtg gct gca gca act cca ctt cca gtc atc ggt 355
 His Leu Pro Gly Met Val Ala Ala Ala Thr Pro Leu Pro Val Ile Gly 85
 70 75 80

gtt cca cgc gca ttg aag gat ctc gac ggt ttg gat tcc ttg ctg tcc 403
 Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu Asp Ser Leu Leu Ser 100
 90 95

atc gtc cag atg cca ggc ggc gtt cca gtc gcc act gtc tcc atc ggt 451
 Ile Val Gln Met Pro Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly 115
 105 110

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 Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly 130
 120 125

gat cct tct ttg gtc acg aag atg gcc gat tac caa gag aat atg gcg 547
 Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala 145
 135 140

aag gaa gtt gaa gcc aag gac gaa gca ctg aag aag cgc ttg ctc ggc 595
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 35 40 45
 Tyr Ala Lys Thr Ala His Glu Arg Gly Ile Lys Thr Ile Ile Ala Cys
 50 55 60
 Ala Gly Gly Ala Ala His Leu Pro Gly Met Val Ala Ala Ala Thr Pro
 65 70 75 80
 Leu Pro Val Ile Gly Val Pro Arg Ala Leu Lys Asp Leu Asp Gly Leu
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 Asp Ser Leu Leu Ser Ile Val Gln Met Pro Gly Gly Val Pro Val Ala
 100 105 110
 Thr Val Ser Ile Gly Gly Ala Lys Asn Ala Gly Leu Leu Ala Val Arg
 115 120 125
 Ile Leu Gly Ala Gly Asp Pro Ser Leu Val Thr Lys Met Ala Asp Tyr
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 Val Gly Pro Leu Val
 1 5
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 Gly Leu Ile Met Gly Ser Asp Ser Asp Trp Asp Thr Val Ala Pro Ala

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Ala Glu Val Leu Ala Glu Phe Gly Ile Pro Phe Glu Val Gly Val Val				
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Gly Gly Val Pro Val Ala Thr Val Ser Ile Gly Gly Ala Lys Asn Ala				
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Gly Leu Leu Ala Val Arg Ile Leu Gly Ala Gly Asp Pro Ser Leu Val				
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Thr Lys Met Ala Asp Tyr Gln Glu Asn Met Ala Lys Glu Val Glu Ala				
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 Met Gln Thr Leu Ala
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 Leu Asp Ala Pro Arg Pro Asp Glu Val Gln Ile Arg Val Ile Ala Ala
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 Gly Val Arg His Thr Asp Ala Ile Val Arg Asp Gln Ile Tyr Pro Thr
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 Phe Leu Pro Ala Val Phe Gly His Glu Gly Ala Gly Val Val Val Ala
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Ala	Gly	His	Thr	Thr	Leu	Phe	Thr	Arg	Ala	Thr	Lys	Glu	Gln	Ala	Glu	
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gcc	atc	atc	gac	acc	ctt	gat	gat	gtt	ttc	tac	gat	gcg	gat	gcg	ggt	547
Ala	Ile	Ile	Asp	Thr	Leu	Asp	Asp	Val	Phe	Tyr	Asp	Ala	Asp	Ala	Gly	
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Pro	Gly	Val	Val	Ala	Gly	Leu	Val	Ser	Ala	Pro	Val	Val	Ala	Leu	Pro	
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Thr	Ser	Val	Gly	Tyr	Gly	Ala	Gly	Ala	Gly	Gly	Ile	Ala	Pro	Leu	Leu	
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Thr	Met	Leu	Asn	Ala	Cys	Ala	Pro	Gly	Val	Gly	Val	Val	Asn	Ile	Asp	
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Asn	Gly	Tyr	Gly	Ala	Gly	His	Leu	Ala	Ala	Gln	Ile	Ala	Ala	Arg		
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 50 55 60
 Gly Val Val Val Ala Val Gly Ser Ala Val Thr Ser Val Lys Pro Asp
 65 70 75 80
 Asp Lys Val Val Leu Gly Phe Asn Ser Cys Gly Gln Cys Leu Lys Cys
 85 90 95
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 100 105 110
 Ala Cys Thr Arg Asp Ala Gly His Thr Thr Leu Phe Thr Arg Ala Thr
 115 120 125
 Lys Glu Gln Ala Glu Ala Ile Ile Asp Thr Leu Asp Asp Val Phe Tyr
 130 135 140
 Asp Ala Asp Ala Gly Phe Leu Ala Tyr Pro Ala Thr Pro Pro Glu Ala
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 Ser Gly Val Ser Val Leu Val Val Ala Ala Gly Thr Ser Asp Leu Pro
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 Gln Ala Lys Glu Ala Leu His Thr Ala Ser Tyr Leu Gly Arg Ser Thr
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 Ser Leu Ile Val Asp Phe Gly Val Ala Gly Ile His Arg Leu Leu Ser
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 Tyr Glu Glu Glu Leu Arg Ala Ala Gly Val Leu Ile Val Ala Ala Gly
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 Met Asp Gly Ala Leu Pro Gly Val Val Ala Gly Leu Val Ser Ala Pro
 225 230 235 240
 Val Val Ala Leu Pro Thr Ser Val Gly Tyr Gly Ala Gly Ala Gly Gly
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Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser
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Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
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Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala
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Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala
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Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg
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Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly
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Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His
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cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499
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Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg
                                   135 140 145

tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca 595
Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala
                                   150 155 160 165

acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg 643
Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu
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ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc 691
Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly Pro Met Gly Thr Ala
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	295					300					305						
gtt	gct	gat	ctt	tcc	ggc	cag	cag	tgg	aac	gaa	ggc	gat	gtc	ttc	tgc		
	1075																
Val	Ala	Asp	Leu	Ser	Gly	Gln	Gln	Trp	Asn	Glu	Gly	Asp	Val	Phe	Cys		
	310				315					320					325		
tcc	gtg	atc	cgc	cgc	gtt	gca	ctg	cca	gac	gca	ttc	ttc	gcg	att	gac		
	1123																
Ser	Val	Ile	Arg	Arg	Val	Ala	Leu	Pro	Asp	Ala	Phe	Phe	Ala	Ile	Asp		
				330					335					340			
gga	atg	ttt	gaa	act	ttc	ctg	aca	gtc	ctg	gat	gaa	ttc	ggc	gca	ttc		
	1171																
Gly	Met	Phe	Glu	Thr	Phe	Leu	Thr	Val	Leu	Asp	Glu	Phe	Gly	Ala	Phe		
			345					350					355				
cct	gcc	atg	atc	gag	cgc	gaa	ctt	gag	cgt	tac	ctg	cca	ttc	ctg	gca		
	1219																
Pro	Ala	Met	Ile	Glu	Arg	Glu	Leu	Glu	Arg	Tyr	Leu	Pro	Phe	Leu	Ala		
		360					365					370					
act	acc	cgt	atc	ctc	atg	gcc	gct	gtc	cgc	gca	ggc	gtt	ggc	cgc	gaa		
	1267																
Thr	Thr	Arg	Ile	Leu	Met	Ala	Ala	Val	Arg	Ala	Gly	Val	Gly	Arg	Glu		
	375					380					385						
acc	gca	cac	gaa	gta	atc	aag	gaa	aac	gct	gtc	gcg	gtt	gcc	ctc	aac		
	1315																
Thr	Ala	His	Glu	Val	Ile	Lys	Glu	Asn	Ala	Val	Ala	Val	Ala	Leu	Asn		
	390				395					400					405		
atg	cgc	gaa	aat	ggc	ggc	gac	cag	gac	ctt	atc	cag	cgc	ctc	gct	gct		
	1363																
Met	Arg	Glu	Asn	Gly	Gly	Asp	Gln	Asp	Leu	Ile	Gln	Arg	Leu	Ala	Ala		

410	415	420
gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct 1411		
Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala 425 430 435		
gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg 1459		
Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val 440 445 450		
ctc gac cgc att cag gtg ctt gtc gac gcc cac ccc ggc gcc gca gac 1507		
Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp 455 460 465		
tac cga cca ggt gag att ctt taaaggtttt taacggcgtt cac 1551		
Tyr Arg Pro Gly Glu Ile Leu 470 475		
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Ser Ala Glu Leu Ser Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met 20 25 30		
Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly 35 40 45		
Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp 50 55 60		
Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His 65 70 75 80		
Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu 85 90 95		
His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu 100 105 110		
Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile 115 120 125		
Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu 130 135 140		
Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu 145 150 155 160		
Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu 165 170 175		

Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly
 180 185 190
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu
 195 200 205
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe
 210 215 220
 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp
 225 230 235 240
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser
 245 250 255
 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu
 260 265 270
 Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met
 275 280 285
 Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg
 290 295 300
 Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu
 305 310 315 320
 Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala
 325 330 335
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp
 340 345 350
 Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr
 355 360 365
 Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala
 370 375 380
 Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val
 385 390 395 400
 Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile
 405 410 415
 Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu
 420 425 430
 Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser
 435 440 445
 Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His
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 Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu
 465 470 475

<210> 943

<211> 1683

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1660)

<223> RXA02622

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 Met Ser Asp Asp Arg
 1 5

aag gca att aaa cgc gca cta att agc gtg tat gac aag act ggc ctg 163
 Lys Ala Ile Lys Arg Ala Leu Ile Ser Val Tyr Asp Lys Thr Gly Leu
 10 15 20

gag gat cta gcc cag gca ctt cac cgc gag aac gtg gaa att gtt tcc 211
 Glu Asp Leu Ala Gln Ala Leu His Arg Glu Asn Val Glu Ile Val Ser
 25 30 35

acc gga tcc act gcg gcg aag att gct gag ctt ggt att cct gtt acc 259
 Thr Gly Ser Thr Ala Ala Lys Ile Ala Glu Leu Gly Ile Pro Val Thr
 40 45 50

ccg gtt gag gag ctc acc ggt ttc cct gag tgc ctt gag ggc cgt gtg 307
 Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys Leu Glu Gly Arg Val
 55 60 65

aag aca ctg cac cct aag gtt cac gct ggc atc ttg gcg gac acc cgc 355
 Lys Thr Leu His Pro Lys Val His Ala Gly Ile Leu Ala Asp Thr Arg
 70 75 80 85

aag gaa gac cac ctg cgt cag ctc aag gaa ctt gag gtc gcc cca ttc 403
 Lys Glu Asp His Leu Arg Gln Leu Lys Glu Leu Glu Val Ala Pro Phe
 90 95 100

cag ctt gtc gtg gtg aac ctg tac cca ttt gct gag acc gtt gcg tcc 451
 Gln Leu Val Val Val Asn Leu Tyr Pro Phe Ala Glu Thr Val Ala Ser
 105 110 115

ggc gcc gat ttc gat gct tgc gtt gag cag atc gac atc gga ggc cca 499
 Gly Ala Asp Phe Asp Ala Cys Val Glu Gln Ile Asp Ile Gly Gly Pro
 120 125 130

tcc atg gtt cgt gct gcg gca aag aac cac cca tct gtc gct gtg gtt 547
 Ser Met Val Arg Ala Ala Ala Lys Asn His Pro Ser Val Ala Val Val
 135 140 145

gtt tca ccg aac cgc tac gag gat gtc cag gaa gct ttg aag acc ggt 595
 Val Ser Pro Asn Arg Tyr Glu Asp Val Gln Glu Ala Leu Lys Thr Gly
 150 155 160 165

gga ttc tcc cgc gcg gag cgc acc aag ttg gct gct gag gct ttc cgc 643
 Gly Phe Ser Arg Ala Glu Arg Thr Lys Leu Ala Ala Glu Ala Phe Arg
 170 175 180

cac acc gca acc tac gat gtc acc gtt gca acc tgg atg agc gag cag 691
 His Thr Ala Thr Tyr Asp Val Thr Val Ala Thr Trp Met Ser Glu Gln

185						190						195						
ctg gct gcc gaa gat tct gag act gag ttc cca ggt tgg atc ggc acc	739																	
Leu Ala Ala Glu Asp Ser Glu Thr Glu Phe Pro Gly Trp Ile Gly Thr																		
200 205 210																		
acc aac acc ttg tcc cgc agc ttg cgt tac ggt gag aac cct cac cag	787																	
Thr Asn Thr Leu Ser Arg Ser Leu Arg Tyr Gly Glu Asn Pro His Gln																		
215 220 225																		
tct gca gct ttg tac gtg ggc aac acc cgc gga ctt gca cag gct aag	835																	
Ser Ala Ala Leu Tyr Val Gly Asn Thr Arg Gly Leu Ala Gln Ala Lys																		
230 235 240 245																		
cag ttc cac ggc aag gaa atg agc tac aac aac tac acc gat tct gat	883																	
Gln Phe His Gly Lys Glu Met Ser Tyr Asn Asn Tyr Thr Asp Ser Asp																		
250 255 260																		
gct gca tgg cgt gca gcg tgg gat cac gag cgt cct tgt gta gct atc	931																	
Ala Ala Trp Arg Ala Ala Trp Asp His Glu Arg Pro Cys Val Ala Ile																		
265 270 275																		
atc aag cat gca aac cct tgt ggc att gct gtt tct gat gag tcc atc	979																	
Ile Lys His Ala Asn Pro Cys Gly Ile Ala Val Ser Asp Glu Ser Ile																		
280 285 290																		
gca gcg gca cac cgc gag gca cac gca tgt gac tct gtg tcc gca ttc																		
1027																		
Ala Ala Ala His Arg Glu Ala His Ala Cys Asp Ser Val Ser Ala Phe																		
295 300 305																		
ggt ggc gtc atc gcg tcc aac cgt gaa gtc agc gtt gag atg gct aac																		
1075																		
Gly Gly Val Ile Ala Ser Asn Arg Glu Val Ser Val Glu Met Ala Asn																		
310 315 320 325																		
cag gtt gca gag atc ttc act gag gtc atc atc gct cct tcc tat gaa																		
1123																		
Gln Val Ala Glu Ile Phe Thr Glu Val Ile Ile Ala Pro Ser Tyr Glu																		
330 335 340																		
gag ggc gct gtg gag atc ctg agc cag aag aag aac atc cgt att ctt																		
1171																		
Glu Gly Ala Val Glu Ile Leu Ser Gln Lys Lys Asn Ile Arg Ile Leu																		
345 350 355																		
cag gct gaa gca cct gtg cgt aag ggc ttt gag tcc cgt gag atc tcc																		
1219																		
Gln Ala Glu Ala Pro Val Arg Lys Gly Phe Glu Ser Arg Glu Ile Ser																		
360 365 370																		
ggc ggt ctg ctt gtt cag gaa cgc gac ttg atc cac gct gag ggc gac																		
1267																		
Gly Gly Leu Leu Val Gln Glu Arg Asp Leu Ile His Ala Glu Gly Asp																		
375 380 385																		
aac tcc gca aac tgg act ctt gct gcc ggc tct gct gtt tct cct gag																		
1315																		
Asn Ser Ala Asn Trp Thr Leu Ala Ala Gly Ser Ala Val Ser Pro Glu																		
390 395 400 405																		

gtt ctg aag gac ctg gag ttc gcg tgg act gca gtt cgt tcc gtg aag
 1363
 Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala Val Arg Ser Val Lys
 410 415 420

tcc aac gca att ctg ttg gct aag aac ggc gct acc gtt ggc gtt ggc
 1411
 Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala Thr Val Gly Val Gly
 425 430 435

atg gga cag gtc aac cgc gtt gac tct gct cgc ttg gct gtc gac cgt
 1459
 Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg Leu Ala Val Asp Arg
 440 445 450

gca ggt gca gag cgc gct acc ggt tcc gtt gct gct tcc gat gcg ttc
 1507
 Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala Ala Ser Asp Ala Phe
 455 460 465

ttc cca ttc gct gat ggc ttt gag gtt ctc gct gag gct ggc atc act
 1555
 Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala Glu Ala Gly Ile Thr
 470 475 480 485

gct gtt gtg cag cct ggt gga tcc att cgc gac aac gag gtc att gag
 1603
 Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp Asn Glu Val Ile Glu
 490 495 500

gca gcc aac aag gct ggc gtg acc atg tac ctg act ggt gcg cga cac
 1651
 Ala Ala Asn Lys Ala Gly Val Thr Met Tyr Leu Thr Gly Ala Arg His
 505 510 515

ttc gct cac taaagttttt aaagatttcg ctt
 1683
 Phe Ala His
 520

<210> 944
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 944
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 Asp Lys Thr Gly Leu Glu Asp Leu Ala Gln Ala Leu His Arg Glu Asn
 20 25 30
 Val Glu Ile Val Ser Thr Gly Ser Thr Ala Ala Lys Ile Ala Glu Leu
 35 40 45
 Gly Ile Pro Val Thr Pro Val Glu Glu Leu Thr Gly Phe Pro Glu Cys
 50 55 60
 Leu Glu Gly Arg Val Lys Thr Leu His Pro Lys Val His Ala Gly Ile
 65 70 75 80

Leu	Ala	Asp	Thr	Arg	Lys	Glu	Asp	His	Leu	Arg	Gln	Leu	Lys	Glu	Leu	85	90	95
Glu	Val	Ala	Pro	Phe	Gln	Leu	Val	Val	Val	Asn	Leu	Tyr	Pro	Phe	Ala	100	105	110
Glu	Thr	Val	Ala	Ser	Gly	Ala	Asp	Phe	Asp	Ala	Cys	Val	Glu	Gln	Ile	115	120	125
Asp	Ile	Gly	Gly	Pro	Ser	Met	Val	Arg	Ala	Ala	Ala	Lys	Asn	His	Pro	130	135	140
Ser	Val	Ala	Val	Val	Val	Ser	Pro	Asn	Arg	Tyr	Glu	Asp	Val	Gln	Glu	145	150	155
Ala	Leu	Lys	Thr	Gly	Gly	Phe	Ser	Arg	Ala	Glu	Arg	Thr	Lys	Leu	Ala	165	170	175
Ala	Glu	Ala	Phe	Arg	His	Thr	Ala	Thr	Tyr	Asp	Val	Thr	Val	Ala	Thr	180	185	190
Trp	Met	Ser	Glu	Gln	Leu	Ala	Ala	Glu	Asp	Ser	Glu	Thr	Glu	Phe	Pro	195	200	205
Gly	Trp	Ile	Gly	Thr	Thr	Asn	Thr	Leu	Ser	Arg	Ser	Leu	Arg	Tyr	Gly	210	215	220
Glu	Asn	Pro	His	Gln	Ser	Ala	Ala	Leu	Tyr	Val	Gly	Asn	Thr	Arg	Gly	225	230	235
Leu	Ala	Gln	Ala	Lys	Gln	Phe	His	Gly	Lys	Glu	Met	Ser	Tyr	Asn	Asn	245	250	255
Tyr	Thr	Asp	Ser	Asp	Ala	Ala	Trp	Arg	Ala	Ala	Trp	Asp	His	Glu	Arg	260	265	270
Pro	Cys	Val	Ala	Ile	Ile	Lys	His	Ala	Asn	Pro	Cys	Gly	Ile	Ala	Val	275	280	285
Ser	Asp	Glu	Ser	Ile	Ala	Ala	Ala	His	Arg	Glu	Ala	His	Ala	Cys	Asp	290	295	300
Ser	Val	Ser	Ala	Phe	Gly	Gly	Val	Ile	Ala	Ser	Asn	Arg	Glu	Val	Ser	305	310	315
Val	Glu	Met	Ala	Asn	Gln	Val	Ala	Glu	Ile	Phe	Thr	Glu	Val	Ile	Ile	325	330	335
Ala	Pro	Ser	Tyr	Glu	Glu	Gly	Ala	Val	Glu	Ile	Leu	Ser	Gln	Lys	Lys	340	345	350
Asn	Ile	Arg	Ile	Leu	Gln	Ala	Glu	Ala	Pro	Val	Arg	Lys	Gly	Phe	Glu	355	360	365
Ser	Arg	Glu	Ile	Ser	Gly	Gly	Leu	Leu	Val	Gln	Glu	Arg	Asp	Leu	Ile	370	375	380
His	Ala	Glu	Gly	Asp	Asn	Ser	Ala	Asn	Trp	Thr	Leu	Ala	Ala	Gly	Ser	385	390	395

Ala Val Ser Pro Glu Val Leu Lys Asp Leu Glu Phe Ala Trp Thr Ala
 405 410 415

Val Arg Ser Val Lys Ser Asn Ala Ile Leu Leu Ala Lys Asn Gly Ala
 420 425 430

Thr Val Gly Val Gly Met Gly Gln Val Asn Arg Val Asp Ser Ala Arg
 435 440 445

Leu Ala Val Asp Arg Ala Gly Ala Glu Arg Ala Thr Gly Ser Val Ala
 450 455 460

Ala Ser Asp Ala Phe Phe Pro Phe Ala Asp Gly Phe Glu Val Leu Ala
 465 470 475 480

Glu Ala Gly Ile Thr Ala Val Val Gln Pro Gly Gly Ser Ile Arg Asp
 485 490 495

Asn Glu Val Ile Glu Ala Ala Asn Lys Ala Gly Val Thr Met Tyr Leu
 500 505 510

Thr Gly Ala Arg His Phe Ala His
 515 520

<210> 945

<211> 1641

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1618)

<223> RXN00488

<400> 945

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 Met Thr Thr Gln Ser
 1 5

cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163
 Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly
 10 15 20

tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211
 Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val
 25 30 35

cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259
 Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu
 40 45 50

aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307
 Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg
 55 60 65

atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355
 Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg
 70 75 80 85

aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt	403
Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg	
90 95 100	
tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg	451
Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met	
105 110 115	
agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt	499
Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly	
120 125 130	
ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac	547
Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn	
135 140 145	
cgc gat atg cgt ttt gaa agc gac atg aac cgt cgt gtc gct gaa gtt	595
Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg Arg Val Ala Glu Val	
150 155 160 165	
atg acc cca atg cct ttg gtt gtt gct gaa gag ggc gtc acc aag gag	643
Met Thr Pro Met Pro Leu Val Val Ala Glu Glu Gly Val Thr Lys Glu	
170 175 180	
cag gct ctt gct ttg ctg tct gca aac aag gtg gag aag ctt cct atc	691
Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val Glu Lys Leu Pro Ile	
185 190 195	
atc gca aag gac ggc aag ctt gtc ggt ctg atc acg gtg aag gac ttc	739
Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile Thr Val Lys Asp Phe	
200 205 210	
gtt aag act gag cag cac ccg aac gca tcc aag gat gca tca ggt cgt	787
Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys Asp Ala Ser Gly Arg	
215 220 225	
ctg ctg gtt gcg gct ggc atc ggc acg ggc gag gag tca ttc cag cga	835
Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu Glu Ser Phe Gln Arg	
230 235 240 245	
gct ggt gcg ctt gcc gac gcc ggc gtc gac att ttg gtc gta gac tct	883
Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile Leu Val Val Asp Ser	
250 255 260	
gca cac gcc cat agc cgt gga gtt ttg gac atg gtg tcc cgc gtg aag	931
Ala His Ala His Ser Arg Gly Val Leu Asp Met Val Ser Arg Val Lys	
265 270 275	
aag tcg ttc ccc aag gtc gat atc gtt ggc ggc aac ttg gcg acc cgc	979
Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly Asn Leu Ala Thr Arg	
280 285 290	
gag gct gcg cag gcc atg att gaa gct ggc gca gac gct atc aag gtg	
1027	
Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala Asp Ala Ile Lys Val	
295 300 305	
ggt att ggc cca ggt tct att tgc acc act cgc gtt gtc gca ggt gtc	
1075	
Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg Val Val Ala Gly Val	

310	315	320	325
ggt gca cct cag atc act gcg atc atg gag gca gct gtt cca gct cac 1123			
Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His 330 335 340			
aag gct ggc gtt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt 1171			
Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly 345 350 355			
gat atc gct aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc 1219			
Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly 360 365 370			
tcc atg ctg gct ggt acc gct gag gct cct ggt gag acc atc acc atc 1267			
Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile 375 380 385			
aac ggc aag cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct 1315			
Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala 390 395 400 405			
atg cag ggc cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac 1363			
Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp 410 415 420			
cgt tac ttc cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa 1411			
Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu 425 430 435			
ggc atc gaa ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att 1459			
Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile 440 445 450			
cac cag cag gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc 1507			
His Gln Gln Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser 455 460 465			
tcc acc att gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc 1555			
Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser 470 475 480 485			
gcg ggt ctg aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa 1603			
Ala Gly Leu Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu 490 495 500			
gct cct aac tac cac tagattttgc tcacttaaag agc 1641			
Ala Pro Asn Tyr His 505			

<210> 946

<211> 506

<212> PRT

<213> Corynebacterium glutamicum

<400> 946

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 20 25 30

Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr
 35 40 45

Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr
 50 55 60

Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile
 65 70 75 80

Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val
 85 90 95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr
 100 105 110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg
 115 120 125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val
 130 135 140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met Asn Arg
 145 150 155 160

Arg Val Ala Glu Val Met Thr Pro Met Pro Leu Val Val Ala Glu Glu
 165 170 175

Gly Val Thr Lys Glu Gln Ala Leu Ala Leu Leu Ser Ala Asn Lys Val
 180 185 190

Glu Lys Leu Pro Ile Ile Ala Lys Asp Gly Lys Leu Val Gly Leu Ile
 195 200 205

Thr Val Lys Asp Phe Val Lys Thr Glu Gln His Pro Asn Ala Ser Lys
 210 215 220

Asp Ala Ser Gly Arg Leu Leu Val Ala Ala Gly Ile Gly Thr Gly Glu
 225 230 235 240

Glu Ser Phe Gln Arg Ala Gly Ala Leu Ala Asp Ala Gly Val Asp Ile
 245 250 255

Leu Val Val Asp Ser Ala His Ala His Ser Arg Gly Val Leu Asp Met
 260 265 270

Val Ser Arg Val Lys Lys Ser Phe Pro Lys Val Asp Ile Val Gly Gly
 275 280 285

Asn Leu Ala Thr Arg Glu Ala Ala Gln Ala Met Ile Glu Ala Gly Ala
 290 295 300
 Asp Ala Ile Lys Val Gly Ile Gly Pro Gly Ser Ile Cys Thr Thr Arg
 305 310 315 320
 Val Val Ala Gly Val Gly Ala Pro Gln Ile Thr Ala Ile Met Glu Ala
 325 330 335
 Ala Val Pro Ala His Lys Ala Gly Val Pro Ile Ile Ala Asp Gly Gly
 340 345 350
 Met Gln Phe Ser Gly Asp Ile Ala Lys Ala Leu Ala Ala Gly Ala Asn
 355 360 365
 Ser Val Met Leu Gly Ser Met Leu Ala Gly Thr Ala Glu Ala Pro Gly
 370 375 380
 Glu Thr Ile Thr Ile Asn Gly Lys Gln Tyr Lys Arg Tyr Arg Gly Met
 385 390 395 400
 Gly Ser Met Gly Ala Met Gln Gly Arg Gly Leu Ser Gly Glu Lys Arg
 405 410 415
 Ser Tyr Ser Lys Asp Arg Tyr Phe Gln Ser Asp Val Lys Ser Glu Asp
 420 425 430
 Lys Leu Val Pro Glu Gly Ile Glu Gly Arg Val Pro Phe Arg Gly Pro
 435 440 445
 Ile Gly Asp Ile Ile His Gln Gln Val Gly Gly Leu Arg Ala Ala Met
 450 455 460
 Gly Tyr Thr Gly Ser Ser Thr Ile Glu Glu Leu His Asn Ala Arg Phe
 465 470 475 480
 Val Gln Ile Thr Ser Ala Gly Leu Lys Glu Ser His Pro His His Ile
 485 490 495
 Gln Gln Thr Val Glu Ala Pro Asn Tyr His
 500 505

<210> 947

<211> 574

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(574)

<223> FRXA00492

<400> 947

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tagataattg tggacacact atgaggagga actgtcgcac atg aca acc cag agc 115

Met Thr Thr Gln Ser

1

5

cga gtt tct acc gga gga gac aac cca aac aag gtt gcc ctt gtt gga 163
 Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys Val Ala Leu Val Gly
 10 15 20
 tta acc ttt gat gac gta ctt ttg ctt cca gat gcg tcg gac gtt gtt 211
 Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp Ala Ser Asp Val Val
 25 30 35
 cct tca gag gta gat acc tcg acg cag tta aca cgt aat att cgc ctt 259
 Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr Arg Asn Ile Arg Leu
 40 45 50
 aac acc cct att ctt tct gcc gca atg gat act gtc acc gag gct cgc 307
 Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr Val Thr Glu Ala Arg
 55 60 65
 atg gct atc ggc atg gca cgc cat ggc ggc att ggt gtt ttg cac cgc 355
 Met Ala Ile Gly Met Ala Arg His Gly Gly Ile Gly Val Leu His Arg
 70 75 80 85
 aac ctg tct att caa gag cag gca gaa aac gtt gag ctg gtg aag cgt 403
 Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val Glu Leu Val Lys Arg
 90 95 100
 tct gag tct gga atg gtc act gat cct gtt acc tgt act cct gac atg 451
 Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr Cys Thr Pro Asp Met
 105 110 115
 agc atc caa gaa gtg gat gat ctg tgt gca cgc ttc cgc att tcc ggt 499
 Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg Phe Arg Ile Ser Gly
 120 125 130
 ctg cct gtt gtt gat gag gcc gga aag ttg gtt ggt att tgc acc aac 547
 Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val Gly Ile Cys Thr Asn
 135 140 145
 cgc gat atg cgt ttt gaa agc gac atg 574
 Arg Asp Met Arg Phe Glu Ser Asp Met
 150 155

<210> 948

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 948

Met Thr Thr Gln Ser Arg Val Ser Thr Gly Gly Asp Asn Pro Asn Lys
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 Val Ala Leu Val Gly Leu Thr Phe Asp Asp Val Leu Leu Leu Pro Asp
 20 25 30
 Ala Ser Asp Val Val Pro Ser Glu Val Asp Thr Ser Thr Gln Leu Thr
 35 40 45
 Arg Asn Ile Arg Leu Asn Thr Pro Ile Leu Ser Ala Ala Met Asp Thr
 50 55 60
 Val Thr Glu Ala Arg Met Ala Ile Gly Met Ala Arg His Gly Gly Ile
 65 70 75 80

Gly Val Leu His Arg Asn Leu Ser Ile Gln Glu Gln Ala Glu Asn Val
85 90 95

Glu Leu Val Lys Arg Ser Glu Ser Gly Met Val Thr Asp Pro Val Thr
100 105 110

Cys Thr Pro Asp Met Ser Ile Gln Glu Val Asp Asp Leu Cys Ala Arg
115 120 125

Phe Arg Ile Ser Gly Leu Pro Val Val Asp Glu Ala Gly Lys Leu Val
130 135 140

Gly Ile Cys Thr Asn Arg Asp Met Arg Phe Glu Ser Asp Met
145 150 155

<210> 949

<211> 557

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) . . (534)

<223> FRXA00488

<400> 949

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Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His Lys Ala Gly
1 5 10 15

gtt cct atc atc gcc gat ggc ggc atg cag ttc tct ggt gat atc gct 96
Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala
20 25 30

aag gct ttg gct gct ggc gct aac tcc gtg atg ctg ggc tcc atg ctg 144
Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu
35 40 45

gct ggt acc gct gag gct cct ggt gag acc atc acc atc aac ggc aag 192
Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys
50 55 60

cag tac aag cgt tac cgc ggc atg ggc tcc atg ggc gct atg cag ggc 240
Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly
65 70 75 80

cgt gga ctt agt ggt gag aag cgt tcc tac tcc aag gac cgt tac ttc 288
Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe
85 90 95

cag tct gac gtt aag agc gaa gac aag ctc gtt cca gaa ggc atc gaa 336
Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu
100 105 110

ggt cgc gtg cct ttc cgc ggt ccc atc gga gac atc att cac cag cag 384
Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln
115 120 125

gtc ggt gga ctt cgt gca gca atg ggc tac acc ggt tcc tcc acc att 432

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile
 130 135 140

gaa gag ctg cac aac gct cgt ttc gtg cag atc acc agc gcg ggt ctg 480
 Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu
 145 150 155 160

aag gaa tcc cac ccg cac cac atc cag cag act gtg gaa gct cct aac 528
 Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn
 165 170 175

tac cac tagattttgc tcacttaaagc agc 557
 Tyr His

<210> 950
 <211> 178
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 950
 Gln Ile Thr Ala Ile Met Glu Ala Ala Val Pro Ala His Lys Ala Gly
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Val Pro Ile Ile Ala Asp Gly Gly Met Gln Phe Ser Gly Asp Ile Ala
 20 25 30

Lys Ala Leu Ala Ala Gly Ala Asn Ser Val Met Leu Gly Ser Met Leu
 35 40 45

Ala Gly Thr Ala Glu Ala Pro Gly Glu Thr Ile Thr Ile Asn Gly Lys
 50 55 60

Gln Tyr Lys Arg Tyr Arg Gly Met Gly Ser Met Gly Ala Met Gln Gly
 65 70 75 80

Arg Gly Leu Ser Gly Glu Lys Arg Ser Tyr Ser Lys Asp Arg Tyr Phe
 85 90 95

Gln Ser Asp Val Lys Ser Glu Asp Lys Leu Val Pro Glu Gly Ile Glu
 100 105 110

Gly Arg Val Pro Phe Arg Gly Pro Ile Gly Asp Ile Ile His Gln Gln
 115 120 125

Val Gly Gly Leu Arg Ala Ala Met Gly Tyr Thr Gly Ser Ser Thr Ile
 130 135 140

Glu Glu Leu His Asn Ala Arg Phe Val Gln Ile Thr Ser Ala Gly Leu
 145 150 155 160

Lys Glu Ser His Pro His His Ile Gln Gln Thr Val Glu Ala Pro Asn
 165 170 175

Tyr His

<210> 951
 <211> 1554

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1531)

<223> RXA02469

<400> 951

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gccgtgttca gggataactg attaatacaac taggagaccc atg cgt ttt ctt aac 115
 Met Arg Phe Leu Asn
 1 5

aat tcc aat ccg ccc tat gag ctg aca tat tcc gat gtg ttt atg gtg 163
 Asn Ser Asn Pro Pro Tyr Glu Leu Thr Tyr Ser Asp Val Phe Met Val
 10 15 20

cct tcg cgt tct gac gta ggc tcc cgc atg tcc gtg gat ctg cgc acc 211
 Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser Val Asp Leu Arg Thr
 25 30 35

aat gac gga act gga aca acc atc ccg ctc gtt gtg gca aac atg act 259
 Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val Val Ala Asn Met Thr
 40 45 50

gct gtt gct ggc cga cgc atg gct gag acc att gcg cgc cgc ggt ggc 307
 Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile Ala Arg Arg Gly Gly
 55 60 65

atg gcg att ctt ccg cag gat gtg ccc gcc gat att gct gca gag act 355
 Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp Ile Ala Ala Glu Thr
 70 75 80 85

atc gcg aat gtg aag aaa gcg gac ctg gtt ttt gat acc cca att acc 403
 Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe Asp Thr Pro Ile Thr
 90 95 100

gta aaa ccg cac cac acc gtg ggt tat gca cgc aac ttg atc cac aag 451
 Val Lys Pro His His Thr Val Gly Tyr Ala Arg Asn Leu Ile His Lys
 105 110 115

cgt gcg cac ggt gca gcc att gtt ttg gag ggc gat cag ccg gtc ggc 499
 Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly Asp Gln Pro Val Gly
 120 125 130

atc gtc acc gac aag gac ctc gaa ggc gca gac aac ttc act cag gtg 547
 Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp Asn Phe Thr Gln Val
 135 140 145

ggc acc ctc atg tcc acc tcc cta ttg acg ctg cct gag gat att tcc 595
 Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu Pro Glu Asp Ile Ser
 150 155 160 165

ccc gaa gac gcc ttc gga atc ctc cac gaa cac agc cgc aaa ctc gcc 643
 Pro Glu Asp Ala Phe Gly Ile Leu His Glu His Ser Arg Lys Leu Ala
 170 175 180

ccc gtc gtc gcg gct gac ggc tca ctc cgc ggc atc ctc acc cgc acc 691
 Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly Ile Leu Thr Arg Thr

185				190				195					
ggc gcc ctg cgc gcc acc atg tac aag ccg gct atc gac gcc aac ggc													739
Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala Ile Asp Ala Asn Gly													
	200						205				210		
cgc ctg cga gtc ggc gcc gcc atc ggc atc aac ggc gac atc gaa gga													787
Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn Gly Asp Ile Glu Gly													
	215						220				225		
cgc acc aaa acg ctt ctc gac gcc ggc gcc gac gtt cta gtc gtc gac													835
Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp Val Leu Val Val Asp													
	230					235				240			245
aca gca cac ggc cac caa tcc acc atg atc agc gcc ctc aaa cgc atc													883
Thr Ala His Gly His Gln Ser Thr Met Ile Ser Ala Leu Lys Arg Ile													
				250					255				260
cgc gca ctc gac gtc aac gtc ccc atc gtt gct ggc aac gtg gtc acc													931
Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala Gly Asn Val Val Thr													
			265					270				275	
gcc gat ggt gtc cgc gac cta gtt gaa gca ggc gca aac atc atc aag													979
Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly Ala Asn Ile Ile Lys													
	280						285				290		
gta ggc gtt gga cca ggc gca atg tgc acc acc cgc atg caa acc ggc													
1027													
Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr Arg Met Gln Thr Gly													
	295					300					305		
gtt ggc cga cca cag ttc tcc gca gtg ctg gaa tgc gca gcc gaa gcc													
1075													
Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu Cys Ala Ala Glu Ala													
	310					315				320			325
cgc aaa ctc ggc gca cac gta tgg gca gac ggc gga gtc cgc gac ccc													
1123													
Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly Gly Val Arg Asp Pro													
				330				335					340
cgc gac gtc gcc ctg gca ctc gca gct ggc gcc tcc aac gtg atg gtc													
1171													
Arg Asp Val Ala Leu Ala Leu Ala Ala Gly Ala Ser Asn Val Met Val													
			345					350				355	
gga tcc tgg ttc tcc gga acc tac gaa tcc ccc ggc gac ctc cgc ttc													
1219													
Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro Gly Asp Leu Arg Phe													
	360						365				370		
gaa tcc gac gga cgc atg tac aaa gaa tcc ttc ggt atg gca tcc cgg													
1267													
Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe Gly Met Ala Ser Arg													
	375					380				385			
cgc gcc gtg gaa agc cga aac caa aag gtc gaa gct ttc gaa aaa gca													
1315													
Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu Ala Phe Glu Lys Ala													
	390				395				400				405

cgc cgc gca atg ttc gaa gaa ggc atc tcc act gcc cgc atc tac att
1363
Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr Ala Arg Ile Tyr Ile
410 415 420

gac aaa cgc cac ggc gga gtc gag gac ctg gta gat caa atc atc tcc
1411
Asp Lys Arg His Gly Gly Val Glu Asp Leu Val Asp Gln Ile Ile Ser
425 430 435

ggc gtc cgc tcc tca ttc acc tac gca ggc gcc gat tcg att gaa acc
1459
Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala Asp Ser Ile Glu Thr
440 445 450

ttc ttc gaa cgc gcc acc gtc gga gtt caa tcc acc gaa ggc tac gca
1507
Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser Thr Glu Gly Tyr Ala
455 460 465

gaa gga aag cca cgc gct tcg cgt taagtgttgt tgtgcctttg aga
1554
Glu Gly Lys Pro Arg Ala Ser Arg
470 475

<210> 952
<211> 477
<212> PRT
<213> Corynebacterium glutamicum

<400> 952
Met Arg Phe Leu Asn Asn Ser Asn Pro Pro Tyr Glu Leu Thr Tyr Ser
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Asp Val Phe Met Val Pro Ser Arg Ser Asp Val Gly Ser Arg Met Ser
20 25 30

Val Asp Leu Arg Thr Asn Asp Gly Thr Gly Thr Thr Ile Pro Leu Val
35 40 45

Val Ala Asn Met Thr Ala Val Ala Gly Arg Arg Met Ala Glu Thr Ile
50 55 60

Ala Arg Arg Gly Gly Met Ala Ile Leu Pro Gln Asp Val Pro Ala Asp
65 70 75 80

Ile Ala Ala Glu Thr Ile Ala Asn Val Lys Lys Ala Asp Leu Val Phe
85 90 95

Asp Thr Pro Ile Thr Val Lys Pro His His Thr Val Gly Tyr Ala Arg
100 105 110

Asn Leu Ile His Lys Arg Ala His Gly Ala Ala Ile Val Leu Glu Gly
115 120 125

Asp Gln Pro Val Gly Ile Val Thr Asp Lys Asp Leu Glu Gly Ala Asp
130 135 140

Asn Phe Thr Gln Val Gly Thr Leu Met Ser Thr Ser Leu Leu Thr Leu
145 150 155 160

Pro Glu Asp Ile Ser Pro Glu Asp Ala Phe Gly Ile Leu His Glu His
 165 170 175
 Ser Arg Lys Leu Ala Pro Val Val Ala Ala Asp Gly Ser Leu Arg Gly
 180 185 190
 Ile Leu Thr Arg Thr Gly Ala Leu Arg Ala Thr Met Tyr Lys Pro Ala
 195 200 205
 Ile Asp Ala Asn Gly Arg Leu Arg Val Gly Ala Ala Ile Gly Ile Asn
 210 215 220
 Gly Asp Ile Glu Gly Arg Thr Lys Thr Leu Leu Asp Ala Gly Ala Asp
 225 230 235 240
 Val Leu Val Val Asp Thr Ala His Gly His Gln Ser Thr Met Ile Ser
 245 250 255
 Ala Leu Lys Arg Ile Arg Ala Leu Asp Val Asn Val Pro Ile Val Ala
 260 265 270
 Gly Asn Val Val Thr Ala Asp Gly Val Arg Asp Leu Val Glu Ala Gly
 275 280 285
 Ala Asn Ile Ile Lys Val Gly Val Gly Pro Gly Ala Met Cys Thr Thr
 290 295 300
 Arg Met Gln Thr Gly Val Gly Arg Pro Gln Phe Ser Ala Val Leu Glu
 305 310 315 320
 Cys Ala Ala Glu Ala Arg Lys Leu Gly Ala His Val Trp Ala Asp Gly
 325 330 335
 Gly Val Arg Asp Pro Arg Asp Val Ala Leu Ala Leu Ala Ala Gly Ala
 340 345 350
 Ser Asn Val Met Val Gly Ser Trp Phe Ser Gly Thr Tyr Glu Ser Pro
 355 360 365
 Gly Asp Leu Arg Phe Glu Ser Asp Gly Arg Met Tyr Lys Glu Ser Phe
 370 375 380
 Gly Met Ala Ser Arg Arg Ala Val Glu Ser Arg Asn Gln Lys Val Glu
 385 390 395 400
 Ala Phe Glu Lys Ala Arg Arg Ala Met Phe Glu Glu Gly Ile Ser Thr
 405 410 415
 Ala Arg Ile Tyr Ile Asp Lys Arg His Gly Gly Val Glu Asp Leu Val
 420 425 430
 Asp Gln Ile Ile Ser Gly Val Arg Ser Ser Phe Thr Tyr Ala Gly Ala
 435 440 445
 Asp Ser Ile Glu Thr Phe Phe Glu Arg Ala Thr Val Gly Val Gln Ser
 450 455 460
 Thr Glu Gly Tyr Ala Glu Gly Lys Pro Arg Ala Ser Arg
 465 470 475

cag gca gtt ctg acc cgc ttc ctc act gag atc gca ggt cta gag cag	691
Gln Ala Val Leu Thr Arg Phe Leu Thr Glu Ile Ala Gly Leu Glu Gln	
185 190 195	
aac tgg acc gca gca aac atc gct gaa gaa ctc atc gaa aag gtc cgc	739
Asn Trp Thr Ala Ala Asn Ile Ala Glu Glu Leu Ile Glu Lys Val Arg	
200 205 210	
gag cag atc ggc gaa gat ggc cgc gct att tgt ggc cta tcc ggt ggt	787
Glu Gln Ile Gly Glu Asp Gly Arg Ala Ile Cys Gly Leu Ser Gly Gly	
215 220 225	
gtg gac tcc gct gtt gcc ggt gct ttg gtg cag cgc gcc att ggt gac	835
Val Asp Ser Ala Val Ala Gly Ala Leu Val Gln Arg Ala Ile Gly Asp	
230 235 240 245	
cgt ttg acc tgt gtc ttt gtt gac cac ggt ctg ctg cgt gcc ggt gag	883
Arg Leu Thr Cys Val Phe Val Asp His Gly Leu Leu Arg Ala Gly Glu	
250 255 260	
cgc gag cag gtg gaa aaa gac ttc gtc gca gca acc ggc gcc aag ctg	931
Arg Glu Gln Val Glu Lys Asp Phe Val Ala Ala Thr Gly Ala Lys Leu	
265 270 275	
gtt acc gtt gat gag cgc cag gca ttc cta tcc aag ctg gcc gga gtt	979
Val Thr Val Asp Glu Arg Gln Ala Phe Leu Ser Lys Leu Ala Gly Val	
280 285 290	
acc gaa cca gaa gca aag cgc aag gct atc ggc gct gag ttc atc cgc	
1027 Thr Glu Pro Glu Ala Lys Arg Lys Ala Ile Gly Ala Glu Phe Ile Arg	
295 300 305	
tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt	
1075 Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly	
310 315 320 325	
tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg	
1123 Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val	
330 335 340	
gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac	
1171 Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn	
345 350 355	
gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg	
1219 Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu	
360 365 370	
cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc	
1267 Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly	
375 380 385	
ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt	
1315	

Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu
390 395 400 405

ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc
1363

Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu
410 415 420

cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt
1411

Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu
425 430 435

gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc
1459

Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg
440 445 450

tct gtt ggt gtt caa ggc gat ggc cgc acc tac gga cac cca atc gtg
1507

Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr Gly His Pro Ile Val
455 460 465

ctg cgc cca gtg tct tcc gaa gac gca atg acc gcc gac tgg acc cgc
1555

Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr Ala Asp Trp Thr Arg
470 475 480 485

ctg cca tac gag gtt ctg gag aag atc tcc acc cgc atc acc aac gaa
1603

Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr Arg Ile Thr Asn Glu
490 495 500

gtt cca gat gtg aac cgc gtg gtg ctg gac gta acc tcc aag cca cca
1651

Val Pro Asp Val Asn Arg Val Val Leu Asp Val Thr Ser Lys Pro Pro
505 510 515

gga acc atc gaa tgg gag taggccttaa atgagccttc gtt
1692

Gly Thr Ile Glu Trp Glu
520

<210> 954

<211> 523

<212> PRT

<213> Corynebacterium glutamicum

<400> 954

Val Ser Leu Gln Thr Asn His Arg Pro Val Leu Val Val Asp Phe Gly
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Ala Gln Tyr Ala Gln Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile
20 25 30

Tyr Ser Glu Val Ile Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala
35 40 45

Lys Asn Ala Ala Ala Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr
50 55 60

Ala	Glu	Gly	Ala	Pro	Ser	Leu	Asp	Ala	Glu	Ile	Leu	Asp	Leu	Gly	Leu	65	70	75	80
Pro	Val	Phe	Gly	Ile	Cys	Tyr	Gly	Phe	Gln	Ala	Met	Thr	His	Ala	Leu	85	90	95	
Gly	Gly	Thr	Val	Ala	Asn	Thr	Gly	Lys	Arg	Glu	Tyr	Gly	Arg	Thr	Asp	100	105	110	
Ile	Asn	Val	Ala	Gly	Gly	Val	Leu	His	Glu	Gly	Leu	Glu	Ala	Cys	His	115	120	125	
Lys	Val	Trp	Met	Ser	His	Gly	Asp	Ala	Val	Ser	Glu	Ala	Pro	Glu	Gly	130	135	140	
Phe	Val	Val	Thr	Ala	Ser	Ser	Glu	Gly	Ala	Pro	Val	Ala	Ala	Phe	Glu	145	150	155	160
Asn	Lys	Glu	Arg	Lys	Met	Ala	Gly	Val	Gln	Tyr	His	Pro	Glu	Val	Leu	165	170	175	
His	Ser	Pro	His	Gly	Gln	Ala	Val	Leu	Thr	Arg	Phe	Leu	Thr	Glu	Ile	180	185	190	
Ala	Gly	Leu	Glu	Gln	Asn	Trp	Thr	Ala	Ala	Asn	Ile	Ala	Glu	Glu	Leu	195	200	205	
Ile	Glu	Lys	Val	Arg	Glu	Gln	Ile	Gly	Glu	Asp	Gly	Arg	Ala	Ile	Cys	210	215	220	
Gly	Leu	Ser	Gly	Gly	Val	Asp	Ser	Ala	Val	Ala	Gly	Ala	Leu	Val	Gln	225	230	235	240
Arg	Ala	Ile	Gly	Asp	Arg	Leu	Thr	Cys	Val	Phe	Val	Asp	His	Gly	Leu	245	250	255	
Leu	Arg	Ala	Gly	Glu	Arg	Glu	Gln	Val	Glu	Lys	Asp	Phe	Val	Ala	Ala	260	265	270	
Thr	Gly	Ala	Lys	Leu	Val	Thr	Val	Asp	Glu	Arg	Gln	Ala	Phe	Leu	Ser	275	280	285	
Lys	Leu	Ala	Gly	Val	Thr	Glu	Pro	Glu	Ala	Lys	Arg	Lys	Ala	Ile	Gly	290	295	300	
Ala	Glu	Phe	Ile	Arg	Ser	Phe	Glu	Arg	Ala	Val	Ala	Gly	Val	Leu	Glu	305	310	315	320
Glu	Ala	Pro	Glu	Gly	Ser	Thr	Val	Asp	Phe	Leu	Val	Gln	Gly	Thr	Leu	325	330	335	
Tyr	Pro	Asp	Val	Val	Glu	Ser	Gly	Gly	Gly	Ser	Gly	Thr	Ala	Asn	Ile	340	345	350	
Lys	Ser	His	His	Asn	Val	Gly	Gly	Leu	Pro	Asp	Asp	Val	Glu	Phe	Lys	355	360	365	
Leu	Val	Glu	Pro	Leu	Arg	Asp	Leu	Phe	Lys	Asp	Glu	Val	Arg	Ala	Val	370	375	380	

Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe
 385 390 395 400
 Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp
 405 410 415
 Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu
 420 425 430
 Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu
 435 440 445
 Leu Ala Asp Val Arg Ser Val Gly Val Gln Gly Asp Gly Arg Thr Tyr
 450 455 460
 Gly His Pro Ile Val Leu Arg Pro Val Ser Ser Glu Asp Ala Met Thr
 465 470 475 480
 Ala Asp Trp Thr Arg Leu Pro Tyr Glu Val Leu Glu Lys Ile Ser Thr
 485 490 495
 Arg Ile Thr Asn Glu Val Pro Asp Val Asn Arg Val Val Leu Asp Val
 500 505 510
 Thr Ser Lys Pro Pro Gly Thr Ile Glu Trp Glu
 515 520

<210> 955
 <211> 1486
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1486)
 <223> FRXA00487

<400> 955
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 Val Ser Leu Gln Thr 5
 aat cat cgc cca gta ctc gtc gtt gac ttc ggc gca cag tac gcg cag 163
 Asn His Arg Pro Val Leu Val Val Asp Phe Gly Ala Gln Tyr Ala Gln 20
 10 15
 ctg atc gca cgt cgt gtg cgt gag gcc ggc atc tac tcc gaa gtc atc 211
 Leu Ile Ala Arg Arg Val Arg Glu Ala Gly Ile Tyr Ser Glu Val Ile 35
 25 30
 ccg cac acc gcc acc gca gac gat gtg cgc gct aaa aat gca gca gcc 259
 Pro His Thr Ala Thr Ala Asp Asp Val Arg Ala Lys Asn Ala Ala Ala 50
 40 45
 ctc gtc ctt tcc ggt ggc cca tcc tcc gtg tat gcc gag gga gca cca 307
 Leu Val Leu Ser Gly Gly Pro Ser Ser Val Tyr Ala Glu Gly Ala Pro 65
 55 60

tcc	ctt	gac	gct	gag	att	ctt	gat	ctc	gga	ttg	cca	gta	ttt	ggc	att	355
Ser	Leu	Asp	Ala	Glu	Ile	Leu	Asp	Leu	Gly	Leu	Pro	Val	Phe	Gly	Ile	
70					75					80					85	
tgc	tac	ggc	ttc	caa	gcc	atg	acc	cac	gcg	ctt	ggg	ggc	acc	gtt	gcc	403
Cys	Tyr	Gly	Phe	Gln	Ala	Met	Thr	His	Ala	Leu	Gly	Gly	Thr	Val	Ala	
				90					95					100		
aac	acc	ggg	aag	cgc	gaa	tac	gga	cgc	acc	gac	atc	aac	gtt	gcc	ggg	451
Asn	Thr	Gly	Lys	Arg	Glu	Tyr	Gly	Arg	Thr	Asp	Ile	Asn	Val	Ala	Gly	
			105					110					115			
ggc	gtc	ctc	cac	gaa	ggc	ctc	gaa	gcc	tgc	cac	aag	gtg	tgg	atg	agc	499
Gly	Val	Leu	His	Glu	Gly	Leu	Glu	Ala	Cys	His	Lys	Val	Trp	Met	Ser	
		120					125					130				
cac	ggc	gac	gcc	gtc	tct	gaa	gcc	cca	gaa	ggg	ttc	gta	gtc	acc	gcg	547
His	Gly	Asp	Ala	Val	Ser	Glu	Ala	Pro	Glu	Gly	Phe	Val	Val	Thr	Ala	
		135				140					145					
tcc	tcc	gaa	ggg	gag	cct	gtc	gca	gct	ttc	gaa	aac	aag	gaa	cgc	aaa	595
Ser	Ser	Glu	Gly	Ala	Pro	Val	Ala	Ala	Phe	Glu	Asn	Lys	Glu	Arg	Lys	
150					155					160					165	
atg	gct	ggc	gtg	cag	tac	cac	cca	gag	gta	ttg	cac	tca	cca	cac	ggc	643
Met	Ala	Gly	Val	Gln	Tyr	His	Pro	Glu	Val	Leu	His	Ser	Pro	His	Gly	
				170					175					180		
cag	gca	gtt	ctg	acc	cgc	ttc	ctc	act	gag	atc	gca	ggg	cta	gag	cag	691
Gln	Ala	Val	Leu	Thr	Arg	Phe	Leu	Thr	Glu	Ile	Ala	Gly	Leu	Glu	Gln	
			185					190					195			
aac	tgg	acc	gca	gca	aac	atc	gct	gaa	gaa	ctc	atc	gaa	aag	gtc	cgc	739
Asn	Trp	Thr	Ala	Ala	Asn	Ile	Ala	Glu	Glu	Leu	Ile	Glu	Lys	Val	Arg	
		200					205					210				
gag	cag	atc	ggc	gaa	gat	ggc	cgc	gct	att	tgt	ggc	cta	tcc	ggg	ggg	787
Glu	Gln	Ile	Gly	Glu	Asp	Gly	Arg	Ala	Ile	Cys	Gly	Leu	Ser	Gly	Gly	
		215				220					225					
gtg	gac	tcc	gct	gtt	gcc	ggg	gct	ttg	gtg	cag	cgc	gcc	att	ggg	gac	835
Val	Asp	Ser	Ala	Val	Ala	Gly	Ala	Leu	Val	Gln	Arg	Ala	Ile	Gly	Asp	
230					235					240					245	
cgt	ttg	acc	tgt	gtc	ttt	gtt	gac	cac	ggg	ctg	ctg	cgt	gcc	ggg	gag	883
Arg	Leu	Thr	Cys	Val	Phe	Val	Asp	His	Gly	Leu	Leu	Arg	Ala	Gly	Glu	
				250					255					260		
cgc	gag	cag	gtg	gaa	aaa	gac	ttc	gtc	gca	gca	acc	ggc	gcc	aag	ctg	931
Arg	Glu	Gln	Val	Glu	Lys	Asp	Phe	Val	Ala	Ala	Thr	Gly	Ala	Lys	Leu	
			265					270					275			
gtt	acc	gtt	gat	gag	cgc	cag	gca	ttc	cta	tcc	aag	ctg	gcc	gga	gtt	979
Val	Thr	Val	Asp	Glu	Arg	Gln	Ala	Phe	Leu	Ser	Lys	Leu	Ala	Gly	Val	
		280					285					290				
acc	gaa	cca	gaa	gca	aag	cgc	aag	gct	atc	ggc	gct	gag	ttc	atc	cgc	
1027																
Thr	Glu	Pro	Glu	Ala	Lys	Arg	Lys	Ala	Ile	Gly	Ala	Glu	Phe	Ile	Arg	
	295					300					305					

tcc ttc gag cgc gca gtt gcc ggt gtg ctg gaa gaa gct cca gaa ggt
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 Ser Phe Glu Arg Ala Val Ala Gly Val Leu Glu Glu Ala Pro Glu Gly
 310 315 320 325

tcc acc gtg gac ttc ctg gtt cag ggc acc ctg tac cca gac gtc gtg
 1123
 Ser Thr Val Asp Phe Leu Val Gln Gly Thr Leu Tyr Pro Asp Val Val
 330 335 340

gaa tcc ggt ggt gga tct ggt acc gca aac atc aag agc cac cac aac
 1171
 Glu Ser Gly Gly Gly Ser Gly Thr Ala Asn Ile Lys Ser His His Asn
 345 350 355

gtc ggt gga ctg cca gac gat gtg gaa ttc aag ctt gtt gag cca ctg
 1219
 Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys Leu Val Glu Pro Leu
 360 365 370

cgt gac ctc ttc aaa gac gaa gtc cgt gcc gtt ggc cgt gaa ctt ggc
 1267
 Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val Gly Arg Glu Leu Gly
 375 380 385

ctg cct gag gaa atc gtt ggc cgc cag cca ttc cca gga cca gga ctt
 1315
 Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe Pro Gly Pro Gly Leu
 390 395 400 405

ggt atc cgc atc atc ggt gaa gtc acc gaa gat cgc cta gaa acc ctc
 1363
 Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp Arg Leu Glu Thr Leu
 410 415 420

cgc cac gct gac ctg atc gcc cgc acc gag ctc acc gaa gcc gga ctt
 1411
 Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu Thr Glu Ala Gly Leu
 425 430 435

gac ggc gtg atc tgg cag tgc cca gta gtc ctc ctg gca gat gtc cgc
 1459
 Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu Leu Ala Asp Val Arg
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 Ser Val Gly Val Gln Gly Asp Gly Arg
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Lys	Asn	Ala	Ala	Ala	Leu	Val	Leu	Ser	Gly	Gly	Pro	Ser	Ser	Val	Tyr
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Ala	Glu	Gly	Ala	Pro	Ser	Leu	Asp	Ala	Glu	Ile	Leu	Asp	Leu	Gly	Leu
65					70					75					80
Pro	Val	Phe	Gly	Ile	Cys	Tyr	Gly	Phe	Gln	Ala	Met	Thr	His	Ala	Leu
				85					90					95	
Gly	Gly	Thr	Val	Ala	Asn	Thr	Gly	Lys	Arg	Glu	Tyr	Gly	Arg	Thr	Asp
			100					105					110		
Ile	Asn	Val	Ala	Gly	Gly	Val	Leu	His	Glu	Gly	Leu	Glu	Ala	Cys	His
	115						120					125			
Lys	Val	Trp	Met	Ser	His	Gly	Asp	Ala	Val	Ser	Glu	Ala	Pro	Glu	Gly
	130					135					140				
Phe	Val	Val	Thr	Ala	Ser	Ser	Glu	Gly	Ala	Pro	Val	Ala	Ala	Phe	Glu
145					150					155					160
Asn	Lys	Glu	Arg	Lys	Met	Ala	Gly	Val	Gln	Tyr	His	Pro	Glu	Val	Leu
				165					170					175	
His	Ser	Pro	His	Gly	Gln	Ala	Val	Leu	Thr	Arg	Phe	Leu	Thr	Glu	Ile
			180					185					190		
Ala	Gly	Leu	Glu	Gln	Asn	Trp	Thr	Ala	Ala	Asn	Ile	Ala	Glu	Glu	Leu
		195					200					205			
Ile	Glu	Lys	Val	Arg	Glu	Gln	Ile	Gly	Glu	Asp	Gly	Arg	Ala	Ile	Cys
	210					215					220				
Gly	Leu	Ser	Gly	Gly	Val	Asp	Ser	Ala	Val	Ala	Gly	Ala	Leu	Val	Gln
225					230					235					240
Arg	Ala	Ile	Gly	Asp	Arg	Leu	Thr	Cys	Val	Phe	Val	Asp	His	Gly	Leu
				245					250					255	
Leu	Arg	Ala	Gly	Glu	Arg	Glu	Gln	Val	Glu	Lys	Asp	Phe	Val	Ala	Ala
			260					265					270		
Thr	Gly	Ala	Lys	Leu	Val	Thr	Val	Asp	Glu	Arg	Gln	Ala	Phe	Leu	Ser
		275					280					285			
Lys	Leu	Ala	Gly	Val	Thr	Glu	Pro	Glu	Ala	Lys	Arg	Lys	Ala	Ile	Gly
	290					295					300				
Ala	Glu	Phe	Ile	Arg	Ser	Phe	Glu	Arg	Ala	Val	Ala	Gly	Val	Leu	Glu
305					310					315					320
Glu	Ala	Pro	Glu	Gly	Ser	Thr	Val	Asp	Phe	Leu	Val	Gln	Gly	Thr	Leu
				325					330					335	
Tyr	Pro	Asp	Val	Val	Glu	Ser	Gly	Gly	Gly	Ser	Gly	Thr	Ala	Asn	Ile
			340					345					350		

Lys Ser His His Asn Val Gly Gly Leu Pro Asp Asp Val Glu Phe Lys
 355 360 365
 Leu Val Glu Pro Leu Arg Asp Leu Phe Lys Asp Glu Val Arg Ala Val
 370 375 380
 Gly Arg Glu Leu Gly Leu Pro Glu Glu Ile Val Gly Arg Gln Pro Phe
 385 390 395 400
 Pro Gly Pro Gly Leu Gly Ile Arg Ile Ile Gly Glu Val Thr Glu Asp
 405 410 415
 Arg Leu Glu Thr Leu Arg His Ala Asp Leu Ile Ala Arg Thr Glu Leu
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 Thr Glu Ala Gly Leu Asp Gly Val Ile Trp Gln Cys Pro Val Val Leu
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 Val Ser Gly Asp Asn
 1 5

caa cta gga cgg ctc gta att ctt gcg ggc ccc tca gcg gtc ggt aaa 163
 Gln Leu Gly Arg Leu Val Ile Leu Ala Gly Pro Ser Ala Val Gly Lys
 10 15 20

tcg act gtg gtt gat cgc ctc cgc aat gac gtt cca aac ctg tat ttc 211
 Ser Thr Val Val Asp Arg Leu Arg Asn Asp Val Pro Asn Leu Tyr Phe
 25 30 35

agt gtg tcg atg acc act agg gca cct cgt cct ggt gaa gtc gat gga 259
 Ser Val Ser Met Thr Thr Arg Ala Pro Arg Pro Gly Glu Val Asp Gly
 40 45 50

cgt gac tac ttc tat gtc act gca cag gaa ttt cag gac aaa atc gac 307
 Arg Asp Tyr Phe Tyr Val Thr Ala Gln Glu Phe Gln Asp Lys Ile Asp
 55 60 65

tgt gga gag atg ctt gaa tgg gca gat atc cac ggc ggt ttg cag cgt 355
 Cys Gly Glu Met Leu Glu Trp Ala Asp Ile His Gly Gly Leu Gln Arg
 70 75 80 85

tca ggc act cca gca ggt ccc gtc aat gag gct cgc caa aat ggt cgg 403

Ser	Gly	Thr	Pro	Ala	Gly	Pro	Val	Asn	Glu	Ala	Arg	Gln	Asn	Gly	Arg		
				90					95					100			
cca	gta	ttg	gtt	gag	gtt	gat	ctt	gca	gga	gcc	cga	aac	atc	gct	agc	451	
Pro	Val	Leu	Val	Glu	Val	Asp	Leu	Ala	Gly	Ala	Arg	Asn	Ile	Ala	Ser		
			105					110					115				
tta	att	cca	gat	gca	gaa	acc	atc	ttc	ctt	gct	cca	cct	tca	tgg	gaa	499	
Leu	Ile	Pro	Asp	Ala	Glu	Thr	Ile	Phe	Leu	Ala	Pro	Pro	Ser	Trp	Glu		
		120					125					130					
gtt	ttg	gtt	gaa	cgc	ctc	act	gga	cgt	ggc	acc	gaa	agc	gaa	gac	gtt	547	
Val	Leu	Val	Glu	Arg	Leu	Thr	Gly	Arg	Gly	Thr	Glu	Ser	Glu	Asp	Val		
	135					140					145						
att	gct	cgc	agg	ctc	gag	acc	gca	cgc	gaa	gaa	ttg	gct	gct	cag	agc	595	
Ile	Ala	Arg	Arg	Leu	Glu	Thr	Ala	Arg	Glu	Glu	Leu	Ala	Ala	Gln	Ser		
150				155					160						165		
gaa	ttt	aag	cac	gtc	att	atc	aat	gat	gat	gtg	gat	aca	gcc	gtc	aag	643	
Glu	Phe	Lys	His	Val	Ile	Ile	Asn	Asp	Asp	Val	Asp	Thr	Ala	Val	Lys		
			170					175						180			
gct	att	gag	gat	gtt	ctc	ctc	ggc	gct	tagccaaaac	atagagcggt						690	
Ala	Ile	Glu	Asp	Val	Leu	Leu	Gly	Ala									
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agg																693	

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<212> PRT

<213> Corynebacterium glutamicum

<400> 958

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Ser	Ala	Val	Gly	Lys	Ser	Thr	Val	Val	Asp	Arg	Leu	Arg	Asn	Asp	Val		
		20					25						30				
Pro	Asn	Leu	Tyr	Phe	Ser	Val	Ser	Met	Thr	Thr	Arg	Ala	Pro	Arg	Pro		
		35					40					45					
Gly	Glu	Val	Asp	Gly	Arg	Asp	Tyr	Phe	Tyr	Val	Thr	Ala	Gln	Glu	Phe		
	50					55				60							
Gln	Asp	Lys	Ile	Asp	Cys	Gly	Glu	Met	Leu	Glu	Trp	Ala	Asp	Ile	His		
65				70					75					80			
Gly	Gly	Leu	Gln	Arg	Ser	Gly	Thr	Pro	Ala	Gly	Pro	Val	Asn	Glu	Ala		
			85					90					95				
Arg	Gln	Asn	Gly	Arg	Pro	Val	Leu	Val	Glu	Val	Asp	Leu	Ala	Gly	Ala		
		100					105					110					
Arg	Asn	Ile	Ala	Ser	Leu	Ile	Pro	Asp	Ala	Glu	Thr	Ile	Phe	Leu	Ala		
	115					120						125					
Pro	Pro	Ser	Trp	Glu	Val	Leu	Val	Glu	Arg	Leu	Thr	Gly	Arg	Gly	Thr		

130		135		140
Glu Ser Glu Asp Val Ile Ala Arg Arg Leu Glu Thr Ala Arg Glu Glu				
145		150		155
Leu Ala Ala Gln Ser Glu Phe Lys His Val Ile Ile Asn Asp Asp Val				
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Asp Thr Ala Val Lys Ala Ile Glu Asp Val Leu Leu Gly Ala				
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<213> Corynebacterium glutamicum

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<222> (101)..(1390)

<223> RXA01446

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Met Ala Ala Ile Val	
1 5	

att gtc ggc gct caa tgg ggc gat gaa ggc aaa ggt aag gcc acg gat	163
Ile Val Gly Ala Gln Trp Gly Asp Glu Gly Lys Gly Lys Ala Thr Asp	
10 15 20	

att ctc ggc gga ctc gtc gat tac gtg gtt aag ccc aat ggc ggt aac	211
Ile Leu Gly Gly Leu Val Asp Tyr Val Val Lys Pro Asn Gly Gly Asn	
25 30 35	

aac gct gga cac act gtt gtg gtc ggc ggc gag aag tac gag cta aag	259
Asn Ala Gly His Thr Val Val Val Gly Gly Glu Lys Tyr Glu Leu Lys	
40 45 50	

ctc ctt cct gcc ggc gtc ctc tcc gaa acg gcc acc cca att ttg ggc	307
Leu Leu Pro Ala Gly Val Leu Ser Glu Thr Ala Thr Pro Ile Leu Gly	
55 60 65	

aac ggc gtt gtg atc aac ctt gag gca ctg ttc gaa gaa atc gac ggc	355
Asn Gly Val Val Ile Asn Leu Glu Ala Leu Phe Glu Glu Ile Asp Gly	
70 75 80 85	

ctt gag gct cgc ggt gcg gat gca tcc cgc ctg cgc atc tct gca aac	403
Leu Glu Ala Arg Gly Ala Asp Ala Ser Arg Leu Arg Ile Ser Ala Asn	
90 95 100	

gct cac ctg gtt gct cca tac cac cag gtg atg gac cgt gtt cag gaa	451
Ala His Leu Val Ala Pro Tyr His Gln Val Met Asp Arg Val Gln Glu	
105 110 115	

cgc ttc ctg ggc aag cgc gca atc ggc acc acc ggc cgt ggc atc ggc	499
Arg Phe Leu Gly Lys Arg Ala Ile Gly Thr Thr Gly Arg Gly Ile Gly	
120 125 130	

cca acc tac gcg gac aaa gta tcc cgc gtg gga atc cgt gtt caa gac	547
Pro Thr Tyr Ala Asp Lys Val Ser Arg Val Gly Ile Arg Val Gln Asp	
135 140 145	
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Ile Phe Asp Glu Ser Ile Leu Arg Gln Lys Val Glu Ser Ala Leu Asp	
150 155 160 165	
tac aaa aac cag gtg ctg gtg aag atg tac aac cgc aag gcc atc gtc	643
Tyr Lys Asn Gln Val Leu Val Lys Met Tyr Asn Arg Lys Ala Ile Val	
170 175 180	
gct gag gaa atc gtg cag tac ttc ctc tcc tac gct gat cgt ctg cgc	691
Ala Glu Glu Ile Val Gln Tyr Phe Leu Ser Tyr Ala Asp Arg Leu Arg	
185 190 195	
ccc atg gtc atc gat gcc acc ttg gtg ctc aac gag gca ctt gat cag	739
Pro Met Val Ile Asp Ala Thr Leu Val Leu Asn Glu Ala Leu Asp Gln	
200 205 210	
ggc aag cac gtt ctt atg gaa ggt ggc cag gca acc atg ctc gac gtg	787
Gly Lys His Val Leu Met Glu Gly Gly Gln Ala Thr Met Leu Asp Val	
215 220 225	
gac cac ggc acc tac cca ttc gtc acc tcc tcc aac cca acc gcc ggt	835
Asp His Gly Thr Tyr Pro Phe Val Thr Ser Ser Asn Pro Thr Ala Gly	
230 235 240 245	
ggc gca agt gtt ggt tca ggt atc ggc cca acc aag atc acc agc tcc	883
Gly Ala Ser Val Gly Ser Gly Ile Gly Pro Thr Lys Ile Thr Ser Ser	
250 255 260	
ttg ggt atc atc aag gcc tac acc act cgt gtt ggt gcc ggc cca ttc	931
Leu Gly Ile Ile Lys Ala Tyr Thr Thr Arg Val Gly Ala Gly Pro Phe	
265 270 275	
cca act gag ctg ttt gat aag tgg ggc gag tac ctg cag acc gtc ggt	979
Pro Thr Glu Leu Phe Asp Lys Trp Gly Glu Tyr Leu Gln Thr Val Gly	
280 285 290	
ggc gag gtc ggc gtg aac acc ggc cgt aag cgt cgc tgt ggc tgg tac	
1027 Gly Glu Val Gly Val Asn Thr Gly Arg Lys Arg Arg Cys Gly Trp Tyr	
295 300 305	
gac tcc gtg att gct cgt tac gca tcc cgc gtc aac gga ttc acc gac	
1075 Asp Ser Val Ile Ala Arg Tyr Ala Ser Arg Val Asn Gly Phe Thr Asp	
310 315 320 325	
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1123 Tyr Phe Leu Thr Lys Leu Asp Val Leu Thr Gly Ile Gly Glu Ile Pro	
330 335 340	
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1171 Ile Cys Val Ala Tyr Asp Val Asp Gly Val Arg His Asp Glu Met Pro	
345 350 355	

Ile	Arg	Val	Gln	Asp	Ile	Phe	Asp	Glu	Ser	Ile	Leu	Arg	Gln	Lys	Val	145	150	155	160
Glu	Ser	Ala	Leu	Asp	Tyr	Lys	Asn	Gln	Val	Leu	Val	Lys	Met	Tyr	Asn	165	170	175	
Arg	Lys	Ala	Ile	Val	Ala	Glu	Glu	Ile	Val	Gln	Tyr	Phe	Leu	Ser	Tyr	180	185	190	
Ala	Asp	Arg	Leu	Arg	Pro	Met	Val	Ile	Asp	Ala	Thr	Leu	Val	Leu	Asn	195	200	205	
Glu	Ala	Leu	Asp	Gln	Gly	Lys	His	Val	Leu	Met	Glu	Gly	Gly	Gln	Ala	210	215	220	
Thr	Met	Leu	Asp	Val	Asp	His	Gly	Thr	Tyr	Pro	Phe	Val	Thr	Ser	Ser	225	230	235	240
Asn	Pro	Thr	Ala	Gly	Gly	Ala	Ser	Val	Gly	Ser	Gly	Ile	Gly	Pro	Thr	245	250	255	
Lys	Ile	Thr	Ser	Ser	Leu	Gly	Ile	Ile	Lys	Ala	Tyr	Thr	Thr	Arg	Val	260	265	270	
Gly	Ala	Gly	Pro	Phe	Pro	Thr	Glu	Leu	Phe	Asp	Lys	Trp	Gly	Glu	Tyr	275	280	285	
Leu	Gln	Thr	Val	Gly	Gly	Glu	Val	Gly	Val	Asn	Thr	Gly	Arg	Lys	Arg	290	295	300	
Arg	Cys	Gly	Trp	Tyr	Asp	Ser	Val	Ile	Ala	Arg	Tyr	Ala	Ser	Arg	Val	305	310	315	320
Asn	Gly	Phe	Thr	Asp	Tyr	Phe	Leu	Thr	Lys	Leu	Asp	Val	Leu	Thr	Gly	325	330	335	
Ile	Gly	Glu	Ile	Pro	Ile	Cys	Val	Ala	Tyr	Asp	Val	Asp	Gly	Val	Arg	340	345	350	
His	Asp	Glu	Met	Pro	Leu	Thr	Gln	Ser	Glu	Phe	His	His	Ala	Thr	Pro	355	360	365	
Ile	Phe	Glu	Thr	Met	Pro	Ala	Trp	Asp	Glu	Asp	Ile	Thr	Asp	Cys	Lys	370	375	380	
Thr	Phe	Glu	Asp	Leu	Pro	Gln	Lys	Ala	Gln	Asp	Tyr	Val	Arg	Arg	Leu	385	390	395	400
Glu	Glu	Leu	Ser	Gly	Ala	Arg	Phe	Ser	Tyr	Ile	Gly	Val	Gly	Pro	Gly	405	410	415	
Arg	Asp	Gln	Thr	Ile	Val	Leu	His	Asp	Val	Leu	Ala	Asp	Asn			420	425	430	

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<211> 1551

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1528)

<223> RXA00619

<400> 961

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 Val Ala Asp Lys Lys
 1 5

aag atc gca aac gtc ctg tcg aac cgt tac gcc tcc gcg gaa ctt tct 163
 Lys Ile Ala Asn Val Leu Ser Asn Arg Tyr Ala Ser Ala Glu Leu Ser
 10 15 20

aac ctg tgg agt gcc gaa gag aag atc atc atg gag cgc cag ctc tgg 211
 Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met Glu Arg Gln Leu Trp
 25 30 35

atc gcc gtg atg aaa gcc cag aaa gat ttg gga gtt gag atc cct gcc 259
 Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly Val Glu Ile Pro Ala
 40 45 50

gag gca att gaa tcc tat gaa gca gtg atc gac cag gtt gat ttg gca 307
 Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp Gln Val Asp Leu Ala
 55 60 65

agc atc gcc gat cgt gag cgc gtc acc cgc cac gat gtg aag gcc cgc 355
 Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His Asp Val Lys Ala Arg
 70 75 80 85

atc gaa gaa ttc aat gca ctg gct ggc cat gag cac atc cac aag ggc 403
 Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu His Ile His Lys Gly
 90 95 100

atg acc tcc cgc gac ctc acc gaa aat gtt gaa cag ctg cag atc cac 451
 Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu Gln Leu Gln Ile His
 105 110 115

cgc tcc ctt gag ctg gtc cgc aac aag ggc att gca gtt gtt gca gct 499
 Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile Ala Val Val Ala Ala
 120 125 130

atc gga tcc cgc gca gcg cag tac caa agc ctg gtc atg gct ggc cgt 547
 Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu Val Met Ala Gly Arg
 135 140 145

tcc cac aac gtg gca gcg cag gca act acc ttg ggc aag cgt ttc gca 595
 Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu Gly Lys Arg Phe Ala
 150 155 160 165

acc gca gct gat gaa atg ctc gtg gca ctt gag cgc gtc acc gaa ctg 643
 Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu Arg Val Thr Glu Leu
 170 175 180

ctc aac cgc tac cca ctt cgc gga atc aag ggc cca atg gga acc gcc 691
 Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly Pro Met Gly Thr Ala
 185 190 195

caa gac atg ctt gac ctc atg gaa ggc gac gag gct cgt ctc tcc gat 739

Gln	Asp	Met	Leu	Asp	Leu	Met	Glu	Gly	Asp	Glu	Ala	Arg	Leu	Ser	Asp		
		200					205					210					
ctg	gaa	acc	cgc	atc	gca	gca	cac	ctc	ggc	ttt	gat	cgc	gtc	ttc	gac	787	
Leu	Glu	Thr	Arg	Ile	Ala	Ala	His	Leu	Gly	Phe	Asp	Arg	Val	Phe	Asp		
	215					220					225						
tcc	gtc	ggc	cag	gtc	tac	cca	cgt	tcc	ctt	gac	ttc	gat	gca	gta	tct	835	
Ser	Val	Gly	Gln	Val	Tyr	Pro	Arg	Ser	Leu	Asp	Phe	Asp	Ala	Val	Ser		
	230				235					240					245		
gct	ctg	gtt	cag	ctt	ggc	tcc	ggc	cca	tca	tcg	ctg	tcc	cac	acc	att	883	
Ala	Leu	Val	Gln	Leu	Gly	Ser	Gly	Pro	Ser	Ser	Leu	Ser	His	Thr	Ile		
				250				255						260			
cgt	ctc	atg	gcc	ggc	acc	gaa	act	gtt	acc	gaa	ggc	ttt	aag	gaa	ggc	931	
Arg	Leu	Met	Ala	Gly	Thr	Glu	Thr	Val	Thr	Glu	Gly	Phe	Lys	Glu	Gly		
			265					270					275				
cag	gtc	ggc	tcc	tct	gca	atg	cct	cac	aag	atg	aac	gct	cgc	tcc	tgt	979	
Gln	Val	Gly	Ser	Ser	Ala	Met	Pro	His	Lys	Met	Asn	Ala	Arg	Ser	Cys		
		280					285					290					
gag	cgc	gtg	ggc	ggc	ctg	cag	gtt	att	ctt	cgc	gga	tac	ctc	acc	atg		
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Glu	Arg	Val	Gly	Gly	Leu	Gln	Val	Ile	Leu	Arg	Gly	Tyr	Leu	Thr	Met		
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gtt	gct	gat	ctt	tcc	ggc	cag	cag	tgg	aac	gaa	ggc	gat	gtc	ttc	tgc		
	1075																
Val	Ala	Asp	Leu	Ser	Gly	Gln	Gln	Trp	Asn	Glu	Gly	Asp	Val	Phe	Cys		
	310				315					320					325		
tcc	gtg	atc	cgc	cgc	gtt	gca	ctg	cca	gac	gca	ttc	ttc	gcg	att	gac		
	1123																
Ser	Val	Ile	Arg	Arg	Val	Ala	Leu	Pro	Asp	Ala	Phe	Phe	Ala	Ile	Asp		
				330					335					340			
gga	atg	ttt	gaa	act	ttc	ctg	aca	gtc	ctg	gat	gaa	ttc	ggc	gca	ttc		
	1171																
Gly	Met	Phe	Glu	Thr	Phe	Leu	Thr	Val	Leu	Asp	Glu	Phe	Gly	Ala	Phe		
			345					350					355				
cct	gcc	atg	atc	gag	cgc	gaa	ctt	gag	cgt	tac	ctg	cca	ttc	ctg	gca		
	1219																
Pro	Ala	Met	Ile	Glu	Arg	Glu	Leu	Glu	Arg	Tyr	Leu	Pro	Phe	Leu	Ala		
		360					365					370					
act	acc	cgt	atc	ctc	atg	gcc	gct	gtc	cgc	gca	ggc	gtt	ggc	cgc	gaa		
	1267																
Thr	Thr	Arg	Ile	Leu	Met	Ala	Ala	Val	Arg	Ala	Gly	Val	Gly	Arg	Glu		
	375					380					385						
acc	gca	cac	gaa	gta	atc	aag	gaa	aac	gct	gtc	gcg	gtt	gcc	ctc	aac		
	1315																
Thr	Ala	His	Glu	Val	Ile	Lys	Glu	Asn	Ala	Val	Ala	Val	Ala	Leu	Asn		
	390				395				400						405		
atg	cgc	gaa	aat	ggc	ggt	gac	cag	gac	ctt	atc	cag	cgc	ctc	gct	gct		
	1363																
Met	Arg	Glu	Asn	Gly	Gly	Asp	Gln	Asp	Leu	Ile	Gln	Arg	Leu	Ala	Ala		

410	415	420
gat gag cgc ctc cca atg agc gaa gct gac ctt gag gca gcg ctg gct 1411		
Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu Glu Ala Ala Leu Ala 425 430 435		
gac cgc cac gcc ttc atc ggt gcc gct gag tcc cag gtc tcc cgt gtg 1459		
Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser Gln Val Ser Arg Val 440 445 450		
ctc gac cgc att cag gtg ctt gtc gac gcc cac ccc ggc gcc gca gac 1507		
Leu Asp Arg Ile Gln Val Leu Val Asp Ala His Pro Gly Ala Ala Asp 455 460 465		
tac cga cca ggt gag att ctt taaaggtttt taacggcgtt cac 1551		
Tyr Arg Pro Gly Glu Ile Leu 470 475		
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Ser Ala Glu Leu Ser Asn Leu Trp Ser Ala Glu Glu Lys Ile Ile Met 20 25 30		
Glu Arg Gln Leu Trp Ile Ala Val Met Lys Ala Gln Lys Asp Leu Gly 35 40 45		
Val Glu Ile Pro Ala Glu Ala Ile Glu Ser Tyr Glu Ala Val Ile Asp 50 55 60		
Gln Val Asp Leu Ala Ser Ile Ala Asp Arg Glu Arg Val Thr Arg His 65 70 75 80		
Asp Val Lys Ala Arg Ile Glu Glu Phe Asn Ala Leu Ala Gly His Glu 85 90 95		
His Ile His Lys Gly Met Thr Ser Arg Asp Leu Thr Glu Asn Val Glu 100 105 110		
Gln Leu Gln Ile His Arg Ser Leu Glu Leu Val Arg Asn Lys Gly Ile 115 120 125		
Ala Val Val Ala Ala Ile Gly Ser Arg Ala Ala Gln Tyr Gln Ser Leu 130 135 140		
Val Met Ala Gly Arg Ser His Asn Val Ala Ala Gln Ala Thr Thr Leu 145 150 155 160		
Gly Lys Arg Phe Ala Thr Ala Ala Asp Glu Met Leu Val Ala Leu Glu 165 170 175		

Arg Val Thr Glu Leu Leu Asn Arg Tyr Pro Leu Arg Gly Ile Lys Gly
 180 185 190
 Pro Met Gly Thr Ala Gln Asp Met Leu Asp Leu Met Glu Gly Asp Glu
 195 200 205
 Ala Arg Leu Ser Asp Leu Glu Thr Arg Ile Ala Ala His Leu Gly Phe
 210 215 220
 Asp Arg Val Phe Asp Ser Val Gly Gln Val Tyr Pro Arg Ser Leu Asp
 225 230 235 240
 Phe Asp Ala Val Ser Ala Leu Val Gln Leu Gly Ser Gly Pro Ser Ser
 245 250 255
 Leu Ser His Thr Ile Arg Leu Met Ala Gly Thr Glu Thr Val Thr Glu
 260 265 270
 Gly Phe Lys Glu Gly Gln Val Gly Ser Ser Ala Met Pro His Lys Met
 275 280 285
 Asn Ala Arg Ser Cys Glu Arg Val Gly Gly Leu Gln Val Ile Leu Arg
 290 295 300
 Gly Tyr Leu Thr Met Val Ala Asp Leu Ser Gly Gln Gln Trp Asn Glu
 305 310 315 320
 Gly Asp Val Phe Cys Ser Val Ile Arg Arg Val Ala Leu Pro Asp Ala
 325 330 335
 Phe Phe Ala Ile Asp Gly Met Phe Glu Thr Phe Leu Thr Val Leu Asp
 340 345 350
 Glu Phe Gly Ala Phe Pro Ala Met Ile Glu Arg Glu Leu Glu Arg Tyr
 355 360 365
 Leu Pro Phe Leu Ala Thr Thr Arg Ile Leu Met Ala Ala Val Arg Ala
 370 375 380
 Gly Val Gly Arg Glu Thr Ala His Glu Val Ile Lys Glu Asn Ala Val
 385 390 395 400
 Ala Val Ala Leu Asn Met Arg Glu Asn Gly Gly Asp Gln Asp Leu Ile
 405 410 415
 Gln Arg Leu Ala Ala Asp Glu Arg Leu Pro Met Ser Glu Ala Asp Leu
 420 425 430
 Glu Ala Ala Leu Ala Asp Arg His Ala Phe Ile Gly Ala Ala Glu Ser
 435 440 445
 Gln Val Ser Arg Val Leu Asp Arg Ile Gln Val Leu Val Asp Ala His
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 Pro Gly Ala Ala Asp Tyr Arg Pro Gly Glu Ile Leu
 465 470 475

<210> 963

<211> 666

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) .. (643)

<223> RXA00688

<400> 963

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gccagctcct gcaaagcaac tacgaaggac ttctaaaata atg cga ctc gta ctc 115
 Met Arg Leu Val Leu
 1 5

ctc gga cct ccc ggt gct ggt aag ggc acc cag gct gca att ctc tct 163
 Leu Gly Pro Pro Gly Ala Gly Lys Gly Thr Gln Ala Ala Ile Leu Ser
 10 15 20

gag aag ctt ggc att cct cac att tct act ggc gat ctt ttc cgc gcc 211
 Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly Asp Leu Phe Arg Ala
 25 30 35

aac att ggc gaa ggt acc cct ctg ggt atc gag gcc aag cag tac atc 259
 Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu Ala Lys Gln Tyr Ile
 40 45 50

gac gct ggc aag ctg gtt cca acc gac gtg act gca cgt atg gtt gct 307
 Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr Ala Arg Met Val Ala
 55 60 65

tcc cgc ctt gct gag tcc gat gct gca gaa ggc ttc ctt ttg gat ggt 355
 Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly Phe Leu Leu Asp Gly
 70 75 80 85

ttc cca cgc acc gtt gag cag gct gac atc ttg gct aac ctg ctt tcc 403
 Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu Ala Asn Leu Leu Ser
 90 95 100

gaa gct ggc cag acc ctc gat ggt gtt gtt aac tac cag gtt tct gaa 451
 Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn Tyr Gln Val Ser Glu
 105 110 115

gac gtc gtc gtg gag cgc atg ctg tcc cgt ggt cgc gct gat gac aac 499
 Asp Val Val Val Glu Arg Met Leu Ser Arg Gly Arg Ala Asp Asp Asn
 120 125 130

gaa gag acc atc cgc acc cgt ctc ggt gtc tac cgc gac gag act gct 547
 Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr Arg Asp Glu Thr Ala
 135 140 145

cct ctg atc gat cac tac ggt gac aag atc atc aac att gag gct gaa 595
 Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile Asn Ile Glu Ala Glu
 150 155 160 165

ggc gaa gtc gaa gag atc aac gct cgt acc ctc aag gca ctg ggc aaa 643
 Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu Lys Ala Leu Gly Lys
 170 175 180

taagatttct tctctagtgc tgc 666

<210> 964
 <211> 181
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 964
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 Ala Ala Ile Leu Ser Glu Lys Leu Gly Ile Pro His Ile Ser Thr Gly
 20 25 30
 Asp Leu Phe Arg Ala Asn Ile Gly Glu Gly Thr Pro Leu Gly Ile Glu
 35 40 45
 Ala Lys Gln Tyr Ile Asp Ala Gly Lys Leu Val Pro Thr Asp Val Thr
 50 55 60
 Ala Arg Met Val Ala Ser Arg Leu Ala Glu Ser Asp Ala Ala Glu Gly
 65 70 75 80
 Phe Leu Leu Asp Gly Phe Pro Arg Thr Val Glu Gln Ala Asp Ile Leu
 85 90 95
 Ala Asn Leu Leu Ser Glu Ala Gly Gln Thr Leu Asp Gly Val Val Asn
 100 105 110
 Tyr Gln Val Ser Glu Asp Val Val Val Glu Arg Met Leu Ser Arg Gly
 115 120 125
 Arg Ala Asp Asp Asn Glu Glu Thr Ile Arg Thr Arg Leu Gly Val Tyr
 130 135 140
 Arg Asp Glu Thr Ala Pro Leu Ile Asp His Tyr Gly Asp Lys Ile Ile
 145 150 155 160
 Asn Ile Glu Ala Glu Gly Glu Val Glu Glu Ile Asn Ala Arg Thr Leu
 165 170 175
 Lys Ala Leu Gly Lys
 180

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 <211> 531
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> RXA00266

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 Met Thr Glu Arg Thr
 1 5

ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa 163
 Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu
 10 15 20

 atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat 211
 Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp
 25 30 35

 ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac 259
 Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His
 40 45 50

 gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca 307
 Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala
 55 60 65

 cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg 355
 Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp
 70 75 80 85

 cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc 403
 Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly
 90 95 100

 acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac 451
 Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His
 105 110 115

 ggt tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc 499
 Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu Ile Ser Ile Trp Phe
 120 125 130

 cct aac ctg taatttttac ggtagaaaa aaa 531
 Pro Asn Leu
 135

<210> 966

<211> 136

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 966

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 Gly His Val Gly Glu Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys
 20 25 30

 Leu Ala Ala Leu Asp Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys
 35 40 45

 His Tyr Glu Glu His Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu
 50 55 60

 Phe Ile Thr Ser Ala Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg
 65 70 75 80

 Ala Ile Asp Ala Trp Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala
 85 90 95

Lys Ala Thr Pro Gly Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly
 100 105 110

Glu Asn Val Val His Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu
 115 120 125

Ile Ser Ile Trp Phe Pro Asn Leu
 130 135

<210> 967
 <211> 1245
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1222)
 <223> RXA00489

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gtcttcgtcg tatacgacca tttaagggag gcccgtcaca atg cgt gac cac gtt 115
 Met Arg Asp His Val
 1 5

gaa atc ggt atc ggc cgt gag gca cga cgc acc tac agc ttg gac gat 163
 Glu Ile Gly Ile Gly Arg Glu Ala Arg Arg Thr Tyr Ser Leu Asp Asp
 10 15 20

att tct gtc gtt tct agc cgc cgc acc cgt tca tcc aaa gat gtc gac 211
 Ile Ser Val Val Ser Ser Arg Arg Thr Arg Ser Ser Lys Asp Val Asp
 25 30 35

acc act tgg cat att gac gcc tac aag ttt gat ctg ccg ttc atg aat 259
 Thr Thr Trp His Ile Asp Ala Tyr Lys Phe Asp Leu Pro Phe Met Asn
 40 45 50

cac cca agt gat gca ttg gca agc cct gag ttt gtc att gaa atg ggc 307
 His Pro Ser Asp Ala Leu Ala Ser Pro Glu Phe Val Ile Glu Met Gly
 55 60 65

aag cag ggt ggc ctt ggc gtg atc aac gct gag ggt ctg tgg ggt cgc 355
 Lys Gln Gly Gly Leu Gly Val Ile Asn Ala Glu Gly Leu Trp Gly Arg
 70 75 80 85

cat gct gat ctc gat gag gcg atc gca aag gtg att gct gcg tat gag 403
 His Ala Asp Leu Asp Glu Ala Ile Ala Lys Val Ile Ala Ala Tyr Glu
 90 95 100

gaa ggc gac cag gct gca gcc act cgc act ctt cag gag ctg cac gca 451
 Glu Gly Asp Gln Ala Ala Ala Thr Arg Thr Leu Gln Glu Leu His Ala
 105 110 115

gcg cca ctg gat act gag ctg ctg agt gag cgc att gcg cag gtt cgt 499
 Ala Pro Leu Asp Thr Glu Leu Leu Ser Glu Arg Ile Ala Gln Val Arg
 120 125 130

gat tcc ggt gag atc gtt gct gtg cgc gtg tct cca caa aat gtt cgt 547
 Asp Ser Gly Glu Ile Val Ala Val Arg Val Ser Pro Gln Asn Val Arg

135	140	145	
gag atc gca cca atc gtc atc aag gca ggt gct gat ctg ctg gtt atc Glu Ile Ala Pro Ile Val Ile Lys Ala Gly Ala Asp Leu Leu Val Ile 150 155 160 165			595
cag ggc acc ctg atc tct gca gag cac gtc aac acc ggt gga gag gcc Gln Gly Thr Leu Ile Ser Ala Glu His Val Asn Thr Gly Gly Glu Ala 170 175 180			643
ctg aac cta aag gaa ttc atc ggt tct ttg gat gtt cct gtc atc gct Leu Asn Leu Lys Glu Phe Ile Gly Ser Leu Asp Val Pro Val Ile Ala 185 190 195			691
ggt ggc gtg aac gat tac acc acc gcg ttg cac atg atg cgt acc ggt Gly Gly Val Asn Asp Tyr Thr Thr Ala Leu His Met Met Arg Thr Gly 200 205 210			739
gct gtg ggc atc atc gtc ggt ggc ggc gag aac acc aac agc cta gca Ala Val Gly Ile Ile Val Gly Gly Gly Glu Asn Thr Asn Ser Leu Ala 215 220 225			787
ttg ggc atg gag gta tcc atg gcc act gcg att gct gat gtc gct gcg Leu Gly Met Glu Val Ser Met Ala Thr Ala Ile Ala Asp Val Ala Ala 230 235 240 245			835
gca cgt cgt gat tac ctg gat gag acc ggt gga cgt tac gtg cac atc Ala Arg Arg Asp Tyr Leu Asp Glu Thr Gly Gly Arg Tyr Val His Ile 250 255 260			883
att gca gat gga agc att gaa aac tcc ggt gat gta gtc aag gct att Ile Ala Asp Gly Ser Ile Glu Asn Ser Gly Asp Val Val Lys Ala Ile 265 270 275			931
gcc tgt ggc gca gat gct gtg gtg ctg ggt tca ccg ttg gct cgc gct Ala Cys Gly Ala Asp Ala Val Val Leu Gly Ser Pro Leu Ala Arg Ala 280 285 290			979
gaa gaa gct gct gga aag ggc tac ttc tgg cca gca gtg gca gcg cac 1027 Glu Glu Ala Ala Gly Lys Gly Tyr Phe Trp Pro Ala Val Ala Ala His 295 300 305			
cct cgt ttc cca cgc ggt gtg gtt act gag tcc gtg gac ttg gat gag 1075 Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser Val Asp Leu Asp Glu 310 315 320 325			
gca gca cca agc ttg gag cag att ctg cat ggt ccg tct acg atg ccg 1123 Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly Pro Ser Thr Met Pro 330 335 340			
tgg ggt gtg gaa aac ttc gaa ggt gga tta aag cgt gcg ctg gct aag 1171 Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys Arg Ala Leu Ala Lys 345 350 355			
tgt ggc tac acc gat ttg aag agc ttc caa aag gta agc ctg cac gtt 1219 Cys Gly Tyr Thr Asp Leu Lys Ser Phe Gln Lys Val Ser Leu His Val			

360

365

370

aac taggtgtgtg tactcgcttc ttc

1245

Asn

<210> 968

<211> 374

<212> PRT

<213> Corynebacterium glutamicum

<400> 968

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Tyr	Ser	Leu	Asp	Asp	Ile	Ser	Val	Val	Ser	Ser	Arg	Arg	Thr	Arg	Ser
			20					25					30		

Ser	Lys	Asp	Val	Asp	Thr	Thr	Trp	His	Ile	Asp	Ala	Tyr	Lys	Phe	Asp
		35					40					45			

Leu	Pro	Phe	Met	Asn	His	Pro	Ser	Asp	Ala	Leu	Ala	Ser	Pro	Glu	Phe
	50					55					60				

Val	Ile	Glu	Met	Gly	Lys	Gln	Gly	Gly	Leu	Gly	Val	Ile	Asn	Ala	Glu
65					70					75					80

Gly	Leu	Trp	Gly	Arg	His	Ala	Asp	Leu	Asp	Glu	Ala	Ile	Ala	Lys	Val
				85					90					95	

Ile	Ala	Ala	Tyr	Glu	Glu	Gly	Asp	Gln	Ala	Ala	Ala	Thr	Arg	Thr	Leu
			100					105					110		

Gln	Glu	Leu	His	Ala	Ala	Pro	Leu	Asp	Thr	Glu	Leu	Leu	Ser	Glu	Arg
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Ile	Ala	Gln	Val	Arg	Asp	Ser	Gly	Glu	Ile	Val	Ala	Val	Arg	Val	Ser
	130					135					140				

Pro	Gln	Asn	Val	Arg	Glu	Ile	Ala	Pro	Ile	Val	Ile	Lys	Ala	Gly	Ala
145					150					155					160

Asp	Leu	Leu	Val	Ile	Gln	Gly	Thr	Leu	Ile	Ser	Ala	Glu	His	Val	Asn
				165					170					175	

Thr	Gly	Gly	Glu	Ala	Leu	Asn	Leu	Lys	Glu	Phe	Ile	Gly	Ser	Leu	Asp
			180					185					190		

Val	Pro	Val	Ile	Ala	Gly	Gly	Val	Asn	Asp	Tyr	Thr	Thr	Ala	Leu	His
		195					200					205			

Met	Met	Arg	Thr	Gly	Ala	Val	Gly	Ile	Ile	Val	Gly	Gly	Gly	Glu	Asn
	210					215					220				

Thr	Asn	Ser	Leu	Ala	Leu	Gly	Met	Glu	Val	Ser	Met	Ala	Thr	Ala	Ile
225					230					235					240

Ala	Asp	Val	Ala	Ala	Ala	Arg	Arg	Asp	Tyr	Leu	Asp	Glu	Thr	Gly	Gly
			245						250					255	

Arg Tyr Val His Ile Ile Ala Asp Gly Ser Ile Glu Asn Ser Gly Asp
 260 265 270
 Val Val Lys Ala Ile Ala Cys Gly Ala Asp Ala Val Val Leu Gly Ser
 275 280 285
 Pro Leu Ala Arg Ala Glu Glu Ala Ala Gly Lys Gly Tyr Phe Trp Pro
 290 295 300
 Ala Val Ala Ala His Pro Arg Phe Pro Arg Gly Val Val Thr Glu Ser
 305 310 315 320
 Val Asp Leu Asp Glu Ala Ala Pro Ser Leu Glu Gln Ile Leu His Gly
 325 330 335
 Pro Ser Thr Met Pro Trp Gly Val Glu Asn Phe Glu Gly Gly Leu Lys
 340 345 350
 Arg Ala Leu Ala Lys Cys Gly Tyr Thr Asp Leu Lys Ser Phe Gln Lys
 355 360 365
 Val Ser Leu His Val Asn
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<210> 969

<211> 1545

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1531)

<223> RXN02281

<400> 969

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 Val Gln Lys Asp Ser
 1 5
 gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu
 10 15 20
 att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn
 25 30 35
 aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr
 40 45 50
 gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly
 55 60 65
 tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg

70	75	80	85	
gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat 403				
Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn	90	95	100	
tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg 451				
Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp Ile Arg Ile Pro Pro	105	110	115	
gag tac att cgc ggc gca cct tcc gct acc gaa gct cgc cgt gct ggt 499				
Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu Ala Arg Arg Ala Gly	120	125	130	
gat gtt gca gat atc atc cca cgc ccc acc ctg gat gaa gtc cac gac 547				
Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu Asp Glu Val His Asp	135	140	145	
gca att atc gac ggc gac tgg cac gcc ttc aac ggc ccc gaa ctc ccg 595				
Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn Gly Pro Glu Leu Pro	150	155	160	165
ctt ttc cac ttc ggg ccg caa cgc ttc gac atc gcc tgc gcc cgc atc 643				
Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile Ala Cys Ala Arg Ile	170	175	180	
gag cac tac acc ggc atc aac gtg gaa cac gtg cag aag tac att ctg 691				
Glu His Tyr Thr Gly Ile Asn Val Glu His Val Gln Lys Tyr Ile Leu	185	190	195	
ttc acc aac tac gcc atg cac acc acc gag ttc gtg cat ttt gcc atg 739				
Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe Val His Phe Ala Met	200	205	210	
tcc gaa ctc acc tcg gaa gac tcc cgc tac gtg ggt cta tcc ttg cca 787				
Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val Gly Leu Ser Leu Pro	215	220	225	
aac ggg cag gta att gac cga gag acc gcc acc agc ctc ggt acg gaa 835				
Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr Ser Leu Gly Thr Glu	230	235	240	245
acc ctt gat ctg act agc cgt ttc caa atg cct cgt tac gat ctc atc 883				
Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro Arg Tyr Asp Leu Ile	250	255	260	
acc gaa gcc ggt gac ggt att acc att atc aac atc ggt gtg ggc cca 931				
Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn Ile Gly Val Gly Pro	265	270	275	
tcc aat gca aaa act atc acc gac tgc ctt gct gtg ctc cgc cca gaa 979				
Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala Val Leu Arg Pro Glu	280	285	290	
gcc tgg gtg atg atc ggc cac tgt gct ggc atg gac gcc cgc atg cgc 1027				
Ala Trp Val Met Ile Gly His Cys Ala Gly Met Asp Ala Arg Met Arg	295	300	305	
atc ggc gac ctc atc ctt ggc aac gcc tac cag cgc gaa gac cac att 1075				

Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile
310 315 320 325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa
1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc gac
1171

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp
345 350 355

aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac
1219

Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn
360 365 370

tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc
1267

Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser
375 380 385

acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga
1315

Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly
390 395 400 405

tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg
1363

Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu
410 415 420

cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac
1411

Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr
425 430 435

ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa
1459

Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu
440 445 450

tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg
1507

Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg
455 460 465

acc ttg ggt gag gtg ccg ttt cgc taaagtctcg gaga
1545

Thr Leu Gly Glu Val Pro Phe Arg
470 475

<210> 970

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 970

Val Gln Lys Asp Ser Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp

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Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala	20	25	30
Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val	35	40	45
Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg	50	55	60
Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr	65	70	75
Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu	85	90	95
Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp	100	105	110
Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu	115	120	125
Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu	130	135	140
Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn	145	150	155
Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile	165	170	175
Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val	180	185	190
Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe	195	200	205
Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val	210	215	220
Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr	225	230	235
Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro	245	250	255
Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn	260	265	270
Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala	275	280	285
Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met	290	295	300
Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln	305	310	315
Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile	325	330	335

Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu
 340 345 350

Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser
 355 360 365

Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn
 370 375 380

Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr
 385 390 395 400

Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu
 405 410 415

Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln
 420 425 430

Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala
 435 440 445

Val Arg Ala Met Glu Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr
 450 455 460

Arg Lys Leu Arg Arg Thr Leu Gly Glu Val Pro Phe Arg
 465 470 475

<210> 971

<211> 1191

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1168)

<223> FRXA02281

<400> 971

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cctataaaag cacagttttg aatccacagg gcatcagggc gtg cag aaa gat agt 115
 Val Gln Lys Asp Ser
 1 5

gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu
 10 15 20

att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr
 40 45 50

gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly
 55 60 65

tat	gtg	gat	cga	gcc	ggg	cga	tac	tcc	gcc	acc	ttg	tcc	aaa	cca	cgc	355
Tyr	Val	Asp	Arg	Ala	Gly	Arg	Tyr	Ser	Ala	Thr	Leu	Ser	Lys	Pro	Arg	
70					75					80					85	
gtg	att	gag	cgt	tac	ctc	cgc	gaa	caa	ctc	gag	cgt	ctc	acc	agt	aat	403
Val	Ile	Glu	Arg	Tyr	Leu	Arg	Glu	Gln	Leu	Glu	Arg	Leu	Thr	Ser	Asn	
				90					95					100		
tat	ccc	tgc	aag	att	tac	gta	tct	gag	tca	gat	atc	cgc	atc	cca	ccg	451
Tyr	Pro	Cys	Lys	Ile	Tyr	Val	Ser	Glu	Ser	Asp	Ile	Arg	Ile	Pro	Pro	
			105					110					115			
gag	tac	att	cgc	ggc	gca	cct	tcc	gct	acc	gaa	gct	cgc	cgt	gct	ggc	499
Glu	Tyr	Ile	Arg	Gly	Ala	Pro	Ser	Ala	Thr	Glu	Ala	Arg	Arg	Ala	Gly	
		120					125					130				
gat	gtt	gca	gat	atc	atc	cca	cgc	ccc	acc	ctg	gat	gaa	gtc	cac	gac	547
Asp	Val	Ala	Asp	Ile	Ile	Pro	Arg	Pro	Thr	Leu	Asp	Glu	Val	His	Asp	
	135					140					145					
gca	att	atc	gac	ggc	gac	tgg	cac	gcc	ttc	aac	ggc	ccc	gaa	ctc	ccg	595
Ala	Ile	Ile	Asp	Gly	Asp	Trp	His	Ala	Phe	Asn	Gly	Pro	Glu	Leu	Pro	
150					155					160					165	
ctt	ttc	cac	ttc	ggg	ccg	caa	cgc	ttc	gac	atc	gcc	tgc	gcc	cgc	atc	643
Leu	Phe	His	Phe	Gly	Pro	Gln	Arg	Phe	Asp	Ile	Ala	Cys	Ala	Arg	Ile	
				170					175					180		
gag	cac	tac	acc	ggc	atc	aac	gtg	gaa	cac	gtg	cag	aag	tac	att	ctg	691
Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val	Gln	Lys	Tyr	Ile	Leu	
			185					190					195			
ttc	acc	aac	tac	gcc	atg	cac	acc	acc	gag	ttc	gtg	cat	ttt	gcc	atg	739
Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe	Val	His	Phe	Ala	Met	
		200					205					210				
tcc	gaa	ctc	acc	tcg	gaa	gac	tcc	cgc	tac	gtg	ggc	cta	tcc	ttg	cca	787
Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val	Gly	Leu	Ser	Leu	Pro	
	215					220					225					
aac	ggg	cag	gta	att	gac	cga	gag	acc	gcc	acc	agc	ctc	ggc	acg	gaa	835
Asn	Gly	Gln	Val	Ile	Asp	Arg	Glu	Thr	Ala	Thr	Ser	Leu	Gly	Thr	Glu	
230					235				240						245	
acc	ctt	gat	ctg	act	agc	cgt	ttc	caa	atg	cct	cgt	tac	gat	ctc	atc	883
Thr	Leu	Asp	Leu	Thr	Ser	Arg	Phe	Gln	Met	Pro	Arg	Tyr	Asp	Leu	Ile	
				250				255						260		
acc	gaa	gcc	ggc	gac	ggc	att	acc	att	atc	aac	atc	ggc	gtg	ggc	cca	931
Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn	Ile	Gly	Val	Gly	Pro	
			265				270						275			
tcc	aat	gca	aaa	act	atc	acc	gac	tgc	ctt	gct	gtg	ctc	cgc	cca	gaa	979
Ser	Asn	Ala	Lys	Thr	Ile	Thr	Asp	Cys	Leu	Ala	Val	Leu	Arg	Pro	Glu	
		280					285					290				
gcc	tgg	gtg	atg	atc	ggc	cac	tgt	gct	ggc	atg	gac	gcc	cgc	atg	cgc	
1027																
Ala	Trp	Val	Met	Ile	Gly	His	Cys	Ala	Gly	Met	Asp	Ala	Arg	Met	Arg	
	295					300					305					

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1075

Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln Arg Glu Asp His Ile
310 315 320 325

ctg aat acc cgc atc cca ctt ggt aat ccg atc ccg gca ata cca gaa
1123

Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
330 335 340

atc caa aaa gct cta gaa gcc agc gtc gac gaa atc tac gga tcc
1168

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser
345 350 355

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1191

<210> 972

<211> 356

<212> PRT

<213> Corynebacterium glutamicum

<400> 972

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Ala Ile Ala Lys Leu Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala
20 25 30

Lys Glu Thr Leu Asn Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val
35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
50 55 60

Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
 195 200 205
 Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
 210 215 220
 Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
 225 230 235 240
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
 245 250 255
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
 260 265 270
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
 275 280 285
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
 290 295 300
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
 305 310 315 320
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
 325 330 335
 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu
 340 345 350
 Ile Tyr Gly Ser
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1279)
 <223> RXA00147

<400> 973
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 Val Ser Lys Asp Thr
 1 5
 acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg 163
 Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu
 10 15 20
 gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc 211
 Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile
 25 30 35
 ggc acc acc ctt ggt gag gca gtg ttc act acc gcc atg acc ggt tac 259

Gly	Thr	Thr	Leu	Gly	Glu	Ala	Val	Phe	Thr	Thr	Ala	Met	Thr	Gly	Tyr	
		40					45					50				
caa	gaa	acc	atg	acc	gat	cct	tcc	tat	cac	cgc	cag	att	gtt	gtg	gct	307
Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg	Gln	Ile	Val	Val	Ala	
	55					60					65					
acc	gca	cca	cag	atc	ggc	aac	acc	ggc	tgg	aac	gat	gag	gac	aac	gag	355
Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn	Asp	Glu	Asp	Asn	Glu	
70					75					80					85	
tcc	cgc	gac	ggc	aag	att	tgg	gtt	gca	ggc	ctt	gtt	atc	cgc	gac	ctc	403
Ser	Arg	Asp	Gly	Lys	Ile	Trp	Val	Ala	Gly	Leu	Val	Ile	Arg	Asp	Leu	
				90					95					100		
gca	gca	cgt	gtg	tcc	aac	tgg	cgc	gcc	acc	acc	tcc	ttg	cag	cag	gaa	451
Ala	Ala	Arg	Val	Ser	Asn	Trp	Arg	Ala	Thr	Thr	Ser	Leu	Gln	Gln	Glu	
			105					110					115			
atg	gca	ggc	cag	ggc	atc	gtc	ggc	atc	ggc	gga	atc	gac	acc	cgc	gca	499
Met	Ala	Gly	Gln	Gly	Ile	Val	Gly	Ile	Gly	Gly	Ile	Asp	Thr	Arg	Ala	
		120					125					130				
ctg	gtt	cgc	cac	ctg	cgc	aat	gaa	ggt	tcc	att	gca	gcg	ggc	atc	ttc	547
Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile	Ala	Ala	Gly	Ile	Phe	
	135					140					145					
tcc	ggc	gct	gac	gca	cag	cgc	cca	gtt	gaa	gaa	ctc	gta	gag	atc	gtc	595
Ser	Gly	Ala	Asp	Ala	Gln	Arg	Pro	Val	Glu	Glu	Leu	Val	Glu	Ile	Val	
150					155					160					165	
aag	aat	cag	cca	gca	atg	acc	ggc	gca	aac	ctc	tcc	gtt	gag	gtc	tct	643
Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu	Ser	Val	Glu	Val	Ser	
			170						175					180		
gct	gat	gaa	acc	tac	gtc	atc	gaa	gct	gaa	ggc	gaa	gag	cgc	cac	acc	691
Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly	Glu	Glu	Arg	His	Thr	
			185					190					195			
gtc	gtg	gcc	tac	gac	ctg	ggc	att	aag	caa	aac	acc	cca	cgt	cgt	ttc	739
Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn	Thr	Pro	Arg	Arg	Phe	
		200				205						210				
tct	gca	cgc	ggt	gtt	cgc	acc	gtc	atc	gtg	cct	gct	gaa	acc	cca	ttc	787
Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro	Ala	Glu	Thr	Pro	Phe	
	215					220					225					
gag	gat	atc	aag	cag	tac	aac	cca	tca	ggc	gtg	ttc	atc	tcc	aac	ggc	835
Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val	Phe	Ile	Ser	Asn	Gly	
230					235					240					245	
cct	ggc	gat	cct	gca	gca	gca	gac	gtc	atg	gtt	gat	atc	gtc	cgc	gaa	883
Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val	Asp	Ile	Val	Arg	Glu	
				250					255					260		
gtt	ctt	gaa	gcc	gac	att	cca	ttc	ttt	ggc	atc	tgc	ttc	ggc	aac	cag	931
Val	Leu	Glu	Ala	Asp	Ile	Pro	Phe	Phe	Gly	Ile	Cys	Phe	Gly	Asn	Gln	
			265					270					275			
att	ctt	ggc	cgc	gca	ttc	ggc	atg	gag	acc	tac	aag	ctg	aag	ttc	ggc	979
Ile	Leu	Gly	Arg	Ala	Phe	Gly	Met	Glu	Thr	Tyr	Lys	Leu	Lys	Phe	Gly	

280 285 290
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 1027
 His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile
 295 300 305
 gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc
 1075
 Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly
 310 315 320 325
 cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc
 1123
 Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys
 330 335 340
 ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca
 1171
 Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala
 345 350 355
 tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca
 1219
 Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala
 360 365 370
 agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag
 1267
 Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln
 375 380 385
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 Lys Lys Gly Ala
 390

<210> 974
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<400> 974
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 Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr
 35 40 45
 Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg
 50 55 60
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn
 65 70 75 80
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu
 85 90 95

Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr
 100 105 110
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly
 115 120 125
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile
 130 135 140
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu
 145 150 155 160
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu
 165 170 175
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly
 180 185 190
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn
 195 200 205
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro
 210 215 220
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val
 225 230 235 240
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val
 245 250 255
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile
 260 265 270
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr
 275 280 285
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His
 290 295 300
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu
 305 310 315 320
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile
 325 330 335
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu
 340 345 350
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala
 355 360 365
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 370 375 380
 Asp Ala Asp Ala Gln Lys Lys Gly Ala
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<213> Corynebacterium glutamicum

<220>

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<223> RXA00145

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Ser	Ile	Ser	Asp	Leu	Ser	Lys	Asp	Glu	Ile	Val	Gly	Leu	Leu	Asp	Glu	
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gcg	gat	cgc	ttt	aag	gag	gtg	ctc	gaa	gga	cgt	gaa	gta	aag	aag	ctg	211
Ala	Asp	Arg	Phe	Lys	Glu	Val	Leu	Glu	Gly	Arg	Glu	Val	Lys	Lys	Leu	
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ccc	acg	ctg	cgt	ggc	cgc	acc	att	ttt	acc	ttg	ttc	tat	gag	aac	tcc	259
Pro	Thr	Leu	Arg	Gly	Arg	Thr	Ile	Phe	Thr	Leu	Phe	Tyr	Glu	Asn	Ser	
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Thr	Arg	Thr	Arg	Ser	Ser	Phe	Glu	Thr	Ala	Gly	Lys	Trp	Met	Ser	Ala	
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Asp	Val	Ile	Asn	Ile	Ser	Ala	Ser	Ser	Ser	Ser	Val	Lys	Lys	Gly	Glu	
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Ser	Leu	Lys	Asp	Thr	Gly	Leu	Thr	Leu	Ser	Ala	Ile	Gly	Ala	Asp	Ala	
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atc	atc	atg	cgc	cac	cca	gcc	tca	ggc	gcc	gcg	cag	cag	ctt	gcg	cag	451
Ile	Ile	Met	Arg	His	Pro	Ala	Ser	Gly	Ala	Ala	Gln	Gln	Leu	Ala	Gln	
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ttc	gtc	gca	cca	ggc	ggc	aac	ggc	ccc	agc	gtg	atc	aac	gcg	ggc	gac	499
Phe	Val	Ala	Pro	Gly	Gly	Asn	Gly	Pro	Ser	Val	Ile	Asn	Ala	Gly	Asp	
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ggc	tcg	cac	cag	cac	ccc	acc	cag	gcg	ctt	ctc	gac	gct	tta	acc	atc	547
Gly	Ser	His	Gln	His	Pro	Thr	Gln	Ala	Leu	Leu	Asp	Ala	Leu	Thr	Ile	
	135					140					145					

cgg	cag	cgc	acc	ggc	cgc	att	gag	gga	ctc	aaa	gtt	gtc	atc	gtg	ggc	595
Arg	Gln	Arg	Thr	Gly	Arg	Ile	Glu	Gly	Leu	Lys	Val	Val	Ile	Val	Gly	
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Asp	Cys	Leu	His	Ser	Arg	Val	Val	Arg	Ser	Asn	Val	Asp	Leu	Leu	Ser	
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Thr	Leu	Gly	Ala	Glu	Val	Val	Leu	Val	Ala	Pro	Pro	Thr	Leu	Leu	Pro	

185								190					195					
att	ggt	gtg	gag	aac	tgg	cca	gtc	cga	ttc	tcc	tac	gac	atg	gac	gca	739		
Ile	Gly	Val	Glu	Asn	Trp	Pro	Val	Arg	Phe	Ser	Tyr	Asp	Met	Asp	Ala			
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gaa	att	gcc	gac	gcc	gac	gta	gtg	atg	atg	ctg	cgc	gtt	cag	caa	gaa	787		
Glu	Ile	Ala	Asp	Ala	Asp	Val	Val	Met	Met	Leu	Arg	Val	Gln	Gln	Glu			
215				220			225											
cgc	atg	cag	ggt	ggt	ttc	ttc	ccc	tca	cac	cgt	gag	tac	gca	acg	ctg	835		
Arg	Met	Gln	Gly	Gly	Phe	Phe	Pro	Ser	His	Arg	Glu	Tyr	Ala	Thr	Leu			
230		235				240					245							
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Tyr	Gly	Met	Ser	Lys	Glu	Arg	Glu	Ala	Arg	Leu	Lys	Asp	Ser	Ala	Ile			
250				255					260									
atc	atg	cac	ccc	ggc	ccc	atg	ctt	cgt	ggc	atg	gaa	att	aac	ttc	cag	931		
Ile	Met	His	Pro	Gly	Pro	Met	Leu	Arg	Gly	Met	Glu	Ile	Asn	Phe	Gln			
265			270				275											
gtg	gca	gac	gca	cca	cgc	acc	gcg	gta	ctg	cag	cag	gta	agc	aac	ggt	979		
Val	Ala	Asp	Ala	Pro	Arg	Thr	Ala	Val	Leu	Gln	Gln	Val	Ser	Asn	Gly			
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Val	His	Met	Arg	Met	Ala	Ile	Leu	Phe	Ala	Leu	Val	Ala	Gly	Ser	Asp			
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Ala Thr Ile																		
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Glu	Val	Lys	Lys	Leu	Pro	Thr	Leu	Arg	Gly	Arg	Thr	Ile	Phe	Thr	Leu			
35			40				45											
Phe	Tyr	Glu	Asn	Ser	Thr	Arg	Thr	Arg	Ser	Ser	Phe	Glu	Thr	Ala	Gly			
50		55				60												
Lys	Trp	Met	Ser	Ala	Asp	Val	Ile	Asn	Ile	Ser	Ala	Ser	Ser	Ser	Ser			
65		70				75					80							
Val	Lys	Lys	Gly	Glu	Ser	Leu	Lys	Asp	Thr	Gly	Leu	Thr	Leu	Ser	Ala			
85				90					95									

Ile Gly Ala Asp Ala Ile Ile Met Arg His Pro Ala Ser Gly Ala Ala
 100 105 110
 Gln Gln Leu Ala Gln Phe Val Ala Pro Gly Gly Asn Gly Pro Ser Val
 115 120 125
 Ile Asn Ala Gly Asp Gly Ser His Gln His Pro Thr Gln Ala Leu Leu
 130 135 140
 Asp Ala Leu Thr Ile Arg Gln Arg Thr Gly Arg Ile Glu Gly Leu Lys
 145 150 155 160
 Val Val Ile Val Gly Asp Cys Leu His Ser Arg Val Val Arg Ser Asn
 165 170 175
 Val Asp Leu Leu Ser Thr Leu Gly Ala Glu Val Val Leu Val Ala Pro
 180 185 190
 Pro Thr Leu Leu Pro Ile Gly Val Glu Asn Trp Pro Val Arg Phe Ser
 195 200 205
 Tyr Asp Met Asp Ala Glu Ile Ala Asp Ala Asp Val Val Met Met Leu
 210 215 220
 Arg Val Gln Gln Glu Arg Met Gln Gly Gly Phe Phe Pro Ser His Arg
 225 230 235 240
 Glu Tyr Ala Thr Leu Tyr Gly Met Ser Lys Glu Arg Glu Ala Arg Leu
 245 250 255
 Lys Asp Ser Ala Ile Ile Met His Pro Gly Pro Met Leu Arg Gly Met
 260 265 270
 Glu Ile Asn Phe Gln Val Ala Asp Ala Pro Arg Thr Ala Val Leu Gln
 275 280 285
 Gln Val Ser Asn Gly Val His Met Arg Met Ala Ile Leu Phe Ala Leu
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 Val Ala Gly Ser Asp Ala Thr Ile
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 <223> RXA00146

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 Val Val Asp Ser Asn
 1 5
 acc cag tat cca gaa acc ggc gca ctg gca ccg gct cct gca gac tca 163

Thr	Gln	Tyr	Pro	Glu	Thr	Gly	Ala	Leu	Ala	Pro	Ala	Pro	Ala	Asp	Ser	
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ctc	cta	atc	agc	aac	gtt	ttg	gtc	tac	ggc	gaa	ggc	gag	cca	acg	aat	211
Leu	Leu	Ile	Ser	Asn	Val	Leu	Val	Tyr	Gly	Glu	Gly	Glu	Pro	Thr	Asn	
			25					30					35			
gtg	ttt	gtt	aaa	gat	ggc	gtg	atc	gca	gct	atc	ggc	ggc	act	cat	gag	259
Val	Phe	Val	Lys	Asp	Gly	Val	Ile	Ala	Ala	Ile	Gly	Gly	Thr	His	Glu	
		40					45					50				
gct	gac	cgc	acc	atc	gac	ggc	aat	ggg	gga	gtt	ctc	ctt	cca	ggc	ttc	307
Ala	Asp	Arg	Thr	Ile	Asp	Gly	Asn	Gly	Gly	Val	Leu	Leu	Pro	Gly	Phe	
	55					60					65					
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Val	Asp	Met	His	Val	His	Leu	Arg	Glu	Pro	Gly	Arg	Glu	Asp	Thr	Glu	
	70				75					80					85	
acc	att	gcc	act	ggc	tct	gcc	gcc	gca	gcc	aag	ggc	gga	ttc	acc	gca	403
Thr	Ile	Ala	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Lys	Gly	Gly	Phe	Thr	Ala	
				90					95					100		
gta	ttc	acc	atg	gcg	aac	acc	act	cca	gtg	atg	gat	cag	ccg	gtt	atc	451
Val	Phe	Thr	Met	Ala	Asn	Thr	Thr	Pro	Val	Met	Asp	Gln	Pro	Val	Ile	
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gcg	gaa	tcc	gta	tgg	ttc	aag	ggc	caa	aac	att	ggc	ctg	tgc	gac	gtg	499
Ala	Glu	Ser	Val	Trp	Phe	Lys	Gly	Gln	Asn	Ile	Gly	Leu	Cys	Asp	Val	
		120					125					130				
cat	cca	gtt	gga	tcc	atc	acc	aag	ggc	ctt	gag	ggc	aag	gag	ctt	act	547
His	Pro	Val	Gly	Ser	Ile	Thr	Lys	Gly	Leu	Glu	Gly	Lys	Glu	Leu	Thr	
	135					140					145					
gag	ttc	ggc	atg	atg	gct	cgc	tct	gaa	gcc	aag	gtg	cgc	atg	ttc	tct	595
Glu	Phe	Gly	Met	Met	Ala	Arg	Ser	Glu	Ala	Lys	Val	Arg	Met	Phe	Ser	
	150				155					160					165	
gat	gat	ggc	aag	tgc	gtc	gat	gat	cct	cag	gtc	atg	cgc	cgc	gcg	ctg	643
Asp	Asp	Gly	Lys	Cys	Val	Asp	Asp	Pro	Gln	Val	Met	Arg	Arg	Ala	Leu	
				170					175					180		
gaa	tac	gcc	aag	ggc	atg	gac	gtt	ttg	atc	gcc	cag	cac	gct	gag	gat	691
Glu	Tyr	Ala	Lys	Gly	Met	Asp	Val	Leu	Ile	Ala	Gln	His	Ala	Glu	Asp	
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cac	cgc	ctg	act	gag	ggc	gct	tca	gca	cac	gag	ggc	gaa	aac	gca	gct	739
His	Arg	Leu	Thr	Glu	Gly	Ala	Ser	Ala	His	Glu	Gly	Glu	Asn	Ala	Ala	
		200					205					210				
cgt	ctg	ggc	ctg	cgc	ggc	tgg	cca	cgt	gtg	gct	gag	gaa	tcc	atc	gtg	787
Arg	Leu	Gly	Leu	Arg	Gly	Trp	Pro	Arg	Val	Ala	Glu	Glu	Ser	Ile	Val	
	215					220					225					
gtg	cgc	gat	gcc	atc	atg	gct	cgt	gac	tac	ggc	aac	cgc	gtg	cac	atc	835
Val	Arg	Asp	Ala	Ile	Met	Ala	Arg	Asp	Tyr	Gly	Asn	Arg	Val	His	Ile	
	230				235					240					245	
tgc	cac	gcc	tcc	act	gaa	ggc	acc	gtg	gag	ttg	ctt	cgt	tgg	gct	aag	883
Cys	His	Ala	Ser	Thr	Glu	Gly	Thr	Val	Glu	Leu	Leu	Arg	Trp	Ala	Lys	

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Ser	Gln	Gly	Ile	Pro	Ile	Thr	Ala	Glu	Val	Thr	Pro	His	His	Leu	Thr		
			265					270					275				
ttg	acc	gat	gag	cgc	ctg	gaa	acc	tac	gac	gcg	gtc	aac	aaa	gtc	aat		979
Leu	Thr	Asp	Glu	Arg	Leu	Glu	Thr	Tyr	Asp	Ala	Val	Asn	Lys	Val	Asn		
		280					285					290					
ccg	cca	ctg	cgc	gaa	agc	cgc	gat	gcc	gaa	gcg	ctc	aag	aag	gcg	ctt		
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Pro	Pro	Leu	Arg	Glu	Ser	Arg	Asp	Ala	Glu	Ala	Leu	Lys	Lys	Ala	Leu		
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1171																	
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1219																	
Gly	Leu	Ala	Asp	Trp	Arg	Phe	Val	Ala	Arg	Val	Met	Ser	Glu	Arg	Pro		
		360					365				370						
gca	gaa	atc	acc	cgt	cta	cca	ggc	cag	ggt	cgc	cca	atc	gca	gaa	ggt		
1267																	
Ala	Glu	Ile	Thr	Arg	Leu	Pro	Gly	Gln	Gly	Arg	Pro	Ile	Ala	Glu	Gly		
	375					380					385						
gag	cca	gca	aac	ctc	gcg	att	gtt	gat	cca	gga	aaa	acc	tgg	aca	gca		
1315																	
Glu	Pro	Ala	Asn	Leu	Ala	Ile	Val	Asp	Pro	Gly	Lys	Thr	Trp	Thr	Ala		
390					395					400					405		
tcc	ggt	gca	gac	ttt	gcg	tcc	aag	gct	gaa	aat	acc	cca	ttt	gag	ggc		
1363																	
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<213> Corynebacterium glutamicum

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20 25 30

Gly Glu Pro Thr Asn Val Phe Val Lys Asp Gly Val Ile Ala Ala Ile
35 40 45

Gly Gly Thr His Glu Ala Asp Arg Thr Ile Asp Gly Asn Gly Gly Val
50 55 60

Leu Leu Pro Gly Phe Val Asp Met His Val His Leu Arg Glu Pro Gly
65 70 75 80

Arg Glu Asp Thr Glu Thr Ile Ala Thr Gly Ser Ala Ala Ala Lys
85 90 95

Gly Gly Phe Thr Ala Val Phe Thr Met Ala Asn Thr Thr Pro Val Met
100 105 110

Asp Gln Pro Val Ile Ala Glu Ser Val Trp Phe Lys Gly Gln Asn Ile
115 120 125

Gly Leu Cys Asp Val His Pro Val Gly Ser Ile Thr Lys Gly Leu Glu
130 135 140

Gly Lys Glu Leu Thr Glu Phe Gly Met Met Ala Arg Ser Glu Ala Lys
145 150 155 160

Val Arg Met Phe Ser Asp Asp Gly Lys Cys Val Asp Asp Pro Gln Val
165 170 175

Met Arg Arg Ala Leu Glu Tyr Ala Lys Gly Met Asp Val Leu Ile Ala
180 185 190

Gln His Ala Glu Asp His Arg Leu Thr Glu Gly Ala Ser Ala His Glu
195 200 205

Gly Glu Asn Ala Ala Arg Leu Gly Leu Arg Gly Trp Pro Arg Val Ala
210 215 220

Glu Glu Ser Ile Val Val Arg Asp Ala Ile Met Ala Arg Asp Tyr Gly
225 230 235 240

Asn Arg Val His Ile Cys His Ala Ser Thr Glu Gly Thr Val Glu Leu
245 250 255

Leu Arg Trp Ala Lys Ser Gln Gly Ile Pro Ile Thr Ala Glu Val Thr
260 265 270

Pro His His Leu Thr Leu Thr Asp Glu Arg Leu Glu Thr Tyr Asp Ala
 275 280 285

Val Asn Lys Val Asn Pro Pro Leu Arg Glu Ser Arg Asp Ala Glu Ala
 290 295 300

Leu Lys Lys Ala Leu Leu Asp Gly Thr Ile Asp Val Val Ala Thr Asp
 305 310 315 320

His Ala Pro His Gly Ser Glu Asp Lys Cys Cys Glu Phe Glu Asn Ala
 325 330 335

Lys Pro Gly Met Leu Gly Leu Glu Thr Ser Leu Ser Ile Ile Val Asp
 340 345 350

Thr Phe Val Ala Thr Gly Leu Ala Asp Trp Arg Phe Val Ala Arg Val
 355 360 365

Met Ser Glu Arg Pro Ala Glu Ile Thr Arg Leu Pro Gly Gln Gly Arg
 370 375 380

Pro Ile Ala Glu Gly Glu Pro Ala Asn Leu Ala Ile Val Asp Pro Gly
 385 390 395 400

Lys Thr Trp Thr Ala Ser Gly Ala Asp Phe Ala Ser Lys Ala Glu Asn
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<212> DNA

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<223> RXA02208

<400> 979

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 Ile Ile Ala Val His Asp Asp Ser Leu Ser Gln Glu Val Phe Gly Val
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acc ttc cca cga cca cta ggc ctc gcc gca ggt ttc gac aaa aac gca 144
 Thr Phe Pro Arg Pro Leu Gly Leu Ala Ala Gly Phe Asp Lys Asn Ala
 35 40 45

tca atg gct gat gcc tgg ggt gcc gtt gga ttc gga tac gcc gaa ctt 192
 Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu
 50 55 60

ggc acc gtc acc gcc ttc cca cag cca gga aac ccc acc ccg cgc ctt	240
Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu	
65 70 75 80	
ttc cgc ctg cct gcc gac aaa gct atc ttg aac cgc atg gga ttc aac	288
Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn	
85 90 95	
aac ctg ggt gca gca gaa gtc gca aaa aac ctg cgc aac cgg aaa tcc	336
Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser	
100 105 110	
acc gat gtc atc ggc atc aac atc ggt aaa acc aaa gtg gtt ccc gct	384
Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala	
115 120 125	
gaa cac gca gta gat gac tac cgc cgt tct gca tct ttg tta ggt gat	432
Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp	
130 135 140	
ctt gct gat tac ctg gtt gtc aac gtt tcc tcc ccc aac act ccg ggt	480
Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly	
145 150 155 160	
ctc cgc gat ctg cag gct gtg gaa tct ttg cga cca atc ctc gcc gca	528
Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala	
165 170 175	
gtg cag gaa tcc acc acc gtc cca gtc ttg gtg aaa atc gca cca gac	576
Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp	
180 185 190	
ctc tcc gac gaa gac atc gac gcc gta gct gac ctg gca gtt gag ctc	624
Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu	
195 200 205	
aaa ctc gcc gga atc gta gcc acc aat acc acc att tcc cgc gaa ggc	672
Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly	
210 215 220	
ctc aac act cct tca ggt gaa gtc gaa gcc atg ggt gct ggc gga atc	720
Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile	
225 230 235 240	
tcc ggt gct cca gta gca gcc cga tct ttg gag gta ctc aag cgc ctc	768
Ser Gly Ala Pro Val Ala Ala Arg Ser Leu Glu Val Leu Lys Arg Leu	
245 250 255	
tac gca cgg gta ggc aaa gag atg gtg ttg atc tct gtc ggt ggc atc	816
Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile	
260 265 270	
agc acc cct gag caa gcc tgg gaa cgc atc acc tcc ggc gca acc ctt	864
Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu	
275 280 285	
ctg cag gga tac acc cca ttc atc tac ggt ggc ccc gat tgg atc aga	912
Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg	
290 295 300	
gat atc cac ctt ggt atc gcc aag cag ctg aaa gct cac ggt ctg cgc	960

Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg
 305 310 315 320

aac atc gct gac gct gtg ggc agc gaa ttg gag tgg aag aac
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Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn
 325 330

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<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 980

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 35 40 45

Ser Met Ala Asp Ala Trp Gly Ala Val Gly Phe Gly Tyr Ala Glu Leu
 50 55 60

Gly Thr Val Thr Ala Phe Pro Gln Pro Gly Asn Pro Thr Pro Arg Leu
 65 70 75 80

Phe Arg Leu Pro Ala Asp Lys Ala Ile Leu Asn Arg Met Gly Phe Asn
 85 90 95

Asn Leu Gly Ala Ala Glu Val Ala Lys Asn Leu Arg Asn Arg Lys Ser
 100 105 110

Thr Asp Val Ile Gly Ile Asn Ile Gly Lys Thr Lys Val Val Pro Ala
 115 120 125

Glu His Ala Val Asp Asp Tyr Arg Arg Ser Ala Ser Leu Leu Gly Asp
 130 135 140

Leu Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly
 145 150 155 160

Leu Arg Asp Leu Gln Ala Val Glu Ser Leu Arg Pro Ile Leu Ala Ala
 165 170 175

Val Gln Glu Ser Thr Thr Val Pro Val Leu Val Lys Ile Ala Pro Asp
 180 185 190

Leu Ser Asp Glu Asp Ile Asp Ala Val Ala Asp Leu Ala Val Glu Leu
 195 200 205

Lys Leu Ala Gly Ile Val Ala Thr Asn Thr Thr Ile Ser Arg Glu Gly
 210 215 220

Leu Asn Thr Pro Ser Gly Glu Val Glu Ala Met Gly Ala Gly Gly Ile

225		230		235		240
Ser Gly Ala Pro Val Ala Ala Arg Ser Leu Glu Val Leu Lys Arg Leu						
		245		250		255
Tyr Ala Arg Val Gly Lys Glu Met Val Leu Ile Ser Val Gly Gly Ile						
		260		265		270
Ser Thr Pro Glu Gln Ala Trp Glu Arg Ile Thr Ser Gly Ala Thr Leu						
		275		280		285
Leu Gln Gly Tyr Thr Pro Phe Ile Tyr Gly Gly Pro Asp Trp Ile Arg						
		290		295		300
Asp Ile His Leu Gly Ile Ala Lys Gln Leu Lys Ala His Gly Leu Arg						
		305		310		315
Asn Ile Ala Asp Ala Val Gly Ser Glu Leu Glu Trp Lys Asn						
		325		330		

<210> 981
 <211> 675
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(652)
 <223> RXA01660

<400> 981
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 taaacctcaa tcatcaaatt aggggaagggc tgggaaatcc atg tca tct aat tcc 115
 Met Ser Ser Asn Ser
 1 5
 att aac gca gaa gcg cgc gct gag ctt gct gaa ctg atc aaa gag cta 163
 Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu Leu Ile Lys Glu Leu
 10 15 20
 gct gtc gtc cac ggt gaa gtc acc ttg tct tcg ggc aag aag gct gat 211
 Ala Val Val His Gly Glu Val Thr Leu Ser Ser Gly Lys Lys Ala Asp
 25 30 35
 tac tac atc gat gtc cgt cgt gcc acc ttg cac gcg cgc gca tct cgc 259
 Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His Ala Arg Ala Ser Arg
 40 45 50
 ctg atc ggt cag ctg ctg cgc gaa gcc acc gct gac tgg gac tat gac 307
 Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala Asp Trp Asp Tyr Asp
 55 60 65
 gca gtt ggc ggc ctg acc ttg ggc gct gac ccg gtt gcc acc gcc atc 355
 Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro Val Ala Thr Ala Ile
 70 75 80 85
 atg cac gcc gac ggc cgc gat atc aac gcg ttt gtg gtg cgc aag gag 403
 Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe Val Val Arg Lys Glu
 90 95 100

gcc aag aag cac ggc atg cag cgt cgc att gag ggc cct gac ctg acg 451
 Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu Gly Pro Asp Leu Thr
 105 110 115

 ggc aag aag gtg ctc gtg gtg gaa gat acc acc acc acc gga aat tcc 499
 Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr Thr Thr Gly Asn Ser
 120 125 130

 cct ctg aca gct gtt gcc gcg ttg cgt gaa gct ggc att gag gtt gtg 547
 Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala Gly Ile Glu Val Val
 135 140 145

 ggc gtt gcc acc gtg gtc gat cgc gca acc ggt gca gat gag gtt atc 595
 Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly Ala Asp Glu Val Ile
 150 155 160 165

 gca gcg gaa ggc ctt cct tac cgc agc ttg ctg gga ctt tct gat ctt 643
 Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu Gly Leu Ser Asp Leu
 170 175 180

 gga ctc aac taacaccccc ggccccacgg agt 675
 Gly Leu Asn

<210> 982

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 982

Met Ser Ser Asn Ser Ile Asn Ala Glu Ala Arg Ala Glu Leu Ala Glu
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 Leu Ile Lys Glu Leu Ala Val Val His Gly Glu Val Thr Leu Ser Ser
 20 25 30

 Gly Lys Lys Ala Asp Tyr Tyr Ile Asp Val Arg Arg Ala Thr Leu His
 35 40 45

 Ala Arg Ala Ser Arg Leu Ile Gly Gln Leu Leu Arg Glu Ala Thr Ala
 50 55 60

 Asp Trp Asp Tyr Asp Ala Val Gly Gly Leu Thr Leu Gly Ala Asp Pro
 65 70 75 80

 Val Ala Thr Ala Ile Met His Ala Asp Gly Arg Asp Ile Asn Ala Phe
 85 90 95

 Val Val Arg Lys Glu Ala Lys Lys His Gly Met Gln Arg Arg Ile Glu
 100 105 110

 Gly Pro Asp Leu Thr Gly Lys Lys Val Leu Val Val Glu Asp Thr Thr
 115 120 125

 Thr Thr Gly Asn Ser Pro Leu Thr Ala Val Ala Ala Leu Arg Glu Ala
 130 135 140

 Gly Ile Glu Val Val Gly Val Ala Thr Val Val Asp Arg Ala Thr Gly
 145 150 155 160

Ala Asp Glu Val Ile Ala Ala Glu Gly Leu Pro Tyr Arg Ser Leu Leu
 165 170 175

Gly Leu Ser Asp Leu Gly Leu Asn
 180

<210> 983

<211> 957

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(934)

<223> RXA02235

<400> 983

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cgctgcagga actcgaccac gcagtcaagg cttaagccct atg aca ttc ggc gag 115
 Met Thr Phe Gly Glu
 1 5

aag ctt ctg aac gcc gcc tcc acc cgt ggc agg cta tgc gtg ggc att 163
 Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg Leu Cys Val Gly Ile
 10 15 20

gat ccc cac gaa agc ctg ctg acg tcc tgg ggg ctg ccg gta aac gta 211
 Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly Leu Pro Val Asn Val
 25 30 35

gac gga ctt gcg gag ttc tcc cgc gcc tgc gtg gag gct ttc gcc gac 259
 Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val Glu Ala Phe Ala Asp
 40 45 50

acc gtg gca ttg gtg aag cct cag gtg gcg ttc tat gag cgt ttc ggt 307
 Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe Tyr Glu Arg Phe Gly
 55 60 65

tcc gct ggc ttt gcc atc ttg gaa gaa acc att cag acg ctg cgt gag 355
 Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile Gln Thr Leu Arg Glu
 70 75 80 85

cgt ggc tgt ttg gtg gtc tct gac gcc aaa cgc ggc gat att ggc tcc 403
 Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg Gly Asp Ile Gly Ser
 90 95 100

acc atg gct ggc tat gcc tca gcg tgg tta gat cca gcg tca ccg ctg 451
 Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp Pro Ala Ser Pro Leu
 105 110 115

tct agc gac gct gtg acg gtc tct ccc tac ctt ggt ttt cat tcc ttg 499
 Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu Gly Phe His Ser Leu
 120 125 130

gac cca gtg ttc gaa ctt gcc gag caa cac ggc agg gga gtg ttt gtc 547
 Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly Arg Gly Val Phe Val
 135 140 145

ttg gcc gcg acc tca aac cct gag gcc cgc gaa ctc cag gac cag caa 595
 Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu Leu Gln Asp Gln Gln
 150 155 160 165

 aac gct gac ggc gtg agc att tcc cag cag atc gtg gat cag gca gcg 643
 Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile Val Asp Gln Ala Ala
 170 175 180

 gcg ctt aac gcg cct tat atg gcc cag ggc aag gct ggc aac att ggc 691
 Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys Ala Gly Asn Ile Gly
 185 190 195

 gtc gtc atc ggc gcc acc ttg tcc aaa cca cca cgc tta tcg acg ctc 739
 Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro Arg Leu Ser Thr Leu
 200 205 210

 ggg ggc gcc att ttg atg ccc ggc gtc ggc gcc cag ggc ggc acg gca 787
 Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala Gln Gly Gly Thr Ala
 215 220 225

 agc gac gtt gat gag att gcg gga gac atg gct cat ctt gca ttc cca 835
 Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala His Leu Ala Phe Pro
 230 235 240 245

 aat gtc tct aga agt att ttg gcg aca ggc cca gat atc gct gaa atg 883
 Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro Asp Ile Ala Glu Met
 250 255 260

 aag aat tct gtg gca aaa aat gct gca gac ttt cct ggt ttc ccc agg 931
 Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe Pro Gly Phe Pro Arg
 265 270 275

 tca tagtcgcgga aacggccctt aat 957
 Ser

<210> 984
 <211> 278
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 984
 Met Thr Phe Gly Glu Lys Leu Leu Asn Ala Ala Ser Thr Arg Gly Arg
 1 5 10 15
 Leu Cys Val Gly Ile Asp Pro His Glu Ser Leu Leu Thr Ser Trp Gly
 20 25 30
 Leu Pro Val Asn Val Asp Gly Leu Ala Glu Phe Ser Arg Ala Cys Val
 35 40 45
 Glu Ala Phe Ala Asp Thr Val Ala Leu Val Lys Pro Gln Val Ala Phe
 50 55 60
 Tyr Glu Arg Phe Gly Ser Ala Gly Phe Ala Ile Leu Glu Glu Thr Ile
 65 70 75 80
 Gln Thr Leu Arg Glu Arg Gly Cys Leu Val Val Ser Asp Ala Lys Arg
 85 90 95

Gly Asp Ile Gly Ser Thr Met Ala Gly Tyr Ala Ser Ala Trp Leu Asp
 100 105 110
 Pro Ala Ser Pro Leu Ser Ser Asp Ala Val Thr Val Ser Pro Tyr Leu
 115 120 125
 Gly Phe His Ser Leu Asp Pro Val Phe Glu Leu Ala Glu Gln His Gly
 130 135 140
 Arg Gly Val Phe Val Leu Ala Ala Thr Ser Asn Pro Glu Ala Arg Glu
 145 150 155 160
 Leu Gln Asp Gln Gln Asn Ala Asp Gly Val Ser Ile Ser Gln Gln Ile
 165 170 175
 Val Asp Gln Ala Ala Ala Leu Asn Ala Pro Tyr Met Ala Gln Gly Lys
 180 185 190
 Ala Gly Asn Ile Gly Val Val Ile Gly Ala Thr Leu Ser Lys Pro Pro
 195 200 205
 Arg Leu Ser Thr Leu Gly Gly Ala Ile Leu Met Pro Gly Val Gly Ala
 210 215 220
 Gln Gly Gly Thr Ala Ser Asp Val Asp Glu Ile Ala Gly Asp Met Ala
 225 230 235 240
 His Leu Ala Phe Pro Asn Val Ser Arg Ser Ile Leu Ala Thr Gly Pro
 245 250 255
 Asp Ile Ala Glu Met Lys Asn Ser Val Ala Lys Asn Ala Ala Asp Phe
 260 265 270
 Pro Gly Phe Pro Arg Ser
 275

<210> 985
 <211> 852
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(829)
 <223> RXN01892

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 aaagcgggttg gcacaacccc tactgaagga gaacaccact gtg acc acc tcg agt 115
 Val Thr Thr Ser Ser
 1 5
 gaa caa ccc cgt aca gga tac aag cga gtg atg tta aag ctc gga ggt 163
 Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Gly Gly
 10 15 20
 gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta gac 211
 Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val Asp
 25 30 35

aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag att	259
Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu Ile	
40 45 50	
gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt cag	307
Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu Gln	
55 60 65	
cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc ggc	355
Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu Gly	
70 75 80 85	
aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat ggc	403
Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His Gly	
90 95 100	
gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca gaa	451
Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala Glu	
105 110 115	
cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc gtt	499
Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg Val	
120 125 130	
gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac acc	547
Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp Thr	
135 140 145	
act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg atg	595
Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu Met	
150 155 160 165	
gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac cca	643
Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn Pro	
170 175 180	
gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag aag	691
Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu Lys	
185 190 195	
ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac aac	739
Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp Asn	
200 205 210	
aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att gct	787
Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile Ala	
215 220 225	
cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc	829
Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser	
230 235 240	
tgatacattt agtcttataa aca	852

<210> 986

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 986

Val	Thr	Thr	Ser	Ser	Glu	Gln	Pro	Arg	Thr	Gly	Tyr	Lys	Arg	Val	Met
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Leu	Lys	Leu	Gly	Gly	Glu	Met	Phe	Gly	Gly	Gly	Lys	Val	Gly	Val	Asp
			20					25					30		
Pro	Asp	Val	Val	Asp	Asn	Val	Ala	Arg	Gln	Ile	Ala	Glu	Val	Ala	Lys
		35					40					45			
Thr	Gly	Ala	Glu	Ile	Ala	Val	Val	Ile	Gly	Gly	Gly	Asn	Phe	Phe	Arg
	50					55					60				
Gly	Ala	Glu	Leu	Gln	Gln	Arg	Gly	Met	Asp	Arg	Ala	Arg	Ser	Asp	Tyr
65				70					75						80
Met	Gly	Met	Leu	Gly	Thr	Val	Met	Asn	Cys	Leu	Ala	Leu	Gln	Asp	Phe
				85				90						95	
Leu	Gly	Gln	His	Gly	Val	Glu	Cys	Arg	Val	Gln	Thr	Ala	Ile	Asn	Met
			100					105					110		
Ala	Gln	Val	Ala	Glu	Pro	Tyr	Leu	Pro	Leu	Arg	Ala	Glu	Arg	His	Leu
		115					120					125			
Glu	Lys	Gly	Arg	Val	Val	Ile	Phe	Gly	Ala	Gly	Met	Gly	Met	Pro	Tyr
	130					135					140				
Phe	Ser	Thr	Asp	Thr	Thr	Ala	Ala	Gln	Arg	Ala	Leu	Glu	Ile	Gly	Cys
145					150				155						160
Asp	Val	Leu	Leu	Met	Ala	Lys	Ala	Val	Asp	Gly	Val	Tyr	Ser	Asp	Asp
				165					170					175	
Pro	Arg	Thr	Asn	Pro	Asp	Ala	Glu	Leu	Phe	Thr	Glu	Ile	Thr	Pro	Lys
			180					185					190		
Glu	Val	Ile	Glu	Lys	Gly	Leu	Lys	Val	Ala	Asp	Ala	Thr	Ala	Phe	Ser
		195					200					205			
Leu	Cys	Met	Asp	Asn	Lys	Met	Pro	Ile	Leu	Val	Phe	Asn	Leu	Leu	Thr
	210					215					220				
Glu	Gly	Asn	Ile	Ala	Arg	Ala	Ile	Ser	Gly	Glu	Arg	Ile	Gly	Thr	Leu
225					230					235					240
Val	Glu	Ser													

<210> 987

<211> 798

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (47) .. (775)

<223> FRXA01892

<400> 987

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Val Thr Thr Ser
1

agt gaa caa ccc cgt aca gga tac aaa cga gtg atg tta aag ctc gaa 106
Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met Leu Lys Leu Glu
5 10 15 20

ggt gaa atg ttt ggt ggt ggc aaa gtc ggc gtc gat cct gat gta gta 154
Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp Pro Asp Val Val
25 30 35

gac aat gtt gca cgt cag atc gct gaa gtt gct aaa act gga gca gag 202
Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys Thr Gly Ala Glu
40 45 50

att gcc gtt gtt atc ggt ggc gga aac ttc ttc cgc gga gct gag ctt 250
Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg Gly Ala Glu Leu
55 60 65

cag cag cgt ggc atg gac cgc gca cgg tcc gat tac atg ggt atg ctc 298
Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr Met Gly Met Leu
70 75 80

ggc aca gtc atg aac tgc ctc gcc ttg cag gac ttc ctc ggt cag cat 346
Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe Leu Gly Gln His
85 90 95 100

ggc gtt gaa tgc cgt gtc cag acc gcc atc aac atg gca cag gtc gca 394
Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met Ala Gln Val Ala
105 110 115

gaa cca tat ctg cca ctg cgc gca gaa cgc cac ctg gaa aag ggc cgc 442
Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu Glu Lys Gly Arg
120 125 130

gtt gtc atc ttc ggt gct ggc atg ggt atg ccg tac ttt tcc acg gac 490
Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr Phe Ser Thr Asp
135 140 145

acc act gct gca cag cgt gcg ttg gaa atc ggc tgt gac gtc cta ctg 538
Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys Asp Val Leu Leu
150 155 160

atg gct aag gct gtt gac ggt gtg tac agc gat gat cct cgt acc aac 586
Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp Pro Arg Thr Asn
165 170 175 180

cca gat gct gag ctc ttc acc gaa att act cca aag gaa gta att gag 634
Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys Glu Val Ile Glu
185 190 195

aag ggc ctg aag gtt gcc gat gca act gca ttc agc ctc tgc atg gac 682
Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser Leu Cys Met Asp
200 205 210

aac aag atg cct atc ttg gtg ttt aac ctg ctt act gaa ggc aac att 730
Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr Glu Gly Asn Ile
215 220 225

gct cgc gcc atc agc ggt gaa cgt atc ggt act ctg gtc gag tcc 775

Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu Val Glu Ser
 230 235 240

tgatacattt agtcttataa aca

798

<210> 988

<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 988

Val Thr Thr Ser Ser Glu Gln Pro Arg Thr Gly Tyr Lys Arg Val Met
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Leu Lys Leu Glu Gly Glu Met Phe Gly Gly Gly Lys Val Gly Val Asp
 20 25 30

Pro Asp Val Val Asp Asn Val Ala Arg Gln Ile Ala Glu Val Ala Lys
 35 40 45

Thr Gly Ala Glu Ile Ala Val Val Ile Gly Gly Gly Asn Phe Phe Arg
 50 55 60

Gly Ala Glu Leu Gln Gln Arg Gly Met Asp Arg Ala Arg Ser Asp Tyr
 65 70 75 80

Met Gly Met Leu Gly Thr Val Met Asn Cys Leu Ala Leu Gln Asp Phe
 85 90 95

Leu Gly Gln His Gly Val Glu Cys Arg Val Gln Thr Ala Ile Asn Met
 100 105 110

Ala Gln Val Ala Glu Pro Tyr Leu Pro Leu Arg Ala Glu Arg His Leu
 115 120 125

Glu Lys Gly Arg Val Val Ile Phe Gly Ala Gly Met Gly Met Pro Tyr
 130 135 140

Phe Ser Thr Asp Thr Thr Ala Ala Gln Arg Ala Leu Glu Ile Gly Cys
 145 150 155 160

Asp Val Leu Leu Met Ala Lys Ala Val Asp Gly Val Tyr Ser Asp Asp
 165 170 175

Pro Arg Thr Asn Pro Asp Ala Glu Leu Phe Thr Glu Ile Thr Pro Lys
 180 185 190

Glu Val Ile Glu Lys Gly Leu Lys Val Ala Asp Ala Thr Ala Phe Ser
 195 200 205

Leu Cys Met Asp Asn Lys Met Pro Ile Leu Val Phe Asn Leu Leu Thr
 210 215 220

Glu Gly Asn Ile Ala Arg Ala Ile Ser Gly Glu Arg Ile Gly Thr Leu
 225 230 235 240

Val Glu Ser

gca tct tat gca ctg ctc acc cac atg ttt gcc cag cag gca ggc ttg 691
 Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala Gln Gln Ala Gly Leu
 185 190 195

gaa gtc ggc gag ttc att tgg act ggc ggc gac tgc cac att tat gac 739
 Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp Cys His Ile Tyr Asp
 200 205 210

aac cac aag gaa cag gtc gcg gag cag ctg agc cga taagctcgcc 785
 Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser Arg
 215 220 225

cctacccac ctt 798

<210> 990
 <211> 225
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 990
 Met Thr Val Pro Thr Pro Tyr Glu Asp Leu Leu Arg Lys Ile Ala Glu
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 Glu Gly Ser His Lys Asp Asp Arg Thr Gly Thr Gly Thr Thr Ser Leu
 20 25 30
 Phe Gly Gln Gln Ile Arg Phe Asp Leu Asn Glu Gly Phe Pro Leu Leu
 35 40 45
 Thr Thr Lys Lys Val His Phe His Ser Val Val Gly Glu Leu Leu Trp
 50 55 60
 Phe Leu Gln Gly Asp Ser Asn Val Lys Trp Leu Gln Asp Asn Asn Ile
 65 70 75 80
 Arg Ile Trp Asn Glu Trp Ala Asp Glu Asp Gly Glu Leu Gly Pro Val
 85 90 95
 Tyr Gly Val Gln Trp Arg Ser Trp Pro Thr Pro Asp Gly Arg His Ile
 100 105 110
 Asp Gln Ile Ser Gly Ala Leu Glu Thr Leu Arg Asn Asn Pro Asp Ser
 115 120 125
 Arg Arg Asn Ile Val Ser Ala Trp Asn Val Ser Glu Leu Glu Asn Met
 130 135 140
 Ala Leu Pro Pro Cys His Leu Leu Phe Gln Leu Tyr Val Ala Asp Gly
 145 150 155 160
 Lys Leu Ser Cys Gln Leu Tyr Gln Arg Ser Ala Asp Met Phe Leu Gly
 165 170 175
 Val Pro Phe Asn Ile Ala Ser Tyr Ala Leu Leu Thr His Met Phe Ala
 180 185 190
 Gln Gln Ala Gly Leu Glu Val Gly Glu Phe Ile Trp Thr Gly Gly Asp
 195 200 205
 Cys His Ile Tyr Asp Asn His Lys Glu Gln Val Ala Glu Gln Leu Ser

210 215 220

Arg
225

<210> 991
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXA00131

<400> 991
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acgttgcagg cccattcaag ccggagcact accgctacta atg att gtc agc att 115
Met Ile Val Ser Ile
1 5

gag gga atc gac ggc gcc ggc aaa aac acc ctg gtt tcg gca tta acg 163
Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu Val Ser Ala Leu Thr
10 15 20

cag gtt att gat gca aaa gtc ctt gca ttc cca cgt tat gaa acc tcg 211
Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro Arg Tyr Glu Thr Ser
25 30 35

att cac gcc caa ttg gcc gcg gaa gca ctc cac ggc cgc atg ggc gac 259
Ile His Ala Gln Leu Ala Ala Glu Ala Leu His Gly Arg Met Gly Asp
40 45 50

ctc acc gac agc gcc tac gcc atg gcc acg ctt ttc gcc ctc gac cgc 307
Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu Phe Ala Leu Asp Arg
55 60 65

cac ttc gcg att gat gac tta aat gcg ccc ggc gtg gtg ctg ctc gac 355
His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly Val Val Leu Leu Asp
70 75 80 85

cga tac gtc gcc tcc aac gcg gct tat acc gcc gcc aga ttg ctt gac 403
Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala Ala Arg Leu Leu Asp
90 95 100

gac gac gcc ccc cgc tgg gtt gcc gac ctg gaa ttc ggg cgg ctt ggg 451
Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu Phe Gly Arg Leu Gly
105 110 115

ctc cca cgt ccg acg ctt caa gtg ttg ttg gat acc ccc gcg gag gta 499
Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp Thr Pro Ala Glu Val
120 125 130

gcg caa gat agg gct aga cgt cga gaa gcg ctt gac tcc gcg cgt gcg 547
Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu Asp Ser Ala Arg Ala
135 140 145

cgg gac cgc tat gaa tcg gat tcg gcg ctg cag caa cgc acc gcc gag 595
Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln Gln Arg Thr Ala Glu

150	155	160	165	
cac tat cgc cgc ctc gcg gcg gac aac tgg gaa tca ccg tgg atc gtg				643
His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu Ser Pro Trp Ile Val	170	175	180	
gtt gcc cct gat gaa gac ccc ggc cac gtt gcg cag aga atc gtg gaa				691
Val Ala Pro Asp Glu Asp Pro Gly His Val Ala Gln Arg Ile Val Glu	185	190	195	
ttc ctg ggt act ata aac taatcccaat tagcaggaag gat				732
Phe Leu Gly Thr Ile Asn	200			

<210> 992

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 992

Met Ile Val Ser Ile Glu Gly Ile Asp Gly Ala Gly Lys Asn Thr Leu	1	5	10	15
Val Ser Ala Leu Thr Gln Val Ile Asp Ala Lys Val Leu Ala Phe Pro	20	25	30	
Arg Tyr Glu Thr Ser Ile His Ala Gln Leu Ala Ala Glu Ala Leu His	35	40	45	
Gly Arg Met Gly Asp Leu Thr Asp Ser Ala Tyr Ala Met Ala Thr Leu	50	55	60	
Phe Ala Leu Asp Arg His Phe Ala Ile Asp Asp Leu Asn Ala Pro Gly	65	70	75	80
Val Val Leu Leu Asp Arg Tyr Val Ala Ser Asn Ala Ala Tyr Thr Ala	85	90	95	
Ala Arg Leu Leu Asp Asp Asp Ala Pro Arg Trp Val Ala Asp Leu Glu	100	105	110	
Phe Gly Arg Leu Gly Leu Pro Arg Pro Thr Leu Gln Val Leu Leu Asp	115	120	125	
Thr Pro Ala Glu Val Ala Gln Asp Arg Ala Arg Arg Arg Glu Ala Leu	130	135	140	
Asp Ser Ala Arg Ala Arg Asp Arg Tyr Glu Ser Asp Ser Ala Leu Gln	145	150	155	160
Gln Arg Thr Ala Glu His Tyr Arg Arg Leu Ala Ala Asp Asn Trp Glu	165	170	175	
Ser Pro Trp Ile Val Val Ala Pro Asp Glu Asp Pro Gly His Val Ala	180	185	190	
Gln Arg Ile Val Glu Phe Leu Gly Thr Ile Asn	195	200		

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<210> 993
<211> 531
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(508)  
<223> RXA00266
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agtgcgcgaa gcagaccacc attaggtaga atcacccaac atg act gaa cgt act 115																
Met Thr Glu Arg Thr 5																
1																
ctc atc ctt atc aag cca gac ggt gtt acc aac gga cac gtc ggc gaa 163																
Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn Gly His Val Gly Glu 20																
10 15																
atc atc gca cgt att gag cgc aag ggc ctg aag ctc gct gct ctg gat 211																
Ile Ile Ala Arg Ile Glu Arg Lys Gly Leu Lys Leu Ala Ala Leu Asp 35																
25 30																
ctg cgt gtt gca gac cgc gag acc gct gaa aag cac tac gaa gag cac 259																
Leu Arg Val Ala Asp Arg Glu Thr Ala Glu Lys His Tyr Glu Glu His 50																
40 45																
gct gac aag cca ttc ttc ggt gag ctc gtt gaa ttc atc acc tct gca 307																
Ala Asp Lys Pro Phe Phe Gly Glu Leu Val Glu Phe Ile Thr Ser Ala 65																
55 60																
cct ctg atc gca ggc atc gtc gaa ggc gag cgt gca atc gat gca tgg 355																
Pro Leu Ile Ala Gly Ile Val Glu Gly Glu Arg Ala Ile Asp Ala Trp 85																
70 75 80																
cgt cag ctt gct ggt ggc acc gac cca gtt gct aag gca acc cca ggc 403																
Arg Gln Leu Ala Gly Gly Thr Asp Pro Val Ala Lys Ala Thr Pro Gly 100																
90 95																
acc atc cgc ggc gat ttc gca ctg act gtt gga gag aac gtt gtt cac 451																
Thr Ile Arg Gly Asp Phe Ala Leu Thr Val Gly Glu Asn Val Val His 115																
105 110																
ggt tct gat tcc cca gag tcc gct gag cgc gag atc tcc atc tgg ttc 499																
Gly Ser Asp Ser Pro Glu Ser Ala Glu Arg Glu Ile Ser Ile Trp Phe 130																
120 125																
cct aac ctg taattttttac ggtagaaaa aaa 531																
Pro Asn Leu 135																

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<210> 994
<211> 136
<212> PRT
<213> Corynebacterium glutamicum
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<400> 994
Met Thr Glu Arg Thr Leu Ile Leu Ile Lys Pro Asp Gly Val Thr Asn

1	5	10	15
Gly His Val	Gly Glu Ile Ile	Ala Arg Ile Glu Arg	Lys Gly Leu Lys
	20	25	30
Leu Ala Ala	Leu Asp Leu Arg	Val Ala Asp Arg	Glu Thr Ala Glu Lys
	35	40	45
His Tyr Glu	Glu His Ala Asp	Lys Pro Phe Phe	Gly Glu Leu Val Glu
	50	55	60
Phe Ile Thr	Ser Ala Pro Leu	Ile Ala Gly Ile	Val Glu Gly Glu Arg
	65	70	75
Ala Ile Asp	Ala Trp Arg Gln	Leu Ala Gly Gly	Thr Asp Pro Val Ala
	85	90	95
Lys Ala Thr	Pro Gly Thr Ile	Arg Gly Asp Phe	Ala Leu Thr Val Gly
	100	105	110
Glu Asn Val	Val His Gly Ser	Asp Ser Pro Glu	Ser Ala Glu Arg Glu
	115	120	125
Ile Ser Ile	Trp Phe Pro Asn	Leu	
	130	135	

<210> 995

<211> 831

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(808)

<223> RXA00718

<400> 995

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actcctctga gctgaccagc ttatacaagg tgggtccaact gtg acg gaa att tcc 115
 Val Thr Glu Ile Ser 5

aac atg cct gcc ggt ggc ctc atc gta gcc atc gac ggg ccg tct ggc 163
 Asn Met Pro Ala Gly Gly Leu Ile Val Ala Ile Asp Gly Pro Ser Gly 20

acc gga aaa tcc acc aca tcc cgc gcg ctc gca acc cgt ctc tcg gcc 211
 Thr Gly Lys Ser Thr Thr Ser Arg Ala Leu Ala Thr Arg Leu Ser Ala 35

aag tac cta gat act ggt gcg atg tac cgc gtc gca acc ctt cat gtg 259
 Lys Tyr Leu Asp Thr Gly Ala Met Tyr Arg Val Ala Thr Leu His Val 50

ctt aac cag ggg att gac cct gca gat agc gca gcc gtg atc gct gca 307
 Leu Asn Gln Gly Ile Asp Pro Ala Asp Ser Ala Ala Val Ile Ala Ala 65

acc gct gta ttg ccg ttg tcg att tct gac gat ccc gcc tcc act gag 355

Thr	Ala	Val	Leu	Pro	Leu	Ser	Ile	Ser	Asp	Asp	Pro	Ala	Ser	Thr	Glu	
70					75					80					85	
gtg	ttg	ctc	gcg	ggc	gtc	gat	gtg	caa	aag	gac	atc	cgc	gga	cca	gaa	403
Val	Leu	Leu	Ala	Gly	Val	Asp	Val	Gln	Lys	Asp	Ile	Arg	Gly	Pro	Glu	
				90					95					100		
gtc	acc	caa	aat	gtc	tcc	gca	gtg	tcc	gcg	atc	cct	gag	gtt	cgt	gaa	451
Val	Thr	Gln	Asn	Val	Ser	Ala	Val	Ser	Ala	Ile	Pro	Glu	Val	Arg	Glu	
			105					110					115			
aac	ttg	gtg	gcg	ttg	cag	cgc	gca	ctc	gcc	gcc	aaa	gca	cat	cgc	tgc	499
Asn	Leu	Val	Ala	Leu	Gln	Arg	Ala	Leu	Ala	Ala	Lys	Ala	His	Arg	Cys	
		120					125					130				
gtc	gtc	gaa	ggc	aga	gac	atc	gga	acg	gca	gtg	ctt	gtc	gac	gcg	ccc	547
Val	Val	Glu	Gly	Arg	Asp	Ile	Gly	Thr	Ala	Val	Leu	Val	Asp	Ala	Pro	
		135				140					145					
atc	aag	gcg	ttt	ctc	acc	gcc	tca	gcg	gaa	gtc	cgc	gcc	cag	cga	cgc	595
Ile	Lys	Ala	Phe	Leu	Thr	Ala	Ser	Ala	Glu	Val	Arg	Ala	Gln	Arg	Arg	
150					155					160					165	
ttt	gac	caa	gac	acc	gca	gca	ggg	cgc	gac	gta	gat	ttc	gac	gct	gtg	643
Phe	Asp	Gln	Asp	Thr	Ala	Ala	Gly	Arg	Asp	Val	Asp	Phe	Asp	Ala	Val	
				170					175					180		
ctg	gca	gat	gtt	gtt	cgc	cgc	gat	gaa	cta	gat	tcc	acc	cgt	gcc	gcc	691
Leu	Ala	Asp	Val	Val	Arg	Arg	Asp	Glu	Leu	Asp	Ser	Thr	Arg	Ala	Ala	
			185					190					195			
tca	ccg	ctg	aaa	cca	gca	gat	gat	gca	cac	atc	gtg	gac	acc	tct	gat	739
Ser	Pro	Leu	Lys	Pro	Ala	Asp	Asp	Ala	His	Ile	Val	Asp	Thr	Ser	Asp	
		200					205					210				
atg	acc	atg	gat	caa	gta	ctt	gat	cac	ctc	atc	cac	cta	gtg	gaa	gcc	787
Met	Thr	Met	Asp	Gln	Val	Leu	Asp	His	Leu	Ile	His	Leu	Val	Glu	Ala	
		215				220					225					
tcc	gct	gaa	agg	agc	aac	cag	tgactgataa	acacaccatg	cct							831
Ser	Ala	Glu	Arg	Ser	Asn	Gln										
230					235											

<210> 996

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 996

Val	Thr	Glu	Ile	Ser	Asn	Met	Pro	Ala	Gly	Gly	Leu	Ile	Val	Ala	Ile	
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Asp	Gly	Pro	Ser	Gly	Thr	Gly	Lys	Ser	Thr	Thr	Ser	Arg	Ala	Leu	Ala	
			20					25					30			
Thr	Arg	Leu	Ser	Ala	Lys	Tyr	Leu	Asp	Thr	Gly	Ala	Met	Tyr	Arg	Val	
		35					40					45				
Ala	Thr	Leu	His	Val	Leu	Asn	Gln	Gly	Ile	Asp	Pro	Ala	Asp	Ser	Ala	
	50					55					60					

Ala Val Ile Ala Ala Thr Ala Val Leu Pro Leu Ser Ile Ser Asp Asp
65 70 75 80

Pro Ala Ser Thr Glu Val Leu Leu Ala Gly Val Asp Val Gln Lys Asp
85 90 95

Ile Arg Gly Pro Glu Val Thr Gln Asn Val Ser Ala Val Ser Ala Ile
100 105 110

Pro Glu Val Arg Glu Asn Leu Val Ala Leu Gln Arg Ala Leu Ala Ala
115 120 125

Lys Ala His Arg Cys Val Val Glu Gly Arg Asp Ile Gly Thr Ala Val
130 135 140

Leu Val Asp Ala Pro Ile Lys Ala Phe Leu Thr Ala Ser Ala Glu Val
145 150 155 160

Arg Ala Gln Arg Arg Phe Asp Gln Asp Thr Ala Ala Gly Arg Asp Val
165 170 175

Asp Phe Asp Ala Val Leu Ala Asp Val Val Arg Arg Asp Glu Leu Asp
180 185 190

Ser Thr Arg Ala Ala Ser Pro Leu Lys Pro Ala Asp Asp Ala His Ile
195 200 205

Val Asp Thr Ser Asp Met Thr Met Asp Gln Val Leu Asp His Leu Ile
210 215 220

His Leu Val Glu Ala Ser Ala Glu Arg Ser Asn Gln
225 230 235

<210> 997
<211> 1785
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1762)
<223> RXA01599

<400> 997
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tcgatgttta ggttcaacca ggaagggtcgt ctcagacatc atg acc tct agt cga 115
Met Thr Ser Ser Arg
1 5

aaa gtc cgt ccc acc aaa cac att ttc gtc acc ggt gga gtt gtt tcc 163
Lys Val Arg Pro Thr Lys His Ile Phe Val Thr Gly Gly Val Val Ser
10 15 20

tca ctc ggc aaa ggc ctg acc gca gca agc ctt ggt caa ttg ctg att 211
Ser Leu Gly Lys Gly Leu Thr Ala Ala Ser Leu Gly Gln Leu Leu Ile
25 30 35

gca cgg gga ctg tcg gtg acc atg cag aag ctg gat cca tac ctc aat 259

Ala	Arg	Gly	Leu	Ser	Val	Thr	Met	Gln	Lys	Leu	Asp	Pro	Tyr	Leu	Asn	
		40					45					50				
gtt	gat	ccg	ggc	acc	atg	aat	cct	ttt	gaa	cac	ggg	gaa	gtc	ttt	gtc	307
Val	Asp	Pro	Gly	Thr	Met	Asn	Pro	Phe	Glu	His	Gly	Glu	Val	Phe	Val	
	55					60					65					
acc	gaa	gac	ggg	gca	gaa	aca	gac	ctg	gat	ttg	ggc	cac	tac	gag	cgt	355
Thr	Glu	Asp	Gly	Ala	Glu	Thr	Asp	Leu	Asp	Leu	Gly	His	Tyr	Glu	Arg	
70					75					80					85	
ttc	ctc	gat	cgc	aac	ctg	ggg	ctc	aac	gcc	aat	gtc	acc	acc	ggc	aag	403
Phe	Leu	Asp	Arg	Asn	Leu	Gly	Leu	Asn	Ala	Asn	Val	Thr	Thr	Gly	Lys	
				90					95					100		
gtg	tat	tcc	act	gtg	atc	gcc	aag	gag	cgc	agg	gga	gag	tac	ctg	ggg	451
Val	Tyr	Ser	Thr	Val	Ile	Ala	Lys	Glu	Arg	Arg	Gly	Glu	Tyr	Leu	Gly	
			105					110					115			
aaa	act	gtg	cag	gtc	atc	cca	cac	atc	act	gat	gag	atc	aaa	gct	cgt	499
Lys	Thr	Val	Gln	Val	Ile	Pro	His	Ile	Thr	Asp	Glu	Ile	Lys	Ala	Arg	
		120					125					130				
att	ttg	agc	atg	ggc	gaa	cca	gat	gct	cat	ggg	aac	gcc	cca	gac	gtg	547
Ile	Leu	Ser	Met	Gly	Glu	Pro	Asp	Ala	His	Gly	Asn	Ala	Pro	Asp	Val	
	135					140					145					
gtg	atc	tct	gag	gtc	ggg	ggc	acc	gtc	ggg	gac	att	gaa	tcc	cag	cca	595
Val	Ile	Ser	Glu	Val	Gly	Gly	Thr	Val	Gly	Asp	Ile	Glu	Ser	Gln	Pro	
150					155					160					165	
ttc	ctt	gaa	gca	gct	cgc	cag	gta	cgc	cat	gaa	att	ggg	cgt	gaa	aac	643
Phe	Leu	Glu	Ala	Ala	Arg	Gln	Val	Arg	His	Glu	Ile	Gly	Arg	Glu	Asn	
				170					175					180		
tgc	ttc	ttc	atc	cac	tgt	tct	ttg	gtg	cca	tac	ttg	gct	acc	tca	ggg	691
Cys	Phe	Phe	Ile	His	Cys	Ser	Leu	Val	Pro	Tyr	Leu	Ala	Thr	Ser	Gly	
			185					190					195			
gag	ctg	aag	acc	aaa	ccc	acc	cag	cat	tct	gtc	gca	gag	ctg	cgc	ggc	739
Glu	Leu	Lys	Thr	Lys	Pro	Thr	Gln	His	Ser	Val	Ala	Glu	Leu	Arg	Gly	
		200					205					210				
atc	ggg	att	ttg	ccg	gat	gct	ctc	gtg	ctt	cgt	tgc	gat	cgg	gag	gtc	787
Ile	Gly	Ile	Leu	Pro	Asp	Ala	Leu	Val	Leu	Arg	Cys	Asp	Arg	Glu	Val	
	215					220					225					
cct	caa	ggg	ctg	aaa	gat	aag	atc	gcg	atg	atg	tgc	gat	gtt	gat	tat	835
Pro	Gln	Gly	Leu	Lys	Asp	Lys	Ile	Ala	Met	Met	Cys	Asp	Val	Asp	Tyr	
230					235					240					245	
gaa	ggc	gtt	gta	tct	tgc	cct	gat	tcc	agt	tct	att	tac	aac	att	cca	883
Glu	Gly	Val	Val	Ser	Cys	Pro	Asp	Ser	Ser	Ser	Ile	Tyr	Asn	Ile	Pro	
				250					255					260		
gat	gtc	ctc	tac	cgc	gag	cac	ctg	gac	acc	ttc	att	att	cgt	cgc	ctg	931
Asp	Val	Leu	Tyr	Arg	Glu	His	Leu	Asp	Thr	Phe	Ile	Ile	Arg	Arg	Leu	
			265					270					275			
ggc	ctt	ccg	ttc	cgt	gat	gtt	gac	tgg	agc	acc	tgg	cac	gat	ctg	ctg	979
Gly	Leu	Pro	Phe	Arg	Asp	Val	Asp	Trp	Ser	Thr	Trp	His	Asp	Leu	Leu	

280	285	290
gaa cgg gtg aac aac cca cgc cat gag ctc acc gtc ggc atc gtg ggc 1027		
Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr Val Gly Ile Val Gly 295 300 305		
aag tac att gat ctt ccc gat gct tat ctc tca gtg gtg gaa gct gtt 1075		
Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser Val Val Glu Ala Val 310 315 320 325		
cgc gct gca ggc tac gcc aat tgg acg cgc acc aat atc aag tgg att 1123		
Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr Asn Ile Lys Trp Ile 330 335 340		
acc tca gat gat tgc gaa acc cca tct ggc gcc atg aaa gcg ctc agc 1171		
Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala Met Lys Ala Leu Ser 345 350 355		
ggc ttg gat gcc atc gtg gtt ccc gga ggt ttc ggt atc cga ggt atc 1219		
Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe Gly Ile Arg Gly Ile 360 365 370		
gaa ggc aaa atc ggt gcg att acg ttt gca cgt gag cac aag atc ccg 1267		
Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg Glu His Lys Ile Pro 375 380 385		
ctt ctt ggc cta tgc ctt ggc ctg cag tgc acc gtc atc gag gca gca 1315		
Leu Leu Gly Leu Cys Leu Gly Leu Gln Cys Thr Val Ile Glu Ala Ala 390 395 400 405		
cgc cag gca gga ctg gag cag gca tca tcc act gag ttt gac cca gct 1363		
Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr Glu Phe Asp Pro Ala 410 415 420		
gca acg cag cca gtg atc gcc acc atg gaa gag cag aaa gct gct gtg 1411		
Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu Gln Lys Ala Ala Val 425 430 435		
tcg ggt gaa gct gat ctg ggt ggc acc atg cgt ctt ggc gca tat cct 1459		
Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg Leu Gly Ala Tyr Pro 440 445 450		
gca acc ctg gag gaa ggc tcc tta gta gcg gaa ctg tat ggc aca acg 1507		
Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu Leu Tyr Gly Thr Thr 455 460 465		
gaa gtc tcc gag cgc cac cgt cac cgc tat gag gtc aat aat gcc tac 1555		
Glu Val Ser Glu Arg His Arg His Arg Tyr Glu Val Asn Asn Ala Tyr 470 475 480 485		

cgc gcc cag att gct gaa ggt tca gat ttg gtc ttc tcc gga acc tca
1603

Arg Ala Gln Ile Ala Glu Gly Ser Asp Leu Val Phe Ser Gly Thr Ser
490 495 500

cct gat gga cat ttg gtg gag ttc gtg gag tac ccc aaa gag gtg cat
1651

Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr Pro Lys Glu Val His
505 510 515

cct tat ctg gtg gca acc cag gcg cac cct gag tac aaa tct cgt cca
1699

Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu Tyr Lys Ser Arg Pro
520 525 530

acc cat gct cat cca ctg ttt tac ggc ctg gtg aag acc gct ttg gag
1747

Thr His Ala His Pro Leu Phe Tyr Gly Leu Val Lys Thr Ala Leu Glu
535 540 545

ctg cgt gtc cac cct tagatctaca atgtgatcat ggt
1785

Leu Arg Val His Pro
550

<210> 998

<211> 554

<212> PRT

<213> Corynebacterium glutamicum

<400> 998

Met Thr Ser Ser Arg Lys Val Arg Pro Thr Lys His Ile Phe Val Thr
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Gly Gly Val Val Ser Ser Leu Gly Lys Gly Leu Thr Ala Ala Ser Leu
20 25 30

Gly Gln Leu Leu Ile Ala Arg Gly Leu Ser Val Thr Met Gln Lys Leu
35 40 45

Asp Pro Tyr Leu Asn Val Asp Pro Gly Thr Met Asn Pro Phe Glu His
50 55 60

Gly Glu Val Phe Val Thr Glu Asp Gly Ala Glu Thr Asp Leu Asp Leu
65 70 75 80

Gly His Tyr Glu Arg Phe Leu Asp Arg Asn Leu Gly Leu Asn Ala Asn
85 90 95

Val Thr Thr Gly Lys Val Tyr Ser Thr Val Ile Ala Lys Glu Arg Arg
100 105 110

Gly Glu Tyr Leu Gly Lys Thr Val Gln Val Ile Pro His Ile Thr Asp
115 120 125

Glu Ile Lys Ala Arg Ile Leu Ser Met Gly Glu Pro Asp Ala His Gly
130 135 140

Asn Ala Pro Asp Val Val Ile Ser Glu Val Gly Gly Thr Val Gly Asp

145		150		155		160
Ile Glu Ser Gln Pro Phe Leu Glu Ala Ala Arg Gln Val Arg His Glu						
		165		170		175
Ile Gly Arg Glu Asn Cys Phe Phe Ile His Cys Ser Leu Val Pro Tyr						
		180		185		190
Leu Ala Thr Ser Gly Glu Leu Lys Thr Lys Pro Thr Gln His Ser Val						
		195		200		205
Ala Glu Leu Arg Gly Ile Gly Ile Leu Pro Asp Ala Leu Val Leu Arg						
		210		215		220
Cys Asp Arg Glu Val Pro Gln Gly Leu Lys Asp Lys Ile Ala Met Met						
		225		230		235
Cys Asp Val Asp Tyr Glu Gly Val Val Ser Cys Pro Asp Ser Ser Ser						
		245		250		255
Ile Tyr Asn Ile Pro Asp Val Leu Tyr Arg Glu His Leu Asp Thr Phe						
		260		265		270
Ile Ile Arg Arg Leu Gly Leu Pro Phe Arg Asp Val Asp Trp Ser Thr						
		275		280		285
Trp His Asp Leu Leu Glu Arg Val Asn Asn Pro Arg His Glu Leu Thr						
		290		295		300
Val Gly Ile Val Gly Lys Tyr Ile Asp Leu Pro Asp Ala Tyr Leu Ser						
		305		310		315
Val Val Glu Ala Val Arg Ala Ala Gly Tyr Ala Asn Trp Thr Arg Thr						
		325		330		335
Asn Ile Lys Trp Ile Thr Ser Asp Asp Cys Glu Thr Pro Ser Gly Ala						
		340		345		350
Met Lys Ala Leu Ser Gly Leu Asp Ala Ile Val Val Pro Gly Gly Phe						
		355		360		365
Gly Ile Arg Gly Ile Glu Gly Lys Ile Gly Ala Ile Thr Phe Ala Arg						
		370		375		380
Glu His Lys Ile Pro Leu Leu Gly Leu Cys Leu Gly Leu Gln Cys Thr						
		385		390		395
Val Ile Glu Ala Ala Arg Gln Ala Gly Leu Glu Gln Ala Ser Ser Thr						
		405		410		415
Glu Phe Asp Pro Ala Ala Thr Gln Pro Val Ile Ala Thr Met Glu Glu						
		420		425		430
Gln Lys Ala Ala Val Ser Gly Glu Ala Asp Leu Gly Gly Thr Met Arg						
		435		440		445
Leu Gly Ala Tyr Pro Ala Thr Leu Glu Glu Gly Ser Leu Val Ala Glu						
		450		455		460
Leu Tyr Gly Thr Thr Glu Val Ser Glu Arg His Arg His Arg Tyr Glu						
		465		470		475
						480

Val Asn Asn Ala Tyr Arg Ala Gln Ile Ala Glu Gly Ser Asp Leu Val
 485 490 495

Phe Ser Gly Thr Ser Pro Asp Gly His Leu Val Glu Phe Val Glu Tyr
 500 505 510

Pro Lys Glu Val His Pro Tyr Leu Val Ala Thr Gln Ala His Pro Glu
 515 520 525

Tyr Lys Ser Arg Pro Thr His Ala His Pro Leu Phe Tyr Gly Leu Val
 530 535 540

Lys Thr Ala Leu Glu Leu Arg Val His Pro
 545 550

<210> 999

<211> 3462

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3439)

<223> RXN02234

<400> 999

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tgatggatgc agacgctcag aagaaaggcg cataaataac atg cca aag cgt tca 115
 Met Pro Lys Arg Ser
 1 5

gat att aac cac gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc 163
 Asp Ile Asn His Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly
 10 15 20

cag gca tgt gaa ttc gac tac tcc ggc acc cag gct tgc cgc gtg ctg 211
 Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu
 25 30 35

aag gaa gag gga ctg cgc gtc acc ctc atc aac tcc aac cca gca acg 259
 Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr
 40 45 50

atc atg acc gac cca gaa atg gct gac cac acc tac gtg gag cca atc 307
 Ile Met Thr Asp Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile
 55 60 65

gag ccg gaa tac atc gac aag att ttc gct aag gaa atc gag cag ggc 355
 Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly
 70 75 80 85

cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt 403
 His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu
 90 95 100

aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc 451
 Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly
 105 110 115

gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat	499
Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp	
120 125 130	
cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg	547
Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala	
135 140 145	
cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca	595
Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala	
150 155 160 165	
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Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu	
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Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile	
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985 990 995

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3139

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His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro	Ser		165		170		175	
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Val	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Trp	Lys	Glu	Phe	Glu	Leu	Glu	210		215		220		
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Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val	Ala		245		250		255	
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Lys	Ala	Leu	Arg	Ser	Leu	Glu	Thr	Lys	Gln	Gln	Gly	Phe	Trp	Thr	Lys
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aac	atc	cag	ttc	gcc	atc	aac	cca	gtt	gat	ggc	cgc	atc	atc	acc	att	768
Asn	Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile	
				245					250					255		
gag	atg	aac	cca	cgt	gtg	tct	cgt	tcc	tcc	gct	ctg	gca	tcc	aag	gca	816
Glu	Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala	
			260					265					270			
acg	ggc	ttc	cca	att	gcc	aag	atg	gct	gcc	aag	ctg	gct	atc	gga	tac	864
Thr	Gly	Phe	Pro	Ile	Ala	Lys	Met	Ala	Ala	Lys	Leu	Ala	Ile	Gly	Tyr	
	275						280					285				

acc ctg gat gag atc acc aac gac atc act ggt gaa acc cca gct gcg	912
Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala	
290 295 300	
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Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala	
305 310 315 320	
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1008 Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys	
325 330 335	
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1056 Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu	
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1104 Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr	
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1152 Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala	
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1200 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val	
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1248 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala	
405 410 415	
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1296 Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln	
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1344 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu	
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cgc gaa gca aag ttc atg ggt ctg tcc gac ctg cag atc gca gcc ctt	
1392 Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu	
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1440 Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser	
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1488	

Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu
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 1536
 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro
 500 505 510
 gca gct gag tct gag gtc gca cca cag act gag cgt gaa aag gtc ctg
 1584
 Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu
 515 520 525
 atc ttg ggc tcc ggt cca aac cgc atc ggc cag ggc atc gag ttc gac
 1632
 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp
 530 535 540
 tac tcc tgt gtt cac gca gct ctt gag ctc tcc cgc gtc ggc tac gaa
 1680
 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu
 545 550 555 560
 act gtc atg gtc aac tgc aac cca gag acc gtg tcc acc gac tac gac
 1728
 Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp
 565 570 575
 acc gct gac cgc ctg tac ttc gag cca ctg acc ttc gaa gac gtc atg
 1776
 Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met
 580 585 590
 gag gtc tac cac gct gag gcg cag tcc ggc acc gtc gca ggt gtt atc
 1824
 Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile
 595 600 605
 gtc cag ctt ggt ggc cag act cct ctg ggc ttg gca gat cgt ttg aag
 1872
 Val Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys
 610 615 620
 aag gct ggc gtc cct gtc att ggt acc tcc cca gag gca atc gac atg
 1920
 Lys Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met
 625 630 635 640
 gct gag gac cgt ggc gag ttc ggt gca ctg ctg aac cgc gag cag ctt
 1968
 Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu
 645 650 655
 cct gct cca gca ttc ggc acc gca acc tct ttc gaa gag gct cgc aca
 2016
 Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr
 660 665 670
 gta gcc gat gag atc agc tac cca gtg ctg gtt cgc cct tcc tac gtc
 2064
 Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val

675	680	685
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Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu 690 695 700		
gat tac atc aac cgc gca act gag ttg tct tct gac cac cca gtg ctg 2160		
Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu 705 710 715 720		
gtt gac cgc ttc cta gac aac gct att gag atc gac gtc gac gca ctg 2208		
Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu 725 730 735		
tgc gac ggc gac gag gtc tac ctg gca ggc gtc atg gag cac atc gag 2256		
Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu 740 745 750		
gaa gcc ggc att cac tcc ggt gac tcc gca tgt gca ctt cct cca atg 2304		
Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met 755 760 765		
act ttg ggc gca cag gac atc gag aag gtc cgc gaa gca acc aag aag 2352		
Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys 770 775 780		
ctg gct ctg ggc atc ggt gta cag ggc ctg atg aac gtc cag tac gca 2400		
Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala 785 790 795 800		
ctc aag gac gac atc ctc tac gtc atc gag gca aac cca cgt gca tcc 2448		
Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser 805 810 815		
cgc acc gtg ccg ttc gtc tcc aag gca acg ggc gtc aac ctg gcc aag 2496		
Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys 820 825 830		
gca gca tcc cgt atc gca gtg ggc gcc acc atc aag gat ctc caa gat 2544		
Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp 835 840 845		
gag ggc atg att cct acc gag tac gac ggc ggc tcc ttg cca ctg gac 2592		
Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp 850 855 860		
gct cca atc gct gtg aag gaa gca gtg ttg ccg ttc aac cgc ttc cgt 2640		
Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg 865 870 875 880		

cgc cca gat gga aag acc ctg gac acc ctg ctt tcc cca gag atg aag
2688

Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys
885 890 895

tcc act ggc gag gtc atg ggc ttg gcc aac aac ttc ggc gct gca tat
2736

Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr
900 905 910

gca aag gct gaa gct ggc gcg ttt ggt gca ttg cca acc gaa ggc acc
2784

Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr
915 920 925

gtc ttc gtg acc gtg gct aac cgc gac aag cgc acc ctg atc ctg cca
2832

Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
930 935 940

atc cag cgc ctg gcg ttg atg ggc tac aag atc ctc gcc acc gaa ggc
2880

Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
945 950 955 960

acc gca ggc atg ctg cgc cgc aac ggc att gag tgt gaa gtt gtg ctc
2928

Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
965 970 975

aag gct tcc gac atc cgc gaa ggt gta gag ggc aag tcc atc gtg gat
2976

Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
980 985 990

cgt atc cgc gaa ggc gaa gtt gac ctc atc ctc aac acc cca gct ggt
3024

Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
995 1000 1005

tct gct ggc gct cgc cac gat ggc tac gat atc cgc gca gca gca gtg
3072

Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val
1010 1015 1020

acc gtg ggt gtt ccg ctg atc acc act gtt cag ggt gtc acc gca gct
3120

Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
1025 1030 1035 1040

gtc cag ggc ata gag gcc ctg cgt gag ggc gtt gtc agc gtc cgc gcg
3168

Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
1045 1050 1055

ctg cag gaa ctc gac cac gca gtc aag gct taagccctat gacattcggc
3218

Leu Gln Glu Leu Asp His Ala Val Lys Ala
1060 1065

gag
3221

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<211> 1066
<212> PRT
<213> Corynebacterium glutamicum

<400> 1002

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			20					25					30		
Lys	Glu	Ile	Glu	Gln	Gly	His	Pro	Ile	Asp	Ala	Val	Leu	Ala	Thr	Leu
		35					40					45			
Gly	Gly	Gln	Thr	Ala	Leu	Asn	Ala	Ala	Ile	Gln	Leu	Asp	Arg	Leu	Gly
	50					55					60				
Ile	Leu	Glu	Lys	Tyr	Gly	Val	Glu	Leu	Ile	Gly	Ala	Asp	Ile	Asp	Ala
65					70					75					80
Ile	Glu	Arg	Gly	Glu	Asp	Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr
				85					90					95	
Ile	Gly	Gly	Glu	Ser	Ala	Arg	Ser	Arg	Val	Cys	His	Asn	Met	Glu	Glu
			100					105					110		
Val	His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro
		115					120					125			
Ser	Phe	Thr	Met	Gly	Gly	Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu
	130					135					140				
Asp	Leu	Glu	Arg	Ile	Ala	Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala
145					150					155					160
Asn	Val	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Trp	Lys	Glu	Phe	Glu	Leu
				165					170					175	
Glu	Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile
			180					185					190		
Glu	Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val
		195					200					205			
Ala	Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp
	210					215					220				
Gln	Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys
225					230					235					240
Asn	Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile
			245						250					255	
Glu	Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala
			260					265						270	

Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr
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 Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala
 290 295 300
 Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala
 305 310 315 320
 Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys
 325 330 335
 Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu
 340 345 350
 Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr
 355 360 365
 Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala
 370 375 380
 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val
 385 390 395 400
 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala
 405 410 415
 Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln
 420 425 430
 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu
 435 440 445
 Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu
 450 455 460
 Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser
 465 470 475 480
 Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu
 485 490 495
 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro
 500 505 510
 Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu
 515 520 525
 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp
 530 535 540
 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu
 545 550 555 560
 Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp
 565 570 575
 Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met
 580 585 590
 Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile

595					600					605					
Val	Gln	Leu	Gly	Gly	Gln	Thr	Pro	Leu	Gly	Leu	Ala	Asp	Arg	Leu	Lys
610						615					620				
Lys	Ala	Gly	Val	Pro	Val	Ile	Gly	Thr	Ser	Pro	Glu	Ala	Ile	Asp	Met
625					630					635					640
Ala	Glu	Asp	Arg	Gly	Glu	Phe	Gly	Ala	Leu	Leu	Asn	Arg	Glu	Gln	Leu
				645					650					655	
Pro	Ala	Pro	Ala	Phe	Gly	Thr	Ala	Thr	Ser	Phe	Glu	Glu	Ala	Arg	Thr
			660				665						670		
Val	Ala	Asp	Glu	Ile	Ser	Tyr	Pro	Val	Leu	Val	Arg	Pro	Ser	Tyr	Val
		675					680					685			
Leu	Gly	Gly	Arg	Gly	Met	Glu	Ile	Val	Tyr	Asp	Glu	Ala	Ser	Leu	Glu
	690					695					700				
Asp	Tyr	Ile	Asn	Arg	Ala	Thr	Glu	Leu	Ser	Ser	Asp	His	Pro	Val	Leu
705					710					715					720
Val	Asp	Arg	Phe	Leu	Asp	Asn	Ala	Ile	Glu	Ile	Asp	Val	Asp	Ala	Leu
				725					730					735	
Cys	Asp	Gly	Asp	Glu	Val	Tyr	Leu	Ala	Gly	Val	Met	Glu	His	Ile	Glu
			740					745					750		
Glu	Ala	Gly	Ile	His	Ser	Gly	Asp	Ser	Ala	Cys	Ala	Leu	Pro	Pro	Met
		755					760					765			
Thr	Leu	Gly	Ala	Gln	Asp	Ile	Glu	Lys	Val	Arg	Glu	Ala	Thr	Lys	Lys
	770					775					780				
Leu	Ala	Leu	Gly	Ile	Gly	Val	Gln	Gly	Leu	Met	Asn	Val	Gln	Tyr	Ala
785					790					795					800
Leu	Lys	Asp	Asp	Ile	Leu	Tyr	Val	Ile	Glu	Ala	Asn	Pro	Arg	Ala	Ser
				805					810					815	
Arg	Thr	Val	Pro	Phe	Val	Ser	Lys	Ala	Thr	Gly	Val	Asn	Leu	Ala	Lys
			820					825					830		
Ala	Ala	Ser	Arg	Ile	Ala	Val	Gly	Ala	Thr	Ile	Lys	Asp	Leu	Gln	Asp
		835					840					845			
Glu	Gly	Met	Ile	Pro	Thr	Glu	Tyr	Asp	Gly	Gly	Ser	Leu	Pro	Leu	Asp
	850					855					860				
Ala	Pro	Ile	Ala	Val	Lys	Glu	Ala	Val	Leu	Pro	Phe	Asn	Arg	Phe	Arg
865					870					875					880
Arg	Pro	Asp	Gly	Lys	Thr	Leu	Asp	Thr	Leu	Leu	Ser	Pro	Glu	Met	Lys
				885					890					895	
Ser	Thr	Gly	Glu	Val	Met	Gly	Leu	Ala	Asn	Asn	Phe	Gly	Ala	Ala	Tyr
			900					905					910		
Ala	Lys	Ala	Glu	Ala	Gly	Ala	Phe	Gly	Ala	Leu	Pro	Thr	Glu	Gly	Thr
		915					920					925			

Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
 930 935 940
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
 945 950 955 960
 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
 965 970 975
 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
 980 985 990
 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
 995 1000 1005
 Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val
 1010 1015 1020
 Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
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 Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
 1045 1050 1055
 Leu Gln Glu Leu Asp His Ala Val Lys Ala
 1060 1065

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 <212> DNA
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 <222> (101)..(424)
 <223> RXN00450

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 gttttgataa tgatctggct cgggtggtgg gattcgacta gtg ggc gtt tta cct 115
 Val Gly Val Leu Pro
 1 5
 gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu
 10 15 20
 gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc 211
 Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val
 25 30 35
 att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga 259
 Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg
 40 45 50
 gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga 307
 Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg
 55 60 65

cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc 355
 Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr
 70 75 80 85

gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg 403
 Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val
 90 95 100

ggt gct cga atc gga cgc atc 424
 Gly Ala Arg Ile Gly Arg Ile
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<210> 1004

<211> 108

<212> PRT

<213> Corynebacterium glutamicum

<400> 1004

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Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
 20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
 35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
 50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
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 85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly Arg Ile
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<223> FRXA00450

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 Val Gly Val Leu Pro
 1 5

gtg cag gcg cgc atc aaa gac gat gag cgc cgc atg cgc cat gct ttg 163
 Val Gln Ala Arg Ile Lys Asp Asp Glu Arg Arg Met Arg His Ala Leu

	10	15	20	
gat att gct cgc caa acc cct gag ggg gac gtt ccc gtt ggc gcc gtc				211
Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val Pro Val Gly Ala Val				
	25	30	35	
att tac gcg ccg acc ggg gag atc ctg gcg acc gca acg aac cgt cga				259
Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr Ala Thr Asn Arg Arg				
	40	45	50	
gaa gca gac cgc gat ccc acg gcc cac gcc gaa att att gct tta cga				307
Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu Ile Ile Ala Leu Arg				
	55	60	65	
cga gcc gcc cgc cgt ttt tcc gac ggc tgg cgg ctg agt gac tgc acc				355
Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg Leu Ser Asp Cys Thr				
	70	75	80	85
gcg gtg gtc acc ttg gag ccc tgc agt atg tgc gcc ggc gcc ttg gtg				403
Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys Ala Gly Ala Leu Val				
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Gly Ala Arg Ile Gly				
	105			

<210> 1006

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<213> Corynebacterium glutamicum

<400> 1006

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Met Arg His Ala Leu Asp Ile Ala Arg Gln Thr Pro Glu Gly Asp Val
20 25 30

Pro Val Gly Ala Val Ile Tyr Ala Pro Thr Gly Glu Ile Leu Ala Thr
35 40 45

Ala Thr Asn Arg Arg Glu Ala Asp Arg Asp Pro Thr Ala His Ala Glu
50 55 60

Ile Ile Ala Leu Arg Arg Ala Ala Arg Arg Phe Ser Asp Gly Trp Arg
65 70 75 80

Leu Ser Asp Cys Thr Ala Val Val Thr Leu Glu Pro Cys Ser Met Cys
85 90 95

Ala Gly Ala Leu Val Gly Ala Arg Ile Gly
100 105

<210> 1007

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<212> DNA

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<221> CDS

<222> (101)..(1345)

<223> RXN02272

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 Val Arg Ile Thr Asn
 1 5

gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163
 Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly
 10 15 20

gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211
 Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp
 25 30 35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259
 His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln
 40 45 50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307
 Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile
 55 60 65

cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg 355
 Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp
 70 75 80 85

gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg 403
 Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala
 90 95 100

aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac ggc gtt ggt ttc 451
 Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe
 105 110 115

atc cgc act cac gta gat gtc acc gat ccc acg ttt gct gga ttc gaa 499
 Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu
 120 125 130

gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag 547
 Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln
 135 140 145

att gtc gcc ttc ccg caa aat ggc att tac gcc tac gaa ggt ggc cag 595
 Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln
 150 155 160 165

aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc 643
 Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly
 170 175 180

atc cca cac ctt gaa ccc acc cga gac gat ggc gtc gag tcg gtg aaa 691
 Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys
 185 190 195

tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac 739
 Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His

200						205						210							
act	gat	gaa	att	gac	gat	cca	cat	tcc	cga	ttt	gtc	gaa	gtc	ctc	gcc	787			
Thr	Asp	Glu	Ile	Asp	Asp	Pro	His	Ser	Arg	Phe	Val	Glu	Val	Leu	Ala				
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gca	gaa	gcc	gca	aaa	cgt	gac	atg	ggc	gca	caa	acc	gtg	gtg	tct	cat	835			
Ala	Glu	Ala	Ala	Lys	Arg	Asp	Met	Gly	Ala	Gln	Thr	Val	Val	Ser	His				
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Ser	Val	Ala	Met	Ala	Tyr	Tyr	Ser	Pro	Gly	Tyr	Met	Ala	Arg	Leu	Leu				
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ccc	aag	ctc	gca	gca	tca	aag	gtt	cgt	ttt	gca	gta	tgc	ccc	aat	gaa	931			
Pro	Lys	Leu	Ala	Ala	Ser	Lys	Val	Arg	Phe	Ala	Val	Cys	Pro	Asn	Glu				
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aac	ctc	cat	ctg	caa	gga	ctt	ggt	ttc	caa	gga	ccc	gtc	ccc	cga	ggt	979			
Asn	Leu	His	Leu	Gln	Gly	Leu	Gly	Phe	Gln	Gly	Pro	Val	Pro	Arg	Gly				
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Val	Ala	Pro	Val	Lys	Gln	Leu	Thr	Glu	Trp	Gly	Ile	Pro	Val	Ser	Phe				
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tgc	cag	gac	tca	ctc	aat	gac	ccc	ttc	tac	ccc	atg	ggc	gat	gga	gat				
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cta	ctc	cgc	att	ctc	gat	tct	gga	tta	cac	gtg	tcc	cac	atg	ctc	aca				
1123																			
Leu	Leu	Arg	Ile	Leu	Asp	Ser	Gly	Leu	His	Val	Ser	His	Met	Leu	Thr				
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gcc	agc	cac	ttg	aag	aat	gca	cta	tcg	ttc	atc	acc	acc	aat	cca	gcc				
1171																			
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345						350						355							
gga	aac	cta	ggc	ctg	gac	aat	tac	gac	att	gca	gaa	aac	tcc	ccg	gcg				
1219																			
Gly	Asn	Leu	Gly	Leu	Asp	Asn	Tyr	Asp	Ile	Ala	Glu	Asn	Ser	Pro	Ala				
360						365						370							
aac	ctg	ctg	gtt	ctt	gat	gcg	agc	agc	gag	aag	gaa	gct	gta	cag	aga				
1267																			
Asn	Leu	Leu	Val	Leu	Asp	Ala	Ser	Ser	Glu	Lys	Glu	Ala	Val	Gln	Arg				
375						380						385							
aaa	gct	tcc	gta	ctt	ttg	agc	atc	cac	cgc	ggc	aaa	aag	gtg	ctc	tcc				
1315																			
Lys	Ala	Ser	Val	Leu	Leu	Ser	Ile	His	Arg	Gly	Lys	Lys	Val	Leu	Ser				
390						395						400						405	
agg	gag	ccc	gaa	cag	gtg	gac	tgg	aac	atc	taacagccca gttgggcctc									
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410						415													

ctt
1368

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<211> 415
<212> PRT
<213> Corynebacterium glutamicum

<400> 1008

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Ile Thr Ile Glu Gly Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile
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35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala
50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu
65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys
85 90 95

Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu
100 105 110

His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr
115 120 125

Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu
130 135 140

Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala
145 150 155 160

Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala
165 170 175

Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly
180 185 190

Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala
195 200 205

Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe
210 215 220

Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln
225 230 235 240

Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr
245 250 255

Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala
260 265 270

Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly
 275 280 285

Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly
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Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro
 305 310 315 320

Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val
 325 330 335

Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile
 340 345 350

Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala
 355 360 365

Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys
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Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly
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Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1345)

<223> FRXA02272

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 Val Arg Ile Thr Asn
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gcc cag gtt aag aac tac gca gag tta gtt gat atc acc ata gag ggt 163
 Ala Gln Val Lys Asn Tyr Ala Glu Leu Val Asp Ile Thr Ile Glu Gly
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gaa aaa att tcc tcg att acc ccc tct tca att cga tca gaa gaa gat 211
 Glu Lys Ile Ser Ser Ile Thr Pro Ser Ser Ile Arg Ser Glu Glu Asp
 25 30 35

cac cgc gcg gac gat tac gat gcc gca gga aga ctg gtc gca ccc cag 259
 His Arg Ala Asp Asp Tyr Asp Ala Ala Gly Arg Leu Val Ala Pro Gln
 40 45 50

ttc gcc gaa gca cac atc cac ctt gac tac gca aac acc gct gga atc 307
 Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala Asn Thr Ala Gly Ile
 55 60 65

cct cgc gaa aac tct tcc ggc aca ctt ttt gaa gcc atc gaa atc tgg	355
Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu Ala Ile Glu Ile Trp	
70 75 80 85	
gcc gac cgc aag acc caa ggc ttc cac atc aaa gaa gac att aaa gcg	403
Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys Glu Asp Ile Lys Ala	
90 95 100	
aag gcc ctc cag gca gcc cgt cgg gca gca gaa cac ggc gtt ggt ttc	451
Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu His Gly Val Gly Phe	
105 110 115	
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Ile Arg Thr His Val Asp Val Thr Asp Pro Thr Phe Ala Gly Phe Glu	
120 125 130	
gca att gcg gag ctg cgc gat gaa gtc cgc gag tgg tgc gat atc cag	547
Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu Trp Cys Asp Ile Gln	
135 140 145	
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Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala Tyr Glu Gly Gly Gln	
150 155 160 165	
aag cta atc tca gat gca atg tct gca ggt gca gat gtc gtt ggt ggc	643
Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala Asp Val Val Gly Gly	
170 175 180	
atc cca cac ctt gaa ccc acc cga gac gat ggc gtc gag tcg gtg aaa	691
Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly Val Glu Ser Val Lys	
185 190 195	
tgg ctg ttc gac ctt gca gag aag cac tca gcc ccc atc gat atc cac	739
Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala Pro Ile Asp Ile His	
200 205 210	
act gat gaa att gac gat cca cat tcc cga ttt gtc gaa gtc ctc gcc	787
Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe Val Glu Val Leu Ala	
215 220 225	
gca gaa gcc gca aaa cgt gac atg ggc gca caa acc gtg gtg tct cat	835
Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln Thr Val Val Ser His	
230 235 240 245	
tct gtg gcg atg gcc tat tac tca cct ggc tac atg gcg cga ctt tta	883
Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr Met Ala Arg Leu Leu	
250 255 260	
ccc aag ctc gca gca tca aag gtt cgt ttt gca gta tgc ccc aat gaa	931
Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala Val Cys Pro Asn Glu	
265 270 275	
aac ctc cat ctg caa gga ctt ggt ttc caa gga ccc gtc ccc cga ggt	979
Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly Pro Val Pro Arg Gly	
280 285 290	
gtt gca ccg gta aag caa ctt acc gaa tgg gga att cca gta agt ttt	
1027	
Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly Ile Pro Val Ser Phe	
295 300 305	

tgc cag gac tca ctc aat gac ccc ttc tac ccc atg ggc gat gga gat
1075

Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro Met Gly Asp Gly Asp
310 315 320 325

cta ctc cgc att ctc gat tct gga tta cac gtg tcc cac atg ctc aca
1123

Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val Ser His Met Leu Thr
330 335 340

gcc agc cac ttg aag aat gca cta tcg ttc atc acc acc aat cca gcc
1171

Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile Thr Thr Asn Pro Ala
345 350 355

gga aac cta ggc ctg gac aat tac gac att gca gaa aac tcc ccg gcg
1219

Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala Glu Asn Ser Pro Ala
360 365 370

aac ctg ctg gtt ctt gat gcg agc agc gag aag gaa gct gta cag aga
1267

Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys Glu Ala Val Gln Arg
375 380 385

aaa gct tcc gta ctt ttg agc atc cac cgc ggc aaa aag gtg ctc tcc
1315

Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly Lys Lys Val Leu Ser
390 395 400 405

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1365

Arg Glu Pro Glu Gln Val Asp Trp Asn Ile
410 415

ctt
1368

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<211> 415

<212> PRT

<213> Corynebacterium glutamicum

<400> 1010

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35 40 45

Leu Val Ala Pro Gln Phe Ala Glu Ala His Ile His Leu Asp Tyr Ala
50 55 60

Asn Thr Ala Gly Ile Pro Arg Glu Asn Ser Ser Gly Thr Leu Phe Glu
65 70 75 80

Ala Ile Glu Ile Trp Ala Asp Arg Lys Thr Gln Gly Phe His Ile Lys
 85 90 95
 Glu Asp Ile Lys Ala Lys Ala Leu Gln Ala Ala Arg Arg Ala Ala Glu
 100 105 110
 His Gly Val Gly Phe Ile Arg Thr His Val Asp Val Thr Asp Pro Thr
 115 120 125
 Phe Ala Gly Phe Glu Ala Ile Ala Glu Leu Arg Asp Glu Val Arg Glu
 130 135 140
 Trp Cys Asp Ile Gln Ile Val Ala Phe Pro Gln Asn Gly Ile Tyr Ala
 145 150 155 160
 Tyr Glu Gly Gly Gln Lys Leu Ile Ser Asp Ala Met Ser Ala Gly Ala
 165 170 175
 Asp Val Val Gly Gly Ile Pro His Leu Glu Pro Thr Arg Asp Asp Gly
 180 185 190
 Val Glu Ser Val Lys Trp Leu Phe Asp Leu Ala Glu Lys His Ser Ala
 195 200 205
 Pro Ile Asp Ile His Thr Asp Glu Ile Asp Asp Pro His Ser Arg Phe
 210 215 220
 Val Glu Val Leu Ala Ala Glu Ala Ala Lys Arg Asp Met Gly Ala Gln
 225 230 235 240
 Thr Val Val Ser His Ser Val Ala Met Ala Tyr Tyr Ser Pro Gly Tyr
 245 250 255
 Met Ala Arg Leu Leu Pro Lys Leu Ala Ala Ser Lys Val Arg Phe Ala
 260 265 270
 Val Cys Pro Asn Glu Asn Leu His Leu Gln Gly Leu Gly Phe Gln Gly
 275 280 285
 Pro Val Pro Arg Gly Val Ala Pro Val Lys Gln Leu Thr Glu Trp Gly
 290 295 300
 Ile Pro Val Ser Phe Cys Gln Asp Ser Leu Asn Asp Pro Phe Tyr Pro
 305 310 315 320
 Met Gly Asp Gly Asp Leu Leu Arg Ile Leu Asp Ser Gly Leu His Val
 325 330 335
 Ser His Met Leu Thr Ala Ser His Leu Lys Asn Ala Leu Ser Phe Ile
 340 345 350
 Thr Thr Asn Pro Ala Gly Asn Leu Gly Leu Asp Asn Tyr Asp Ile Ala
 355 360 365
 Glu Asn Ser Pro Ala Asn Leu Leu Val Leu Asp Ala Ser Ser Glu Lys
 370 375 380
 Glu Ala Val Gln Arg Lys Ala Ser Val Leu Leu Ser Ile His Arg Gly
 385 390 395 400
 Lys Lys Val Leu Ser Arg Glu Pro Glu Gln Val Asp Trp Asn Ile

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 <212> DNA
 <213> Corynebacterium glutamicum
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 <223> RXN03004
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 Val Leu Leu Ser Asp
 1 5
 cgt gac att cgt aaa tca att gac gca ggc gac ttg gga att gaa cct 163
 Arg Asp Ile Arg Lys Ser Ile Asp Ala Gly Asp Leu Gly Ile Glu Pro
 10 15 20
 ttc gac gct gag ctg att cag ccg tcg agt gtc gat gtc cgc atg gac 211
 Phe Asp Ala Glu Leu Ile Gln Pro Ser Ser Val Asp Val Arg Met Asp
 25 30 35
 cgc tac ttc cgg gtt ttc aat aac tct aag tac acc cac att gac cct 259
 Arg Tyr Phe Arg Val Phe Asn Asn Ser Lys Tyr Thr His Ile Asp Pro
 40 45 50
 aag ttg aat cag gat gag ctg acc agc ctt gtt gag gtt gag gac ggc 307
 Lys Leu Asn Gln Asp Glu Leu Thr Ser Leu Val Glu Val Glu Asp Gly
 55 60 65
 gag ggc ttt gtg ctg cat ccg ggt gag ttt gtg ctg gcg tcc acg ctg 355
 Glu Gly Phe Val Leu His Pro Gly Glu Phe Val Leu Ala Ser Thr Leu
 70 75 80 85
 gaa aag ttc act ttg cct gcg cat ctg gct ggt cgt ttg gag ggt aag 403
 Glu Lys Phe Thr Leu Pro Ala His Leu Ala Gly Arg Leu Glu Gly Lys
 90 95 100
 tcg tct ctt ggt cgt ctt ggc ttg ttg acg cac tct act gct ggt ttc 451
 Ser Ser Leu Gly Arg Leu Gly Leu Leu Thr His Ser Thr Ala Gly Phe
 105 110 115
 att gat cct ggt ttt agt ggt tac atc acg ttg gag ttg tcc aat gtg 499
 Ile Asp Pro Gly Phe Ser Gly Tyr Ile Thr Leu Glu Leu Ser Asn Val
 120 125 130
 gct aat ctg ccg atc acg ttg tgg ccg ggt atg aag gtg ggg cag ctg 547
 Ala Asn Leu Pro Ile Thr Leu Trp Pro Gly Met Lys Val Gly Gln Leu
 135 140 145
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 Ala Leu Phe Gln Met Ser Ser Pro Ala Glu Thr
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<210> 1012
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1012

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			20					25					30		
Asp	Val	Arg	Met	Asp	Arg	Tyr	Phe	Arg	Val	Phe	Asn	Asn	Ser	Lys	Tyr
		35					40					45			
Thr	His	Ile	Asp	Pro	Lys	Leu	Asn	Gln	Asp	Glu	Leu	Thr	Ser	Leu	Val
	50					55					60				
Glu	Val	Glu	Asp	Gly	Glu	Gly	Phe	Val	Leu	His	Pro	Gly	Glu	Phe	Val
65					70					75					80
Leu	Ala	Ser	Thr	Leu	Glu	Lys	Phe	Thr	Leu	Pro	Ala	His	Leu	Ala	Gly
				85					90					95	
Arg	Leu	Glu	Gly	Lys	Ser	Ser	Leu	Gly	Arg	Leu	Gly	Leu	Leu	Thr	His
			100					105					110		
Ser	Thr	Ala	Gly	Phe	Ile	Asp	Pro	Gly	Phe	Ser	Gly	Tyr	Ile	Thr	Leu
		115					120					125			
Glu	Leu	Ser	Asn	Val	Ala	Asn	Leu	Pro	Ile	Thr	Leu	Trp	Pro	Gly	Met
	130					135					140				
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<222> (101)..(202)

<223> RXN03137

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				Leu Glu Leu Asn Lys		
				1	5	
gca gcg tac atg ttt gag tac agc ttc gat gac atc acc gtg tcc ggc						163
Ala Ala Tyr Met Phe Glu Tyr Ser Phe Asp Asp Ile Thr Val Ser Gly						
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tac gat cca cac cca ttg atc cgc ggc aag gtc gcc gta tgatcgggtgc 212
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<210> 1014

<211> 34

<212> PRT

<213> Corynebacterium glutamicum

<400> 1014

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<210> 1015

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(613)

<223> RXN03171

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 Met Asp Ile Thr Ile
 1 5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
 Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
 10 15 20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
 Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
 25 30 35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
 Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
 40 45 50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
 Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
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ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
 Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
 70 75 80 85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403

Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
 90 95 100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
 Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
 105 110 115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
 Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
 120 125 130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
 Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
 135 140 145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
 Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
 150 155 160 165

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 Asp Ala Leu Ala Glu Ser
 170

613

<210> 1016

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1016

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 20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
 35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
 50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
 65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
 85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
 100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
 115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
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165

170

<210> 1017
 <211> 613
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <223> FRXA02857

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                Met Asp Ile Thr Ile
                1                    5

gtc aac cac cca ctc gtt gct agc cgc cta acc ctg ttg cgc gac gag 163
Val Asn His Pro Leu Val Ala Ser Arg Leu Thr Leu Leu Arg Asp Glu
                10                    15                    20

cgc agc gac aac gca gct ttc cgt gca gca gcc aac gac ctc ggc gcc 211
Arg Ser Asp Asn Ala Ala Phe Arg Ala Ala Ala Asn Asp Leu Gly Ala
                25                    30                    35

atg ctg atc tac gaa gca tcc cga gat ctg gaa gtc gaa cac ttc gac 259
Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu Val Glu His Phe Asp
                40                    45                    50

acc aaa acc ccc gtt gcc atg gct gaa ggt act cgc ctg aag cag cca 307
Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr Arg Leu Lys Gln Pro
                55                    60                    65

ccc atc atc gtt ccc atc atc cgt gca ggt ctc ggc atg atc gac cca 355
Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu Gly Met Ile Asp Pro
                70                    75                    80                    85

gcg ctg tcg atg att ccg gat gca cag gtc ggc ttc att ggc ctt gcc 403
Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly Phe Ile Gly Leu Ala
                90                    95                    100

cgc gat gag gaa acc cat gag cca gtc cca tac ctt gag gcg ctg cca 451
Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr Leu Glu Ala Leu Pro
                105                    110                    115

cag gat cta agc aac cag cct gta ttc ctt gtc gat ccc atg ctg gcc 499
Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val Asp Pro Met Leu Ala
                120                    125                    130

acc ggc ggt tcc ctc ctg cac gcg atc cgc ctt ctt gct gat cgt ggc 547
Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu Leu Ala Asp Arg Gly
                135                    140                    145

gcc acc gac atc acc gcc atc tgc atg gtt tct gcg cag cca ggt gtg 595
Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser Ala Gln Pro Gly Val
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gac gca ttg gcg gaa tct 613

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Asp Ala Leu Ala Glu Ser
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<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 1018

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20 25 30

Asn Asp Leu Gly Ala Met Leu Ile Tyr Glu Ala Ser Arg Asp Leu Glu
35 40 45

Val Glu His Phe Asp Thr Lys Thr Pro Val Ala Met Ala Glu Gly Thr
50 55 60

Arg Leu Lys Gln Pro Pro Ile Ile Val Pro Ile Ile Arg Ala Gly Leu
65 70 75 80

Gly Met Ile Asp Pro Ala Leu Ser Met Ile Pro Asp Ala Gln Val Gly
85 90 95

Phe Ile Gly Leu Ala Arg Asp Glu Glu Thr His Glu Pro Val Pro Tyr
100 105 110

Leu Glu Ala Leu Pro Gln Asp Leu Ser Asn Gln Pro Val Phe Leu Val
115 120 125

Asp Pro Met Leu Ala Thr Gly Gly Ser Leu Leu His Ala Ile Arg Leu
130 135 140

Leu Ala Asp Arg Gly Ala Thr Asp Ile Thr Ala Ile Cys Met Val Ser
145 150 155 160

Ala Gln Pro Gly Val Asp Ala Leu Ala Glu Ser
165 170

<210> 1019

<211> 678

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(655)

<223> RXA02771

<400> 1019

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atggaacatg gaccgttggt ccagaagtga ggaataagta gtg agc gaa caa gct 115
Val Ser Glu Gln Ala
1 5

cta agc acc ttc gac agg gca cgt gag gcc ctg gac aag aaa acc cga 163
 Leu Ser Thr Phe Asp Arg Ala Arg Glu Ala Leu Asp Lys Lys Thr Arg
 10 15 20

tat gtg cag gat ttc cca gaa aaa ggt gtg ctt ttt gaa gac ctc acc 211
 Tyr Val Gln Asp Phe Pro Glu Lys Gly Val Leu Phe Glu Asp Leu Thr
 25 30 35

ccg gtg ttg ggc gat gca gaa tca ttt gtg gcc gtg gtg gac gcc atg 259
 Pro Val Leu Gly Asp Ala Glu Ser Phe Val Ala Val Val Asp Ala Met
 40 45 50

gct gaa gct gca gaa aaa ctg aat gca gaa atc atc ggt ggc ttg gat 307
 Ala Glu Ala Ala Glu Lys Leu Asn Ala Glu Ile Ile Gly Gly Leu Asp
 55 60 65

gcg cga gga ttc ctc ctc gga tct gct gtc gct tac aaa ctc ggc cta 355
 Ala Arg Gly Phe Leu Leu Gly Ser Ala Val Ala Tyr Lys Leu Gly Leu
 70 75 80 85

ggt gtg ctg gct atc cgc aag aag gga aag ctc ccc cca cct gtg gtg 403
 Gly Val Leu Ala Ile Arg Lys Lys Gly Lys Leu Pro Pro Pro Val Val
 90 95 100

acc cag gag tat gaa ctt gaa tac ggc act gca gca ctc gag ctg ccc 451
 Thr Gln Glu Tyr Glu Leu Glu Tyr Gly Thr Ala Ala Leu Glu Leu Pro
 105 110 115

agt gaa gga atc gac att gct ggt aaa aac atc gtt ttg atc gac gat 499
 Ser Glu Gly Ile Asp Ile Ala Gly Lys Asn Ile Val Leu Ile Asp Asp
 120 125 130

gtg ctg gca acc ggc ggc acc ttg ggc gct gca cgt aaa cta att gaa 547
 Val Leu Ala Thr Gly Gly Thr Leu Gly Ala Ala Arg Lys Leu Ile Glu
 135 140 145

tcg tgt gac gga cat gtt tcc gga tat gtt ctt gcc att gag gtc cca 595
 Ser Cys Asp Gly His Val Ser Gly Tyr Val Leu Ala Ile Glu Val Pro
 155 160 165

ggc ctc ggc ggt agg gat aat ctt ggt gat agg ccc gtc att gtg gtc 643
 Gly Leu Gly Gly Arg Asp Asn Leu Gly Asp Arg Pro Val Ile Val Val
 170 175 180

aga gat cct cag tagaaggatc gaaagaaagg cgg 678
 Arg Asp Pro Gln
 185

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<211> 185

<212> PRT

<213> Corynebacterium glutamicum

<400> 1020

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Asp Lys Lys Thr Arg Tyr Val Gln Asp Phe Pro Glu Lys Gly Val Leu
 20 25 30

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Val	Val	Asp	Ala	Met	Ala	Glu	Ala	Ala	Glu	Lys	Leu	Asn	Ala	Glu	Ile
	50					55					60				
Ile	Gly	Gly	Leu	Asp	Ala	Arg	Gly	Phe	Leu	Leu	Gly	Ser	Ala	Val	Ala
65					70					75					80
Tyr	Lys	Leu	Gly	Leu	Gly	Val	Leu	Ala	Ile	Arg	Lys	Lys	Gly	Lys	Leu
				85					90					95	
Pro	Pro	Pro	Val	Val	Thr	Gln	Glu	Tyr	Glu	Leu	Glu	Tyr	Gly	Thr	Ala
			100					105					110		
Ala	Leu	Glu	Leu	Pro	Ser	Glu	Gly	Ile	Asp	Ile	Ala	Gly	Lys	Asn	Ile
		115					120					125			
Val	Leu	Ile	Asp	Asp	Val	Leu	Ala	Thr	Gly	Gly	Thr	Leu	Gly	Ala	Ala
	130					135					140				
Arg	Lys	Leu	Ile	Glu	Ser	Cys	Asp	Gly	His	Val	Ser	Gly	Tyr	Val	Leu
145					150					155					160
Ala	Ile	Glu	Val	Pro	Gly	Leu	Gly	Gly	Arg	Asp	Asn	Leu	Gly	Asp	Arg
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Pro	Val	Ile	Val	Val	Arg	Asp	Pro	Gln							
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tgattgacac ctgaatctac aacacaaggg gaacgcgacg atg agc aac aac gta 115
Met Ser Asn Asn Val
1 5

gaa atg gcc gac cac aaa gat ctc aat gtt cca gcc aac cca tac ggc 163
Glu Met Ala Asp His Lys Asp Leu Asn Val Pro Ala Asn Pro Tyr Gly
10 15 20

acc gac att gaa tca gta ttg atc agc gaa gag aag ctc aag cag cgc 211
Thr Asp Ile Glu Ser Val Leu Ile Ser Glu Glu Lys Leu Lys Gln Arg
25 30 35

atc gcc gaa atg gcc aag cgc gtc tcc gaa gag ttc aaa gac gcc gaa 259
Ile Ala Glu Met Ala Lys Arg Val Ser Glu Glu Phe Lys Asp Ala Glu
40 45 50

gaa gac ctc atc ctg gtg tgc gtg ctc aag ggc gcg ttc tac ttc ctg 307

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Glu	Asp	Leu	Ile	Leu	Val	Cys	Val	Leu	Lys	Gly	Ala	Phe	Tyr	Phe	Leu	
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gca	gat	ttc	tcc	cgc	atg	ctc	gac	atc	ccc	acc	cag	tcc	gag	ttc	atg	355
Ala	Asp	Phe	Ser	Arg	Met	Leu	Asp	Ile	Pro	Thr	Gln	Ser	Glu	Phe	Met	
70					75				80						85	
gcg	gtg	tcc	tct	tac	gga	aac	tcc	acc	tcc	tct	tca	ggc	gtg	gtg	cgc	403
Ala	Val	Ser	Ser	Tyr	Gly	Asn	Ser	Thr	Ser	Ser	Ser	Gly	Val	Val	Arg	
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atc	ctc	aag	gac	ctg	gac	aag	gaa	att	gaa	ggc	cgc	gac	gtt	ttg	atc	451
Ile	Leu	Lys	Asp	Leu	Asp	Lys	Glu	Ile	Glu	Gly	Arg	Asp	Val	Leu	Ile	
			105				110						115			
gtg	gaa	gac	atc	atc	gat	tcc	gga	ctg	acc	ctg	tcc	tgg	ctg	atg	cgc	499
Val	Glu	Asp	Ile	Ile	Asp	Ser	Gly	Leu	Thr	Leu	Ser	Trp	Leu	Met	Arg	
		120					125					130				
aac	ctg	aaa	aac	cgc	aac	cct	aag	tcc	ctc	aac	gtg	atc	acc	ttg	ctg	547
Asn	Leu	Lys	Asn	Arg	Asn	Pro	Lys	Ser	Leu	Asn	Val	Ile	Thr	Leu	Leu	
		135				140					145					
cgt	aag	cca	gag	cgc	ctg	acc	acc	aac	atc	gac	atg	ttc	gac	att	gga	595
Arg	Lys	Pro	Glu	Arg	Leu	Thr	Thr	Asn	Ile	Asp	Met	Phe	Asp	Ile	Gly	
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ttt	gat	att	cca	aat	gag	ttt	gtt	gtg	ggc	tac	gga	ctt	gat	ttc	gca	643
Phe	Asp	Ile	Pro	Asn	Glu	Phe	Val	Val	Gly	Tyr	Gly	Leu	Asp	Phe	Ala	
				170				175						180		
gaa	cgc	tac	cgc	gac	ctg	cca	tat	gtg	ggc	acc	ctc	gag	cct	cac	gtg	691
Glu	Arg	Tyr	Arg	Asp	Leu	Pro	Tyr	Val	Gly	Thr	Leu	Glu	Pro	His	Val	
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tac	tcc	gac	tagtaatcaa	aagtgcgaaa	gag											723
Tyr	Ser	Asp														
		200														

<210> 1022

<211> 200

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<213> Corynebacterium glutamicum

<400> 1022

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Ala	Asn	Pro	Tyr	Gly	Thr	Asp	Ile	Glu	Ser	Val	Leu	Ile	Ser	Glu	Glu	
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Lys	Leu	Lys	Gln	Arg	Ile	Ala	Glu	Met	Ala	Lys	Arg	Val	Ser	Glu	Glu	
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Phe	Lys	Asp	Ala	Glu	Glu	Asp	Leu	Ile	Leu	Val	Cys	Val	Leu	Lys	Gly	
	50					55					60					
Ala	Phe	Tyr	Phe	Leu	Ala	Asp	Phe	Ser	Arg	Met	Leu	Asp	Ile	Pro	Thr	
65					70					75					80	

Gln	Ser	Glu	Phe	Met 85	Ala	Val	Ser	Ser	Tyr 90	Gly	Asn	Ser	Thr	Ser 95	Ser
Ser	Gly	Val	Val 100	Arg	Ile	Leu	Lys	Asp 105	Leu	Asp	Lys	Glu	Ile 110	Glu	Gly
Arg	Asp	Val 115	Leu	Ile	Val	Glu	Asp 120	Ile	Ile	Asp	Ser	Gly 125	Leu	Thr	Leu
Ser	Trp 130	Leu	Met	Arg	Asn	Leu 135	Lys	Asn	Arg	Asn	Pro 140	Lys	Ser	Leu	Asn
Val 145	Ile	Thr	Leu	Leu	Arg 150	Lys	Pro	Glu	Arg	Leu 155	Thr	Thr	Asn	Ile	Asp 160
Met	Phe	Asp	Ile	Gly 165	Phe	Asp	Ile	Pro	Asn 170	Glu	Phe	Val	Val	Gly 175	Tyr
Gly	Leu	Asp	Phe 180	Ala	Glu	Arg	Tyr	Arg 185	Asp	Leu	Pro	Tyr	Val 190	Gly	Thr
Leu	Glu	Pro 195	His	Val	Tyr	Ser	Asp 200								

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<212> DNA
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Met Thr Glu Glu Arg																
1 5																
gag att ctg acc tat gag atg ttc gga aca gca atg cgg gag ctg gcc																163
Glu Ile Leu Thr Tyr Glu Met Phe Gly Thr Ala Met Arg Glu Leu Ala																
10 15 20																
caa gaa att att gat gac tac cag cca gat tgc gtg ctg tcc att gcg																211
Gln Glu Ile Ile Asp Asp Tyr Gln Pro Asp Cys Val Leu Ser Ile Ala																
25 30 35																
cgt ggt ggt ctt cta atc ggt ggc gca ctt ggt tat gcg ctg ggt atc																259
Arg Gly Gly Leu Leu Ile Gly Gly Ala Leu Gly Tyr Ala Leu Gly Ile																
40 45 50																
aag aat gta tcg gtg atc aat gtg gag ttc tac acc gat att gga gag																307
Lys Asn Val Ser Val Ile Asn Val Glu Phe Tyr Thr Asp Ile Gly Glu																
55 60 65																
cac ttg gag gag cca atg atg ctg cct cca act cca aaa gct gtt gat																355
His Leu Glu Glu Pro Met Met Leu Pro Pro Thr Pro Lys Ala Val Asp																
70 75 80 85																

ctc tcg gga atg cgt gtg ctc gtc gct gac gat gtc gcg gat acc gga 403
 Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp Val Ala Asp Thr Gly
 90 95 100
 aag act ctt gag ttg gtc agg gac ttc ctg ggt gac caa gtt gtc gaa 451
 Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly Asp Gln Val Val Glu
 105 110 115
 gtg cgc act gca gtg atc tat cac aag cca aac agt gtg ttt aag ccg 499
 Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn Ser Val Phe Lys Pro
 120 125 130
 gag tat gtg tgg cgt gag act gat aag tgg att aac ttc cca tgg tct 547
 Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile Asn Phe Pro Trp Ser
 135 140 145
 acc ctg cct cca gtg gag cct tct aag taattttttca cccgtgaaag 594
 Thr Leu Pro Pro Val Glu Pro Ser Lys
 150 155
 tgc 597

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<211> 158

<212> PRT

<213> Corynebacterium glutamicum

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 Val Leu Ser Ile Ala Arg Gly Gly Leu Leu Ile Gly Gly Ala Leu Gly
 35 40 45
 Tyr Ala Leu Gly Ile Lys Asn Val Ser Val Ile Asn Val Glu Phe Tyr
 50 55 60
 Thr Asp Ile Gly Glu His Leu Glu Glu Pro Met Met Leu Pro Pro Thr
 65 70 75 80
 Pro Lys Ala Val Asp Leu Ser Gly Met Arg Val Leu Val Ala Asp Asp
 85 90 95
 Val Ala Asp Thr Gly Lys Thr Leu Glu Leu Val Arg Asp Phe Leu Gly
 100 105 110
 Asp Gln Val Val Glu Val Arg Thr Ala Val Ile Tyr His Lys Pro Asn
 115 120 125
 Ser Val Phe Lys Pro Glu Tyr Val Trp Arg Glu Thr Asp Lys Trp Ile
 130 135 140
 Asn Phe Pro Trp Ser Thr Leu Pro Pro Val Glu Pro Ser Lys
 145 150 155

tac tac aaa ttt gaa caa gaa gtt cct cag tca atc ctt gat gag ctc 691
 Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser Ile Leu Asp Glu Leu
 185 190 195

agt gaa gat gga aag aat cca cgg gga agt gaa gtc act taaacctcca 740
 Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu Val Thr
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gttgaaacca ctg 753

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<212> PRT

<213> Corynebacterium glutamicum

<400> 1026

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Asn Tyr Gln Phe Gly Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu
 35 40 45

Lys Thr Glu Phe Ser Gln Leu His Glu Tyr Ala Pro Ile Glu His Val
 50 55 60

Ser Ser Arg Leu Lys Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg
 65 70 75 80

Lys Gly Asp Glu Leu Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp
 85 90 95

Ile Ala Gly Ile Arg Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala
 100 105 110

Ile Ala Asp Met Leu Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala
 115 120 125

Lys Asp Tyr Ile Ala Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His
 130 135 140

Leu Ile Leu Gln Val Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val
 145 150 155 160

Asn Val Glu Val Gln Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser
 165 170 175

Leu Glu His Lys Ile Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser
 180 185 190

Ile Leu Asp Glu Leu Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu
 195 200 205

Val Thr
 210

<210> 1027

<211> 1158
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 <213> Corynebacterium glutamicum

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 <223> RXN02772

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                                         Met Ser Leu Glu Arg
                                         1                               5

aac aca caa aaa tct tcc atg ggt gtg cga agc atg tca gcc agg ctt 163
Asn Thr Gln Lys Ser Ser Met Gly Val Arg Ser Met Ser Ala Arg Leu
                               10                               15                               20

gcc cgc agc ctc aca gga aac cgc gtt cgc acc aac cct gtg ctg gat 211
Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
                               25                               30                               35

ccg ctg ctg agc atc cac cgg caa ttt cac cca cgc gcc gac gta caa 259
Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln
                               40                               45                               50

gtg ttg gaa cgt gca tat gac acc gcg gaa cgt ctt cat gat ggt gtg 307
Val Leu Glu Arg Ala Tyr Asp Thr Ala Glu Arg Leu His Asp Gly Val
                               55                               60                               65

att cga aaa tcg ggc gat ccg tat att acc cac ccg ttg gct gtc gcc 355
Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His Pro Leu Ala Val Ala
                               70                               75                               80                               85

acc atc gcc gcg gaa atc ggc atg gac acc acc acg ctc gtc gca gcc 403
Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr Thr Leu Val Ala Ala
                               90                               95                               100

ttg ttg cat gac acg gtg gaa gac acc gac tac tct ttg gac gat ctc 451
Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr Ser Leu Asp Asp Leu
                               105                               110                               115

acc cga gat ttc gga gaa gaa gtt gcc agg ctt gtc gac ggt gtc acc 499
Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr
                               120                               125                               130

aag ctc gac aaa gtc gca cta ggt gct gcc gcg gag gcc gaa acg att 547
Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala Glu Ala Glu Thr Ile
                               135                               140                               145

cgc aaa atg atc gtc gcc atg agc cag gac ccc cgc gtg ctg gtg att 595
Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile
                               150                               155                               160                               165

aaa gtg gcc gac cgt ttg cac aat atg cgc acc atg cgg ttc ctg ccg 643
Lys Val Ala Asp Arg Leu His Asn Met Arg Thr Met Arg Phe Leu Pro
                               170                               175                               180

ccg gaa aag caa gct aaa aaa gca cgc caa acc ctt gaa gtg att gct 691

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Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr Leu Glu Val Ile Ala
 185 190 195

cct ttg gca cac cgc ctg ggc atg gcc agc gtg aaa tgg gaa ttg gaa 739
 Pro Leu Ala His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu
 200 205 210

gat cta tcc ttt gcc att ttg tac ccc aag aag tac gaa gag atc gtg 787
 Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val
 215 220 225

cgt ctt gtt gcc gac cgc gcg ccc tct aga gac cgg tac ctc aaa gaa 835
 Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp Arg Tyr Leu Lys Glu
 230 235 240 245

att att gat caa gtc acc ggt ggc ttg cgc gaa aac aac atc gcg gca 883
 Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu Asn Asn Ile Ala Ala
 250 255 260

gaa gtg ctt ggt cga cca aag cac tac tgg tct atc tat caa aag atg 931
 Glu Val Leu Gly Arg Pro Lys His Tyr Trp Ser Ile Tyr Gln Lys Met
 265 270 275

atc gtt cgc ggt cgt gat ttt gac gat att ttt gat ctt gtt ggc atc 979
 Ile Val Arg Gly Arg Asp Phe Asp Asp Ile Phe Asp Leu Val Gly Ile
 280 285 290

cgc atc ctg gta gac aac gtg aac aac tgt gta cgc cgc cat cgg tgt
 1027
 Arg Ile Leu Val Asp Asn Val Asn Asn Cys Val Arg Arg His Arg Cys
 295 300 305

cgt gca ctc cct gtt caa tgc tct gcc tgg ccg att caa aga cta tat
 1075
 Arg Ala Leu Pro Val Gln Cys Ser Ala Trp Pro Ile Gln Arg Leu Tyr
 310 315 320 325

ttc agc ccc gcg ctt cgg tgt cta cca atc cct gca cac cac cgt gat
 1123
 Phe Ser Pro Ala Leu Arg Cys Leu Pro Ile Pro Ala His His Arg Asp
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 1158
 Gly Thr Trp Arg
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Arg	Ala	Asp	Val	Gln	Val	Leu	Glu	Arg	Ala	Tyr	Asp	Thr	Ala	Glu	Arg
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Leu	His	Asp	Gly	Val	Ile	Arg	Lys	Ser	Gly	Asp	Pro	Tyr	Ile	Thr	His
65					70					75					80
Pro	Leu	Ala	Val	Ala	Thr	Ile	Ala	Ala	Glu	Ile	Gly	Met	Asp	Thr	Thr
				85					90					95	
Thr	Leu	Val	Ala	Ala	Leu	Leu	His	Asp	Thr	Val	Glu	Asp	Thr	Asp	Tyr
			100					105					110		
Ser	Leu	Asp	Asp	Leu	Thr	Arg	Asp	Phe	Gly	Glu	Glu	Val	Ala	Arg	Leu
		115					120					125			
Val	Asp	Gly	Val	Thr	Lys	Leu	Asp	Lys	Val	Ala	Leu	Gly	Ala	Ala	Ala
	130					135					140				
Glu	Ala	Glu	Thr	Ile	Arg	Lys	Met	Ile	Val	Ala	Met	Ser	Gln	Asp	Pro
145					150					155					160
Arg	Val	Leu	Val	Ile	Lys	Val	Ala	Asp	Arg	Leu	His	Asn	Met	Arg	Thr
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Met	Arg	Phe	Leu	Pro	Pro	Glu	Lys	Gln	Ala	Lys	Lys	Ala	Arg	Gln	Thr
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Leu	Glu	Val	Ile	Ala	Pro	Leu	Ala	His	Arg	Leu	Gly	Met	Ala	Ser	Val
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gcc cgc agc ctc aca gga aac cgc gtt cgc acc aac cct gtg ctg gat 163
Ala Arg Ser Leu Thr Gly Asn Arg Val Arg Thr Asn Pro Val Leu Asp
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Pro Leu Leu Ser Ile His Arg Gln Phe His Pro Arg Ala Asp Val Gln
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Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu Val Asp Gly Val Thr
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aag ctc gac aaa gtc gca cta ggt gct gcc gcg gag gcc gaa acg att 499
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Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro Arg Val Leu Val Ile
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cct ttg gca cac cgc ctg ggc atg gcc agc gtg aaa tgg gaa ttg gaa 691

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Pro Leu Ala His Arg Leu Gly Met Ala Ser Val Lys Trp Glu Leu Glu
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 Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys Tyr Glu Glu Ile Val
 200 205 210

cgt ctt gtt gcc gac cgc gcg ccc tct aga gac cgg tac ctc aaa gaa 787
 Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp Arg Tyr Leu Lys Glu
 215 220 225

att att gat caa gtc acc ggt ggc ttg cgc gaa aac aac atc gcg gca 835
 Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu Asn Asn Ile Ala Ala
 230 235 240 245

gaa gtg ctt ggt cgn ccn aag cac tct ggt ctt tct ttc aaa aga 880
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 35 40 45

Leu His Asp Gly Val Ile Arg Lys Ser Gly Asp Pro Tyr Ile Thr His
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Pro Leu Ala Val Ala Thr Ile Ala Ala Glu Ile Gly Met Asp Thr Thr
 65 70 75 80

Thr Leu Val Ala Ala Leu Leu His Asp Thr Val Glu Asp Thr Asp Tyr
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Ser Leu Asp Asp Leu Thr Arg Asp Phe Gly Glu Glu Val Ala Arg Leu
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Val Asp Gly Val Thr Lys Leu Asp Lys Val Ala Leu Gly Ala Ala Ala
 115 120 125

Glu Ala Glu Thr Ile Arg Lys Met Ile Val Ala Met Ser Gln Asp Pro
 130 135 140

Arg Val Leu Val Ile Lys Val Ala Asp Arg Leu His Asn Met Arg Thr
 145 150 155 160

Met Arg Phe Leu Pro Pro Glu Lys Gln Ala Lys Lys Ala Arg Gln Thr
 165 170 175

Leu Glu Val Ile Ala Pro Leu Ala His Arg Leu Gly Met Ala Ser Val
 180 185 190
 Lys Trp Glu Leu Glu Asp Leu Ser Phe Ala Ile Leu Tyr Pro Lys Lys
 195 200 205
 Tyr Glu Glu Ile Val Arg Leu Val Ala Asp Arg Ala Pro Ser Arg Asp
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 Arg Tyr Leu Lys Glu Ile Ile Asp Gln Val Thr Gly Gly Leu Arg Glu
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 Ser Phe Lys Arg
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 Met Ile Val Arg Gly
 1 5
 cgt gat ttt gac gat att ttt gat ctt gtt ggc atc cgc ntc ctg gna 163
 Arg Asp Phe Asp Asp Ile Phe Asp Leu Val Gly Ile Arg Xaa Leu Xaa
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 Asp Asn Val Asn Asn Trp Val Arg Arg Xaa Arg Cys Arg Ala Leu Pro
 25 30 35
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Tyr Phe Ser Pro Ala Leu
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 Met Asn Thr Ala Ala
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tgg gca cac cgc cac cac gta cgc aaa ggc ggt gga att ccg tat gtc 163
 Trp Ala His Arg His His Val Arg Lys Gly Gly Gly Ile Pro Tyr Val
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agc cat ctt tat tca gtg atg tac ttg ctg gcc agc gtc act aat gat 211
 Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala Ser Val Thr Asn Asp
 25 30 35

gaa gat gtg ctc atc gcc ggg ctg ctc cac gac acc ctc gaa gac gta 259
 Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp Thr Leu Glu Asp Val
 40 45 50

ccc gag gaa tac aat tct gcc caa ctt gaa gct gat ttt ggt ccg cgg 307
 Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala Asp Phe Gly Pro Arg
 55 60 65

gtg cgc gag ttg gtg gaa gag ctc acc aaa cag ccc tta aaa agc tgg 355
 Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln Pro Leu Lys Ser Trp
 70 75 80 85

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 Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu Ser Ala Gly Ala Ser
 90 95 100

tta gag gct gtc tta atc tcc acc gca gat aaa ctg cat aat ctc atg 451
 Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys Leu His Asn Leu Met
 105 110 115

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 Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu Asp Leu Trp Gln Arg
 120 125 130

ttt aac gct ggc aaa gag cag caa atc tgg tgg tat agc gag gtt tat 547

Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp Tyr Ser Glu Val Tyr
 135 140 145

cag ata tct ctc cag cgc tta ggg ttc aat gag ttg aat aaa caa ctg 595
 Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu Leu Asn Lys Gln Leu
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 35 40 45

Thr Leu Glu Asp Val Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala
 50 55 60

Asp Phe Gly Pro Arg Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln
 65 70 75 80

Pro Leu Lys Ser Trp Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu
 85 90 95

Ser Ala Gly Ala Ser Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys
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Leu His Asn Leu Met Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu
 115 120 125

Asp Leu Trp Gln Arg Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp
 130 135 140

Tyr Ser Glu Val Tyr Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu
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 Met Tyr Pro Tyr Ser
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gac gca gac gct ttt cga cgc cag cct gag cgc gcc aag tcc agc caa 163
 Asp Ala Asp Ala Phe Arg Arg Gln Pro Glu Arg Ala Lys Ser Ser Gln
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ctg cgt acc agc gcc gta gac acc cgc agc gcg ttc gcc cgc gac cgg 211
 Leu Arg Thr Ser Ala Val Asp Thr Arg Ser Ala Phe Ala Arg Asp Arg
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gct cgc gtg ctg cat tct gct gct ctt cga cgc ctc gcg gat aaa acc 259
 Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg Leu Ala Asp Lys Thr
 40 45 50

caa gtg gtt ggc ccc aat gat ggt gat act ccg cgc acc cgg ctg acg 307
 Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro Arg Thr Arg Leu Thr
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cac tct ttg gaa gta gct caa att gca cgg gga atc gga gct gga ctg 355
 His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly Ile Gly Ala Gly Leu
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 Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly Leu Cys His Asp Ile
 90 95 100

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 Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn Ala Leu Asn Glu Val
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gct gcg gcc tgt gga gga ttt gag ggc aac gcc caa acc ttg cgt att 499
 Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala Gln Thr Leu Arg Ile
 120 125 130

ctc acg cgt ctg gag cca aaa att gtc tct gat gag ggg gag agc ttt 547
 Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp Glu Gly Glu Ser Phe
 135 140 145

ggg ctg aac ttg tcg cgg gct gct ctt gat gct gca tgt aag tat ccg 595
 Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala Ala Cys Lys Tyr Pro
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 Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn Lys Lys Tyr Ser Ala
 170 175 180

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 Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile Arg Gln Gly His Glu
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Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly Ile Val Ser Gly Arg	
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Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu Leu Ala Ala Leu Ala	
230 235 240 245	
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Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro Ala Glu Leu Ile Glu	
250 255 260	
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Gly Ala Ala Ser Leu Arg Glu Leu Pro Val Val Ala Ala Ala Ala Asp	
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Phe Asp Phe Ser Leu Arg Ser Tyr Ala Ala Leu Lys Ala Met Thr Ser	
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1027	
Glu Leu Val Gly Arg Tyr Val Gly Ser Thr Ile Glu Ser Thr Lys Lys	
295 300 305	
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1171	
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375 380 385	
gaa tcg gaa cag atc cgt gtg att gtt gat cag att gcg tcg atg acg	
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Glu Ser Glu Gln Ile Arg Val Ile Val Asp Gln Ile Ala Ser Met Thr	
390 395 400 405	
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Phe Leu Gly

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Phe Ala Arg Asp Arg Ala Arg Val Leu His Ser Ala Ala Leu Arg Arg
 35 40 45

Leu Ala Asp Lys Thr Gln Val Val Gly Pro Asn Asp Gly Asp Thr Pro
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Arg Thr Arg Leu Thr His Ser Leu Glu Val Ala Gln Ile Ala Arg Gly
 65 70 75 80

Ile Gly Ala Gly Leu Asp Leu Asp Pro Asp Leu Cys Asp Leu Ala Gly
 85 90 95

Leu Cys His Asp Ile Gly His Pro Pro Tyr Gly His Asn Gly Glu Asn
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Ala Leu Asn Glu Val Ala Ala Ala Cys Gly Gly Phe Glu Gly Asn Ala
 115 120 125

Gln Thr Leu Arg Ile Leu Thr Arg Leu Glu Pro Lys Ile Val Ser Asp
 130 135 140

Glu Gly Glu Ser Phe Gly Leu Asn Leu Ser Arg Ala Ala Leu Asp Ala
 145 150 155 160

Ala Cys Lys Tyr Pro Trp Ala Lys Thr Asn Ala Asp Gly Ser Val Asn
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Lys Lys Tyr Ser Ala Tyr Asp Glu Asp Ala Glu Ile Leu Ala Trp Ile
 180 185 190

Arg Gln Gly His Glu Asp Leu Arg Pro Pro Ile Glu Ala Gln Val Met
 195 200 205

Asp Phe Ser Asp Asp Ile Ala Tyr Ser Val His Asp Val Glu Asp Gly
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Ile Val Ser Gly Arg Ile Asp Leu Lys Val Leu Trp Asp Leu Val Glu
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Leu Ala Ala Leu Ala Asp Lys Gly Ala Ala Ala Phe Gly Gly Ser Pro

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 Met Ala Asn Lys Asn
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 Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile
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 aac ggt cgc ctg caa cag atc ccg gcg cgt ccc act gag gaa ttc acc 211
 Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr
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aac	ccg	gac	agc	atc	gag	gtc	gct	gtc	atc	cac	cgc	ccg	cac	tat	gat	307
Asn	Pro	Asp	Ser	Ile	Glu	Val	Ala	Val	Ile	His	Arg	Pro	His	Tyr	Asp	
	55					60					65					
gac	tgg	tcc	ctg	gcc	aag	ggc	aaa	gtc	gat	ccc	ggc	gag	tct	att	ccg	355
Asp	Trp	Ser	Leu	Ala	Lys	Gly	Lys	Val	Asp	Pro	Gly	Glu	Ser	Ile	Pro	
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Thr	Thr	Ala	Ala	Arg	Glu	Ile	Leu	Glu	Glu	Thr	Gly	Tyr	Asp	Ile	Arg	
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ctg	ggc	aag	ctg	atc	ggc	aag	gtt	act	tac	cct	gtg	ctc	gac	cga	acc	451
Leu	Gly	Lys	Leu	Ile	Gly	Lys	Val	Thr	Tyr	Pro	Val	Leu	Asp	Arg	Thr	
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Lys	Val	Val	Tyr	Tyr	Trp	Thr	Ala	Gln	Val	Leu	Gly	Gly	Glu	Phe	Val	
		120					125					130				
ccc	aac	gat	gaa	gtt	gat	gaa	atc	cgt	tgg	ctg	tct	gtt	gat	gaa	gca	547
Pro	Asn	Asp	Glu	Val	Asp	Glu	Ile	Arg	Trp	Leu	Ser	Val	Asp	Glu	Ala	
	135					140					145					
tgc	gag	ttg	ctc	agc	tac	caa	gta	gat	acc	gaa	gtt	ctg	gcc	aag	gca	595
Cys	Glu	Leu	Leu	Ser	Tyr	Gln	Val	Asp	Thr	Glu	Val	Leu	Ala	Lys	Ala	
	150				155					160					165	
gca	aag	cgt	ttc	cgc	act	cct	tcc	acc	act	cgg	gtg	ctg	tat	gtt	cgc	643
Ala	Lys	Arg	Phe	Arg	Thr	Pro	Ser	Thr	Thr	Arg	Val	Leu	Tyr	Val	Arg	
				170					175					180		
cat	gct	cat	gca	cat	ggt	cgc	caa	acc	tgg	ggt	ggc	gac	gac	aat	aag	691
His	Ala	His	Ala	His	Gly	Arg	Gln	Thr	Trp	Gly	Gly	Asp	Asp	Asn	Lys	
			185					190					195			
cgc	cca	ttg	gac	aaa	aag	ggg	cgt	cga	caa	gca	gaa	atg	ctc	gta	ccc	739
Arg	Pro	Leu	Asp	Lys	Lys	Gly	Arg	Arg	Gln	Ala	Glu	Met	Leu	Val	Pro	
		200					205					210				
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Met	Leu	Leu	Pro	Phe	Lys	Pro	Thr	Ala	Ile	Tyr	Ser	Ala	Val	Pro	Asp	
	215					220					225					
cgc	tgc	caa	gcc	acc	gcg	ctc	ccc	ctt	gcc	gat	gag	ctc	ggc	ctc	gac	835
Arg	Cys	Gln	Ala	Thr	Ala	Leu	Pro	Leu	Ala	Asp	Glu	Leu	Gly	Leu	Asp	
	230				235					240					245	
gtg	tcc	gtc	aac	cga	ctg	ttc	ggc	gac	gac	gcc	tgg	gaa	acc	gat	ccc	883
Val	Ser	Val	Asn	Arg	Leu	Phe	Gly	Asp	Asp	Ala	Trp	Glu	Thr	Asp	Pro	
				250				255						260		
gag	gcc	tgc	aag	aag	cgc	ttc	acc	gac	gtg	gtc	gcg	caa	ggc	ggc	gtg	931
Glu	Ala	Cys	Lys	Lys	Arg	Phe	Thr	Asp	Val	Val	Ala	Gln	Gly	Gly	Val	
			265					270					275			
ccg	atg	atc	gtt	ggg	cag	ggc	gac	atc	att	ccg	gaa	atg	atc	aaa	tgg	979

Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met Ile Lys Trp
 280 285 290

ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc aag gcg aaa
 1027

Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile Lys Ala Lys
 295 300 305

aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg ttc acc ggc
 1075

Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val Phe Thr Gly
 310 315 320 325

gct gat tac ctg gcg agt tcc ctg ccg gtt aaa taggagcgcg tttaaggcct
 1128

Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
 330 335

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<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 1038

Met Ala Asn Lys Asn Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp
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Ser Ala Met Leu Ile Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro
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Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp
 35 40 45

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His
 50 55 60

Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro
 65 70 75 80

Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr
 85 90 95

Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro
 100 105 110

Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu
 115 120 125

Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu
 130 135 140

Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu
 145 150 155 160

Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg
 165 170 175

Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly
 180 185 190

Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala
 195 200 205

Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr
 210 215 220

Ser Ala Val Pro Asp Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp
 225 230 235 240

Glu Leu Gly Leu Asp Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala
 245 250 255

Trp Glu Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val
 260 265 270

Ala Gln Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro
 275 280 285

Glu Met Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu
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Lys Ile Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp
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Gly Val Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(757)

<223> FRXA01024

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 Met Ala Asn Lys Asn
 1 5

aat aag cct cat gag gtg gac aaa gac caa gat tca gcc atg ctg atc 163
 Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile
 10 15 20

aac ggt cgc ctg caa cag atc ccg gcg cgt ccc act gag gaa ttc acc 211
 Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr
 25 30 35

cgc cca act ctt gca gca ggt gca gta ctg tgg cgc ggc gac atc acc 259
 Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr

40					45					50						
aac	ccg	gac	agc	atc	gag	gtc	gct	gtc	atc	cac	cgc	ccg	cac	tat	gat	307
Asn	Pro	Asp	Ser	Ile	Glu	Val	Ala	Val	Ile	His	Arg	Pro	His	Tyr	Asp	
55						60					65					
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Asp	Trp	Ser	Leu	Ala	Lys	Gly	Lys	Val	Asp	Pro	Gly	Glu	Ser	Ile	Pro	
70					75					80					85	
aca	acc	gcg	gcc	cgt	gaa	atc	ctt	gaa	gaa	act	ggc	tac	gac	atc	cgt	403
Thr	Thr	Ala	Ala	Arg	Glu	Ile	Leu	Glu	Glu	Thr	Gly	Tyr	Asp	Ile	Arg	
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ctg	ggc	aag	ctg	atc	ggc	aag	gtt	act	tac	cct	gtg	ctc	gac	cga	acc	451
Leu	Gly	Lys	Leu	Ile	Gly	Lys	Val	Thr	Tyr	Pro	Val	Leu	Asp	Arg	Thr	
			105					110					115			
aaa	gtg	gtc	tac	tac	tgg	act	gcc	cag	gtt	ctt	ggc	gga	gag	ttt	gtc	499
Lys	Val	Val	Tyr	Tyr	Trp	Thr	Ala	Gln	Val	Leu	Gly	Gly	Glu	Phe	Val	
		120					125					130				
ccc	aac	gat	gaa	gtt	gat	gaa	atc	cgt	tgg	ctg	tct	gtt	gat	gaa	gca	547
Pro	Asn	Asp	Glu	Val	Asp	Glu	Ile	Arg	Trp	Leu	Ser	Val	Asp	Glu	Ala	
	135					140					145					
tgc	gag	ttg	ctc	agc	tac	caa	gta	gat	acc	gaa	gtt	ctg	gcc	aag	gca	595
Cys	Glu	Leu	Leu	Ser	Tyr	Gln	Val	Asp	Thr	Glu	Val	Leu	Ala	Lys	Ala	
150					155					160					165	
gca	aag	cgt	ttc	cgc	act	cct	tcc	acc	act	cgg	gtg	ctg	tat	gtt	cgc	643
Ala	Lys	Arg	Phe	Arg	Thr	Pro	Ser	Thr	Thr	Arg	Val	Leu	Tyr	Val	Arg	
				170					175					180		
cat	gct	cat	gca	cat	ggc	cgc	caa	acc	tgg	ggc	ggc	gac	gac	aat	aag	691
His	Ala	His	Ala	His	Gly	Arg	Gln	Thr	Trp	Gly	Gly	Asp	Asp	Asn	Lys	
			185					190					195			
cgc	cca	ttg	gac	aaa	aag	ggg	cgt	cga	caa	gca	gaa	atg	ctc	gta	ccc	739
Arg	Pro	Leu	Asp	Lys	Lys	Gly	Arg	Arg	Gln	Ala	Glu	Met	Leu	Val	Pro	
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atg	ttg	ttg	ccc	ttc	aaa											757
Met	Leu	Leu	Pro	Phe	Lys											
		215														

<210> 1040

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 1040

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Ser	Ala	Met	Leu	Ile	Asn	Gly	Arg	Leu	Gln	Gln	Ile	Pro	Ala	Arg	Pro
			20					25					30		

Thr	Glu	Glu	Phe	Thr	Arg	Pro	Thr	Leu	Ala	Ala	Gly	Ala	Val	Leu	Trp
		35					40					45			

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His
 50 55 60
 Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro
 65 70 75 80
 Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr
 85 90 95
 Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro
 100 105 110
 Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu
 115 120 125
 Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu
 130 135 140
 Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu
 145 150 155 160
 Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg
 165 170 175
 Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly
 180 185 190
 Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala
 195 200 205
 Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys
 210 215

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> FRXA01027

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 Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met
 20 25 30
 atc aaa tgg ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc 144
 Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile
 35 40 45
 aag gcg aaa aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg 192
 Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val
 50 55 60

ttc acc ggc gct gat tac ctg gcg agt tcc ctg ccg gtt aaa 234
 Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
 65 70 75

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<210> 1042

<211> 78

<212> PRT

<213> Corynebacterium glutamicum

<400> 1042

Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln
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Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met
 20 25 30

Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile
 35 40 45

Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val
 50 55 60

Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
 65 70 75

<210> 1043

<211> 651

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(628)

<223> RXA01528

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gggtcgtagg tctccaacca ggaggcggtc caacacgagg gtg aat cag gcg tgg 115
 Val Asn Gln Ala Trp
 1 5

cag cag tcc cgt ttg gtt act tct gat gag act tcc gca ggt ggt ctc 163
 Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr Ser Ala Gly Gly Leu
 10 15 20

gtg gtg tca ggt ttg gct gag gcg gtc aac gct aac aat gag gtt gat 211
 Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala Asn Asn Glu Val Asp
 25 30 35

ctg tcg aag att tat gtt gcg ttg att ggt cgc ctt gat cgt cgt ggt 259
 Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg Leu Asp Arg Arg Gly
 40 45 50

cgt ttg ttg tgg tcg atg ccg aag ggc cat gtt gag cct ggt gag gat 307
 Arg Leu Leu Trp Ser Met Pro Lys Gly His Val Glu Pro Gly Glu Asp

55	60	65	
aag gct gcg act gct gag cgt gag gtg tgg gag gag acc ggc atc cac			355
Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu Glu Thr Gly Ile His			
70	75	80	85
ggt gag gtg ttc act gag ttg ggt gtg att gat tat tgg ttc gtt tcg			403
Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp Tyr Trp Phe Val Ser			
	90	95	100
gaa ggg aag cgg atc cat aag acg gtg cat cat cat ttg ttg cgt tat			451
Glu Gly Lys Arg Ile His Lys Thr Val His His His Leu Leu Arg Tyr			
	105	110	115
gtt gat ggc gat ttg aat gat gag gat cca gaa gtc act gag gtg gcg			499
Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu Val Thr Glu Val Ala			
	120	125	130
tgg att ccg gcg aat cag ttg att gag cat ttg gct ttt gcg gat gag			547
Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu Ala Phe Ala Asp Glu			
	135	140	145
cgg aag ttg gct agg cag gcg cat gat ttg ttg cct gag ttt gct ttg			595
Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu Pro Glu Phe Ala Leu			
	150	155	160
aag gaa aag gcg gag gga agg tcc acc cca agg tgattccgaa ccccaacccg			648
Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg			
	170	175	
aac			651

<210> 1044

<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 1044

Val Asn Gln Ala Trp Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr
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Ser Ala Gly Gly Leu Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala
20 25 30

Asn Asn Glu Val Asp Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg
35 40 45

Leu Asp Arg Arg Gly Arg Leu Leu Trp Ser Met Pro Lys Gly His Val
50 55 60

Glu Pro Gly Glu Asp Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu
65 70 75 80

Glu Thr Gly Ile His Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp
85 90 95

Tyr Trp Phe Val Ser Glu Gly Lys Arg Ile His Lys Thr Val His His
100 105 110

His Leu Leu Arg Tyr Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu

115	120	125
Val Thr Glu Val Ala Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu		
130	135	140
Ala Phe Ala Asp Glu Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu		
145	150	155
Pro Glu Phe Ala Leu Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg		
165	170	175

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 <211> 541
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(541)
 <223> RXA00072

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aagaatctct cgaaagacac aaaagagggtg agtcgcaaca atg agc ttt caa cta 115
 Met Ser Phe Gln Leu
 1 5

gtt aac gcc ctg aaa aat act ggt tcg gta aaa gat ccc gag atc tca 163
 Val Asn Ala Leu Lys Asn Thr Gly Ser Val Lys Asp Pro Glu Ile Ser
 10 15 20

ccc gaa gga cct cgc acg acc aca ccg ttg tca cca gag gta gca aaa 211
 Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser Pro Glu Val Ala Lys
 25 30 35

cat aac gag gaa ctc gtc gaa aag cat gct gct gcg ttg tat gac gcc 259
 His Asn Glu Glu Leu Val Glu Lys His Ala Ala Ala Leu Tyr Asp Ala
 40 45 50

agc gcg caa gag atc ctg gaa tgg aca gcc gag cac gcg ccg ggc gct 307
 Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu His Ala Pro Gly Ala
 55 60 65

att gca gtg acc ttg agc atg gaa aac acc gtg ctg gcg gag ctg gct 355
 Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val Leu Ala Glu Leu Ala
 70 75 80 85

gcg cgg cac ctg ccg gaa gct gat ttc ctc ttt ttg gac acc ggt tac 403
 Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe Leu Asp Thr Gly Tyr
 90 95 100

cac ttc aag gag acc ctt gaa gtt gcc cgt cag gta gat gag cgc tat 451
 His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln Val Asp Glu Arg Tyr
 105 110 115

tcc cag aag ctt gtc acc gcg ctg ccg atc ctc aag cgc acg gag cag 499

Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu Lys Arg Thr Glu Gln
 120 125 130

gat tcc att tat ggt ctc aac ctg tac cgc agc aac cca gcg 541
 Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser Asn Pro Ala
 135 140 145

<210> 1046

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 1046

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Asp Pro Glu Ile Ser Pro Glu Gly Pro Arg Thr Thr Thr Pro Leu Ser
 20 25 30

Pro Glu Val Ala Lys His Asn Glu Glu Leu Val Glu Lys His Ala Ala
 35 40 45

Ala Leu Tyr Asp Ala Ser Ala Gln Glu Ile Leu Glu Trp Thr Ala Glu
 50 55 60

His Ala Pro Gly Ala Ile Ala Val Thr Leu Ser Met Glu Asn Thr Val
 65 70 75 80

Leu Ala Glu Leu Ala Ala Arg His Leu Pro Glu Ala Asp Phe Leu Phe
 85 90 95

Leu Asp Thr Gly Tyr His Phe Lys Glu Thr Leu Glu Val Ala Arg Gln
 100 105 110

Val Asp Glu Arg Tyr Ser Gln Lys Leu Val Thr Ala Leu Pro Ile Leu
 115 120 125

Lys Arg Thr Glu Gln Asp Ser Ile Tyr Gly Leu Asn Leu Tyr Arg Ser
 130 135 140

Asn Pro Ala
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<210> 1047

<211> 1002

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(979)

<223> RXA01878

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 Met Glu Glu Pro Ser
 1 5

ggc	gca	cag	ctg	ctc	ggc	ccg	gta	gaa	atc	cgt	gcg	ctg	gca	gaa	aag	163
Gly	Ala	Gln	Leu	Leu	Gly	Pro	Val	Glu	Ile	Arg	Ala	Leu	Ala	Glu	Lys	
			10					15						20		
ctc	gac	gtc	aca	cca	act	aag	aag	ttg	ggg	cag	aac	ttt	gtt	cac	gat	211
Leu	Asp	Val	Thr	Pro	Thr	Lys	Lys	Leu	Gly	Gln	Asn	Phe	Val	His	Asp	
			25					30					35			
ccc	aac	acg	gtg	cgt	cgc	att	gtt	gct	gcg	gca	gag	ctc	acc	cca	aac	259
Pro	Asn	Thr	Val	Arg	Arg	Ile	Val	Ala	Ala	Ala	Glu	Leu	Thr	Pro	Asn	
		40					45					50				
gac	cac	gtg	gtg	gaa	gtt	ggc	cct	ggc	ctg	ggc	tct	ctg	acc	ctt	gcc	307
Asp	His	Val	Val	Glu	Val	Gly	Pro	Gly	Leu	Gly	Ser	Leu	Thr	Leu	Ala	
	55					60					65					
ctg	gtg	gaa	tct	gct	gct	tca	gta	act	gcg	gtg	gaa	att	gat	ccc	cgt	355
Leu	Val	Glu	Ser	Ala	Ala	Ser	Val	Thr	Ala	Val	Glu	Ile	Asp	Pro	Arg	
70				75					80						85	
ttg	gct	gcg	gaa	ttg	ccg	gag	act	ttt	cag	tgg	cgc	gcg	ccg	gcc	ctt	403
Leu	Ala	Ala	Glu	Leu	Pro	Glu	Thr	Phe	Gln	Trp	Arg	Ala	Pro	Ala	Leu	
			90					95					100			
gct	cac	aag	ttg	agc	atc	gtg	ctg	aaa	gac	gcc	ctg	aag	gtt	caa	caa	451
Ala	His	Lys	Leu	Ser	Ile	Val	Leu	Lys	Asp	Ala	Leu	Lys	Val	Gln	Gln	
			105					110					115			
tcc	gat	atg	gct	gtt	caa	ccc	acc	gcc	ttg	gtg	gct	aac	ttg	ccg	tac	499
Ser	Asp	Met	Ala	Val	Gln	Pro	Thr	Ala	Leu	Val	Ala	Asn	Leu	Pro	Tyr	
		120					125					130				
aac	gtc	tct	gtc	cct	gtc	ttg	ttg	cac	atg	atg	gag	gag	ttt	ccc	acc	547
Asn	Val	Ser	Val	Pro	Val	Leu	Leu	His	Met	Met	Glu	Glu	Phe	Pro	Thr	
	135					140					145					
atc	aac	aag	gtg	ctt	gtc	atg	gtg	cag	gca	gag	gtt	gct	gat	cgt	ttg	595
Ile	Asn	Lys	Val	Leu	Val	Met	Val	Gln	Ala	Glu	Val	Ala	Asp	Arg	Leu	
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gct	gcg	gat	cca	gga	tcg	aag	att	tat	ggc	gtg	cct	agc	gtg	aag	gcg	643
Ala	Ala	Asp	Pro	Gly	Ser	Lys	Ile	Tyr	Gly	Val	Pro	Ser	Val	Lys	Ala	
				170					175					180		
tcc	ttc	tac	ggc	cca	gtt	act	cgc	gcc	ggg	tcg	att	ggc	aag	aat	gtc	691
Ser	Phe	Tyr	Gly	Pro	Val	Thr	Arg	Ala	Gly	Ser	Ile	Gly	Lys	Asn	Val	
			185					190					195			
ttt	tgg	cca	gct	cca	aag	atc	gaa	tcc	ggc	ttg	gtg	aag	atc	gtg	cgc	739
Phe	Trp	Pro	Ala	Pro	Lys	Ile	Glu	Ser	Gly	Leu	Val	Lys	Ile	Val	Arg	
		200				205						210				
gaa	gac	acc	gcg	tgg	aag	cag	gac	gat	gag	acg	cgt	aag	aag	gtg	tgg	787
Glu	Asp	Thr	Ala	Trp	Lys	Gln	Asp	Asp	Glu	Thr	Arg	Lys	Lys	Val	Trp	
	215					220					225					
ccg	atc	att	gat	gct	gct	ttc	ttg	cag	cgc	cgt	aaa	acc	cta	aga	gct	835
Pro	Ile	Ile	Asp	Ala	Ala	Phe	Leu	Gln	Arg	Arg	Lys	Thr	Leu	Arg	Ala	
230				235					240						245	

gcg ctt tct gga cac tac ggt tct ggc cag gca gct gag gaa gct ttg 883
 Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala Ala Glu Glu Ala Leu
 250 255 260

cgg gcc gct gat att gat cca acg ctt cgt ggc gaa aag ctt gat gtc 931
 Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly Glu Lys Leu Asp Val
 265 270 275

act gac tat gtg cgc cta gct ggg gtg ttg cag caa aag gat gag aag 979
 Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln Gln Lys Asp Glu Lys
 280 285 290

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 1002

<210> 1048

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 1048

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Ala Leu Ala Glu Lys Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln
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Asn Phe Val His Asp Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala
 35 40 45

Glu Leu Thr Pro Asn Asp His Val Val Glu Val Gly Pro Gly Leu Gly
 50 55 60

Ser Leu Thr Leu Ala Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val
 65 70 75 80

Glu Ile Asp Pro Arg Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp
 85 90 95

Arg Ala Pro Ala Leu Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala
 100 105 110

Leu Lys Val Gln Gln Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val
 115 120 125

Ala Asn Leu Pro Tyr Asn Val Ser Val Pro Val Leu Leu His Met Met
 130 135 140

Glu Glu Phe Pro Thr Ile Asn Lys Val Leu Val Met Val Gln Ala Glu
 145 150 155 160

Val Ala Asp Arg Leu Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val
 165 170 175

Pro Ser Val Lys Ala Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser
 180 185 190

Ile Gly Lys Asn Val Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu
 195 200 205

Val Lys Ile Val Arg Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr
 210 215 220

Arg Lys Lys Val Trp Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg
 225 230 235 240

Lys Thr Leu Arg Ala Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala
 245 250 255

Ala Glu Glu Ala Leu Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly
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Glu Lys Leu Asp Val Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln
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Gln Lys Asp Glu Lys
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 Val Gln Lys Asp Ser
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gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu
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att gac atc tac gac acc tcg acc aaa ctg gcc aaa gaa acc ctc aac 211
 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn
 25 30 35

aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr
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gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly
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tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg
 70 75 80 85

gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat 403
 Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn
 90 95 100

tat ccc tgc aag att tac gta tct gag tca gat atc cgc atc cca ccg 451

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Glu	Tyr	Ile	Arg	Gly	Ala	Pro	Ser	Ala	Thr	Glu	Ala	Arg	Arg	Ala	Gly		
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gat	gtt	gca	gat	atc	atc	cca	cgc	ccc	acc	ctg	gat	gaa	gtc	cac	gac	547	
Asp	Val	Ala	Asp	Ile	Ile	Pro	Arg	Pro	Thr	Leu	Asp	Glu	Val	His	Asp		
	135					140					145						
gca	att	atc	gac	ggc	gac	tgg	cac	gcc	ttc	aac	ggc	ccc	gaa	ctc	ccg	595	
Ala	Ile	Ile	Asp	Gly	Asp	Trp	His	Ala	Phe	Asn	Gly	Pro	Glu	Leu	Pro		
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Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val	Gln	Lys	Tyr	Ile	Leu		
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Phe	Thr	Asn	Tyr	Ala	Met	His	Thr	Thr	Glu	Phe	Val	His	Phe	Ala	Met		
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Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val	Gly	Leu	Ser	Leu	Pro		
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Asn	Gly	Gln	Val	Ile	Asp	Arg	Glu	Thr	Ala	Thr	Ser	Leu	Gly	Thr	Glu		
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Thr	Leu	Asp	Leu	Thr	Ser	Arg	Phe	Gln	Met	Pro	Arg	Tyr	Asp	Leu	Ile		
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Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn	Ile	Gly	Val	Gly	Pro		
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tcc	aat	gca	aaa	act	atc	acc	gac	tgc	ctt	gct	gtg	ctc	cgc	cca	gaa	979	
Ser	Asn	Ala	Lys	Thr	Ile	Thr	Asp	Cys	Leu	Ala	Val	Leu	Arg	Pro	Glu		
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gcc	tgg	gtg	atg	atc	ggc	cac	tgt	gct	ggc	atg	gac	gcc	cgc	atg	cgc		
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Ala	Trp	Val	Met	Ile	Gly	His	Cys	Ala	Gly	Met	Asp	Ala	Arg	Met	Arg		
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1075																	
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1123																	
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1171

Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu Ile Tyr Gly Ser Asp
345 350 355

aac agc ctc atg cgc acc ggt acg gtc tta tcc acc gac gac cga aac
1219

Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser Thr Asp Asp Arg Asn
360 365 370

tgg gaa tgg cac acc cca gaa aac ctc tgg aac tgg ctc aaa gga tcc
1267

Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn Trp Leu Lys Gly Ser
375 380 385

acc gcc gca gct gtt gac atg gaa tct tcc acc ttg gcc acc aac gga
1315

Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr Leu Ala Thr Asn Gly
390 395 400 405

tat cga ttc cgc att cca tac ggc acc ctg ctg agc gtc tct gac ctg
1363

Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu Ser Val Ser Asp Leu
410 415 420

cca cta cac gca gtg ccg aaa ctt tcc gcg caa gcg cag gcg ttt tac
1411

Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln Ala Gln Ala Phe Tyr
425 430 435

ttc aac tcc aag gaa gcc cac gtc atg tgt gct gtt cgt gca atg gaa
1459

Phe Asn Ser Lys Glu Ala His Val Met Cys Ala Val Arg Ala Met Glu
440 445 450

tac ctg gca gta gat cct gaa cgg ttg cgt acc cgt aaa ctg cgc agg
1507

Tyr Leu Ala Val Asp Pro Glu Arg Leu Arg Thr Arg Lys Leu Arg Arg
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<212> PRT

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35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
 50 55 60
 Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
 65 70 75 80
 Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
 85 90 95
 Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
 100 105 110
 Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
 115 120 125
 Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
 130 135 140
 Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
 145 150 155 160
 Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
 165 170 175
 Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
 180 185 190
 Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
 195 200 205
 Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
 210 215 220
 Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
 225 230 235 240
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
 245 250 255
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
 260 265 270
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
 275 280 285
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
 290 295 300
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
 305 310 315 320
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
 325 330 335
 Pro Ala Ile Pro Glu Ile Gln Lys Ala Leu Glu Ala Ser Val Asp Glu
 340 345 350
 Ile Tyr Gly Ser Asp Asn Ser Leu Met Arg Thr Gly Thr Val Leu Ser
 355 360 365

Thr Asp Asp Arg Asn Trp Glu Trp His Thr Pro Glu Asn Leu Trp Asn
 370 375 380
 Trp Leu Lys Gly Ser Thr Ala Ala Ala Val Asp Met Glu Ser Ser Thr
 385 390 395 400
 Leu Ala Thr Asn Gly Tyr Arg Phe Arg Ile Pro Tyr Gly Thr Leu Leu
 405 410 415
 Ser Val Ser Asp Leu Pro Leu His Ala Val Pro Lys Leu Ser Ala Gln
 420 425 430
 Ala Gln Ala Phe Tyr Phe Asn Ser Lys Glu Ala His Val Met Cys Ala
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 Val Gln Lys Asp Ser 5
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 gtg gtg cgc atg gaa gca aca acg atc gat gac gca atc gcg aag ctc 163
 Val Val Arg Met Glu Ala Thr Thr Ile Asp Asp Ala Ile Ala Lys Leu 20
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 Ile Asp Ile Tyr Asp Thr Ser Thr Lys Leu Ala Lys Glu Thr Leu Asn 35
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 aat gag gac tac gcc gca tac gcc gat gtt gtt tac ccc aaa ctc acc 259
 Asn Glu Asp Tyr Ala Ala Tyr Ala Asp Val Val Tyr Pro Lys Leu Thr 50
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 gtt gac gtg ctg gaa tgg aaa ccc atc gac cgc acc gaa ccc ttc ggc 307
 Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg Thr Glu Pro Phe Gly 65
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 tat gtg gat cga gcc ggg cga tac tcc gcc acc ttg tcc aaa cca cgc 355
 Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr Leu Ser Lys Pro Arg 85
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 gtg att gag cgt tac ctc cgc gaa caa ctc gag cgt ctc acc agt aat 403
 Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu Arg Leu Thr Ser Asn

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Tyr	Pro	Cys	Lys	Ile	Tyr	Val	Ser	Glu	Ser	Asp	Ile	Arg	Ile	Pro	Pro		
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Glu	Tyr	Ile	Arg	Gly	Ala	Pro	Ser	Ala	Thr	Glu	Ala	Arg	Arg	Ala	Gly		
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Ala	Ile	Ile	Asp	Gly	Asp	Trp	His	Ala	Phe	Asn	Gly	Pro	Glu	Leu	Pro		
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ctt	ttc	cac	ttc	ggg	ccg	caa	cgc	ttc	gac	atc	gcc	tgc	gcc	cgc	atc	643	
Leu	Phe	His	Phe	Gly	Pro	Gln	Arg	Phe	Asp	Ile	Ala	Cys	Ala	Arg	Ile		
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Glu	His	Tyr	Thr	Gly	Ile	Asn	Val	Glu	His	Val	Gln	Lys	Tyr	Ile	Leu		
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tcc	gaa	ctc	acc	tcg	gaa	gac	tcc	cgc	tac	gtg	ggc	cta	tcc	ttg	cca	787	
Ser	Glu	Leu	Thr	Ser	Glu	Asp	Ser	Arg	Tyr	Val	Gly	Leu	Ser	Leu	Pro		
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aac	ggg	cag	gta	att	gac	cga	gag	acc	gcc	acc	agc	ctc	ggc	acg	gaa	835	
Asn	Gly	Gln	Val	Ile	Asp	Arg	Glu	Thr	Ala	Thr	Ser	Leu	Gly	Thr	Glu		
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acc	ctt	gat	ctg	act	agc	cgt	ttc	caa	atg	cct	cgt	tac	gat	ctc	atc	883	
Thr	Leu	Asp	Leu	Thr	Ser	Arg	Phe	Gln	Met	Pro	Arg	Tyr	Asp	Leu	Ile		
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acc	gaa	gcc	ggc	gac	ggc	att	acc	att	atc	aac	atc	ggc	gtg	ggc	cca	931	
Thr	Glu	Ala	Gly	Asp	Gly	Ile	Thr	Ile	Ile	Asn	Ile	Gly	Val	Gly	Pro		
			265					270								275	
tcc	aat	gca	aaa	act	atc	acc	gac	tgc	ctt	gct	gtg	ctc	cgc	cca	gaa	979	
Ser	Asn	Ala	Lys	Thr	Ile	Thr	Asp	Cys	Leu	Ala	Val	Leu	Arg	Pro	Glu		
			280					285								290	
gcc	tgg	gtg	atg	atc	ggc	cac	tgt	gct	ggc	atg	gac	gcc	cgc	atg	cgc	1027	
Ala	Trp	Val	Met	Ile	Gly	His	Cys	Ala	Gly	Met	Asp	Ala	Arg	Met	Arg		
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atc	ggc	gac	ctc	atc	ctt	ggc	aac	gcc	tac	cag	cgc	gaa	gac	cac	att	1075	
Ile	Gly	Asp	Leu	Ile	Leu	Gly	Asn	Ala	Tyr	Gln	Arg	Glu	Asp	His	Ile		
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																325	

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 1123
 Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile Pro Ala Ile Pro Glu
 330 335 340

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 35 40 45

Tyr Pro Lys Leu Thr Val Asp Val Leu Glu Trp Lys Pro Ile Asp Arg
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Thr Glu Pro Phe Gly Tyr Val Asp Arg Ala Gly Arg Tyr Ser Ala Thr
 65 70 75 80

Leu Ser Lys Pro Arg Val Ile Glu Arg Tyr Leu Arg Glu Gln Leu Glu
 85 90 95

Arg Leu Thr Ser Asn Tyr Pro Cys Lys Ile Tyr Val Ser Glu Ser Asp
 100 105 110

Ile Arg Ile Pro Pro Glu Tyr Ile Arg Gly Ala Pro Ser Ala Thr Glu
 115 120 125

Ala Arg Arg Ala Gly Asp Val Ala Asp Ile Ile Pro Arg Pro Thr Leu
 130 135 140

Asp Glu Val His Asp Ala Ile Ile Asp Gly Asp Trp His Ala Phe Asn
 145 150 155 160

Gly Pro Glu Leu Pro Leu Phe His Phe Gly Pro Gln Arg Phe Asp Ile
 165 170 175

Ala Cys Ala Arg Ile Glu His Tyr Thr Gly Ile Asn Val Glu His Val
 180 185 190

Gln Lys Tyr Ile Leu Phe Thr Asn Tyr Ala Met His Thr Thr Glu Phe
 195 200 205

Val His Phe Ala Met Ser Glu Leu Thr Ser Glu Asp Ser Arg Tyr Val
 210 215 220

Gly Leu Ser Leu Pro Asn Gly Gln Val Ile Asp Arg Glu Thr Ala Thr
 225 230 235 240
 Ser Leu Gly Thr Glu Thr Leu Asp Leu Thr Ser Arg Phe Gln Met Pro
 245 250 255
 Arg Tyr Asp Leu Ile Thr Glu Ala Gly Asp Gly Ile Thr Ile Ile Asn
 260 265 270
 Ile Gly Val Gly Pro Ser Asn Ala Lys Thr Ile Thr Asp Cys Leu Ala
 275 280 285
 Val Leu Arg Pro Glu Ala Trp Val Met Ile Gly His Cys Ala Gly Met
 290 295 300
 Asp Ala Arg Met Arg Ile Gly Asp Leu Ile Leu Gly Asn Ala Tyr Gln
 305 310 315 320
 Arg Glu Asp His Ile Leu Asn Thr Arg Ile Pro Leu Gly Asn Pro Ile
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 <223> RXN01240

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 Met Ser Asp Asn Thr
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 ctc tcc caa ttt ggc agt tac tac cac gaa ttc cga cgt gcc cat ccc 163
 Leu Ser Gln Phe Gly Ser Tyr Tyr His Glu Phe Arg Arg Ala His Pro
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 atg gcc gac gtc gaa ttc ctc cta gca att gaa gaa tta ctt acg gac 211
 Met Ala Asp Val Glu Phe Leu Leu Ala Ile Glu Glu Leu Leu Thr Asp
 25 30 35
 ggt ggt gtc acc ttc gat cgc gtc acc aca cgc atc aaa gaa tgg tca 259
 Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg Ile Lys Glu Trp Ser
 40 45 50
 agc ctg aaa gcc aag gct cgc aag cgt cgc aac gat ggc tcg ttg atc 307
 Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn Asp Gly Ser Leu Ile
 55 60 65

tac cct gat ccg cgc aaa gac atc cac gac atg atc ggt gtt cgg atc	355
Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met Ile Gly Val Arg Ile	
70 75 80 85	
acc acg tac cac tcc acg gaa ata ccc gtg gcc cta aaa gtg ctc caa	403
Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala Leu Lys Val Leu Gln	
90 95 100	
gac tcc ttc atc gtc cac aaa tcc gta gac aaa gcc gct gaa act cgc	451
Asp Ser Phe Ile Val His Lys Ser Val Asp Lys Ala Ala Glu Thr Arg	
105 110 115	
atc tca ggc ggc ttt ggt tac ggc tcc cac cac ctg att ctg gaa gtc	499
Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His Leu Ile Leu Glu Val	
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gat gac acc tcc gat gac ctc cag gac tac aaa ggc ctc gtc ttt gaa	547
Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys Gly Leu Val Phe Glu	
135 140 145	
gtt cag gtg cgc acc gtg ctg caa cac gcc tgg gca gag ttc gaa cac	595
Val Gln Val Arg Thr Val Leu Gln His Ala Trp Ala Glu Phe Glu His	
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Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn Pro Glu Asp Phe Ser	
170 175 180	
gca gaa gta gac cgc atg ttc acc ctc gct gcc gga ctc atc gaa tta	691
Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala Gly Leu Ile Glu Leu	
185 190 195	
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Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu Lys Glu Thr Ser Arg	
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gtt gct gat gaa tcc gtc gaa ctc acc gca gag aca ctt ccc ggc gtt	787
Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu Thr Leu Pro Gly Val	
215 220 225	
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Leu Ala Met Leu Ile Gly Asn Arg Phe Pro Arg Pro Arg Ser Thr Asn	
230 235 240 245	
tac cgc ttc ctc gaa gac atc ctg gtg gcc aac tcc att acc tct gtg	883
Tyr Arg Phe Leu Glu Asp Ile Leu Val Ala Asn Ser Ile Thr Ser Val	
250 255 260	
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Val Gln Leu Arg Glu Leu Leu Asn Pro Thr Asp Ile Glu Val Leu Leu	
265 270 275	
aaa gta atg aac tac cgc ttc cac cca ggc cag atc cgc atc atc gac	979
Lys Val Met Asn Tyr Arg Phe His Pro Gly Gln Ile Arg Ile Ile Asp	
280 285 290	
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295 300 305	

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1075

Ala Thr Asp Ser Gln Pro Leu Asn Ala Lys Arg His Arg Gln Leu Lys
310 315 320 325

cgc aag cta gag ctc atg acc caa gct cat ctt gtg gaa cca cca aac
1123

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<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 1054

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20 25 30

Glu Leu Leu Thr Asp Gly Gly Val Thr Phe Asp Arg Val Thr Thr Arg
35 40 45

Ile Lys Glu Trp Ser Ser Leu Lys Ala Lys Ala Arg Lys Arg Arg Asn
50 55 60

Asp Gly Ser Leu Ile Tyr Pro Asp Pro Arg Lys Asp Ile His Asp Met
65 70 75 80

Ile Gly Val Arg Ile Thr Thr Tyr His Ser Thr Glu Ile Pro Val Ala
85 90 95

Leu Lys Val Leu Gln Asp Ser Phe Ile Val His Lys Ser Val Asp Lys
100 105 110

Ala Ala Glu Thr Arg Ile Ser Gly Gly Phe Gly Tyr Gly Ser His His
115 120 125

Leu Ile Leu Glu Val Asp Asp Thr Ser Asp Asp Leu Gln Asp Tyr Lys
130 135 140

Gly Leu Val Phe Glu Val Gln Val Arg Thr Val Leu Gln His Ala Trp
145 150 155 160

Ala Glu Phe Glu His Asp Ile Arg Tyr Lys Arg Ala Asp Val Ser Asn
165 170 175

Pro Glu Asp Phe Ser Ala Glu Val Asp Arg Met Phe Thr Leu Ala Ala
180 185 190

Gly Leu Ile Glu Leu Ala Asp Gln Gln Phe Asp Gln Ile Ala Ala Leu
195 200 205

Lys Glu Thr Ser Arg Val Ala Asp Glu Ser Val Glu Leu Thr Ala Glu

210					215					220					
Thr	Leu	Pro	Gly	Val	Leu	Ala	Met	Leu	Ile	Gly	Asn	Arg	Phe	Pro	Arg
225					230					235					240
Pro	Arg	Ser	Thr	Asn	Tyr	Arg	Phe	Leu	Glu	Asp	Ile	Leu	Val	Ala	Asn
				245					250					255	
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			260					265					270		
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		275					280					285			
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	290					295					300				
Ile	Asp	Ala	Thr	Val	Ala	Thr	Asp	Ser	Gln	Pro	Leu	Asn	Ala	Lys	Arg
305					310					315					320
His	Arg	Gln	Leu	Lys	Arg	Lys	Leu	Glu	Leu	Met	Thr	Gln	Ala	His	Leu
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Val	Glu	Pro	Pro	Asn											
				340											

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 <213> Corynebacterium glutamicum

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 <222> (101)..(1234)
 <223> RXN02008

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 Val Tyr Ala Ala Ile
 1 5
 ggt gtc gtg cac tcc ctg ttc aat gct ctg cct ggc cga ttc aaa gac 163
 Gly Val Val His Ser Leu Phe Asn Ala Leu Pro Gly Arg Phe Lys Asp
 10 15 20
 tat att tca gcc ccg cgc ttc ggt gtc tac caa tcc ctg cac acc acc 211
 Tyr Ile Ser Ala Pro Arg Phe Gly Val Tyr Gln Ser Leu His Thr Thr
 25 30 35
 gtg atg gga cct ggc ggt aag cct ctg gaa gtt cag gca cgt acc cac 259
 Val Met Gly Pro Gly Gly Lys Pro Leu Glu Val Gln Ala Arg Thr His
 40 45 50
 gac atg cac tac aac gcc gaa ttc ggc att gca gcg cac tgg cga tac 307
 Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala Ala His Trp Arg Tyr
 55 60 65
 aaa gaa acc aaa ggc agc cac agt ggc gag caa gcc gaa gtg gat caa 355

Lys 70	Glu	Thr	Lys	Gly	Ser 75	His	Ser	Gly	Glu	Gln 80	Ala	Glu	Val	Asp	Gln 85	
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Met	Ala	Trp	Met	Arg 90	Gln	Leu	Leu	Asp	Trp 95	Gln	Lys	Glu	Ala	Ala	Asp 100	
ccc	aac	gag	ttc	ctg	gac	agc	ctg	cgc	tac	gat	ctg	act	tcc	aag	cag	451
Pro	Asn	Glu	Phe 105	Leu	Asp	Ser	Leu	Arg 110	Tyr	Asp	Leu	Thr	Ser	Lys	Gln	
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Ser	Thr 135	Pro	Val	Asp	Phe	Ala 140	Tyr	Ala	Val	His	Thr 145	Glu	Val	Gly	His	
cgc	tgc	atc	ggc	gcc	aaa	atc	aac	ggc	aaa	ctg	gtc	gct	ttg	gaa	acg	595
Arg	Cys	Ile	Gly	Ala	Lys 155	Ile	Asn	Gly	Lys	Leu 160	Val	Ala	Leu	Glu	Thr 165	
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Lys	Leu	Lys	Ser 170	Gly	Asp	Arg	Val	Glu	Val 175	Phe	Thr	Ser	Lys	Asp	Gln 180	
aac	gct	ggc	cca	agt	agg	gga	tgg	caa	gaa	ttt	gtt	gtc	tca	cct	cgt	691
Asn	Ala	Gly 185	Pro	Ser	Arg	Gly	Trp	Gln	Glu	Phe	Val	Val	Ser	Pro	Arg	
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Ala	Lys 200	Ala	Lys	Ile	Arg	Gln	Trp 205	Phe	Ala	Lys	Glu	Arg	Arg	Glu	Glu	
tac	cta	gaa	gcc	gga	cgc	gat	gcg	ctg	gca	gca	gtt	att	cag	cgt	ggc	787
Tyr	Leu 215	Glu	Ala	Gly	Arg	Asp 220	Ala	Leu	Ala	Ala	Val 225	Ile	Gln	Arg	Gly	
ggc	ctg	cca	atg	cac	cgc	ttg	ttc	acc	gcg	tcc	tcc	atg	aag	acg	gtg	835
Gly	Leu	Pro	Met	His	Arg 235	Leu	Phe	Thr	Ala	Ser 240	Ser	Met	Lys	Thr	Val 245	
gca	aca	gag	ctg	cac	tac	cca	gat	gta	gat	gcg	ctc	tac	aca	gcc	atc	883
Ala	Thr	Glu	Leu	His 250	Tyr	Pro	Asp	Val	Asp 255	Ala	Leu	Tyr	Thr	Ala	Ile 260	
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Gly	Ser	Gly 265	Ser	Val	Ser	Ala	Gln	His 270	Val	Val	Asn	Arg	Leu	Met	Ala	
atc	ttt	ggt	gac	gaa	gaa	gat	gcc	gaa	gac	gca	ttg	gtt	gca	cgc	acc	979
Ile	Phe	Gly 280	Asp	Glu	Glu	Asp	Ala 285	Glu	Asp	Ala	Leu	Val	Ala	Arg	Thr	
cca	ttc	agc	gag	ctg	gtc	aac	tcc	cgt	gcc	acc	acg	gaa	agc	agc	acc	
Pro 1027	Phe	Ser	Glu	Leu	Val	Asn	Ser	Arg	Ala	Thr	Thr 305	Glu	Ser	Ser	Thr	

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1075
Gly Ile Leu Val Glu Gly Ser Pro Asp Val Met Ala Lys Leu Ala Lys
310 315 320 325

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1123
Cys Cys Met Pro Val Pro Gly Asp Glu Ile Phe Gly Phe Val Thr Arg
330 335 340

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1171
Gly Gly Gly Val Ser Val His Arg Thr Asp Cys Thr Asn Val Glu Lys
345 350 355

ctc aaa gaa gag cca gaa cgc att gtc tcc gtc tcc tgg gct tcg gaa
1219
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375

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<213> Corynebacterium glutamicum

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35 40 45
Gln Ala Arg Thr His Asp Met His Tyr Asn Ala Glu Phe Gly Ile Ala
50 55 60
Ala His Trp Arg Tyr Lys Glu Thr Lys Gly Ser His Ser Gly Glu Gln
65 70 75 80
Ala Glu Val Asp Gln Met Ala Trp Met Arg Gln Leu Leu Asp Trp Gln
85 90 95
Lys Glu Ala Ala Asp Pro Asn Glu Phe Leu Asp Ser Leu Arg Tyr Asp
100 105 110
Leu Thr Ser Lys Gln Ile Phe Val Phe Thr Pro Lys Gly Asp Val Val
115 120 125
Asn Leu Pro Val Asn Ser Thr Pro Val Asp Phe Ala Tyr Ala Val His
130 135 140
Thr Glu Val Gly His Arg Cys Ile Gly Ala Lys Ile Asn Gly Lys Leu
145 150 155 160

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Val Ala Leu Glu Thr Lys Leu Lys Ser Gly Asp Arg Val Glu Val Phe
      165                      170                      175
Thr Ser Lys Asp Gln Asn Ala Gly Pro Ser Arg Gly Trp Gln Glu Phe
      180                      185                      190
Val Val Ser Pro Arg Ala Lys Ala Lys Ile Arg Gln Trp Phe Ala Lys
      195                      200                      205
Glu Arg Arg Glu Glu Tyr Leu Glu Ala Gly Arg Asp Ala Leu Ala Ala
      210                      215                      220
Val Ile Gln Arg Gly Gly Leu Pro Met His Arg Leu Phe Thr Ala Ser
      225                      230                      235                      240
Ser Met Lys Thr Val Ala Thr Glu Leu His Tyr Pro Asp Val Asp Ala
      245                      250                      255
Leu Tyr Thr Ala Ile Gly Ser Gly Ser Val Ser Ala Gln His Val Val
      260                      265                      270
Asn Arg Leu Met Ala Ile Phe Gly Asp Glu Glu Asp Ala Glu Asp Ala
      275                      280                      285
Leu Val Ala Arg Thr Pro Phe Ser Glu Leu Val Asn Ser Arg Ala Thr
      290                      295                      300
Thr Glu Ser Ser Thr Gly Ile Leu Val Glu Gly Ser Pro Asp Val Met
      305                      310                      315                      320
Ala Lys Leu Ala Lys Cys Cys Met Pro Val Pro Gly Asp Glu Ile Phe
      325                      330                      335
Gly Phe Val Thr Arg Gly Gly Gly Val Ser Val His Arg Thr Asp Cys
      340                      345                      350
Thr Asn Val Glu Lys Leu Lys Glu Glu Pro Glu Arg Ile Val Ser Val
      355                      360                      365
Ser Trp Ala Ser Glu Gly Gln Gly Ser Val
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<213> Corynebacterium glutamicum

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<223> RXN01940

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gccagctaaa tccacaaact gaactaagga gttttaccct atg acc acc aag atc 115
              Met Thr Thr Lys Ile
              1                      5

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atc ctc gac tgc gat cca gga cac gac gac gct gta gcc atg ctg ctc	163
Ile Leu Asp Cys Asp Pro Gly His Asp Asp Ala Val Ala Met Leu Leu	
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gca gcc ggc agc cca gaa att gaa ctg ctt gga atc acc acg gtc ggc	211
Ala Ala Gly Ser Pro Glu Ile Glu Leu Leu Gly Ile Thr Thr Val Gly	
25 30 35	
ggc aac cag acc ttg gac aag gtc acc cac aat acg cag gtc gta gcc	259
Gly Asn Gln Thr Leu Asp Lys Val Thr His Asn Thr Gln Val Val Ala	
40 45 50	
acc atc gct gat atc aat gcg ccc atc tac cgc ggt gtc acc cga cca	307
Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg Gly Val Thr Arg Pro	
55 60 65	
ttg gtg cgc ccc gtt gag gta gcc gaa gat atc cac ggc gat acc ggc	355
Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile His Gly Asp Thr Gly	
70 75 80 85	
atg gaa atc cac aag tac gaa ctg cct gaa cca acc aag cag gta gaa	403
Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro Thr Lys Gln Val Glu	
90 95 100	
gac acc cac gcg gtg gat ttc atc atc gat acc atc atg aat aac gag	451
Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr Ile Met Asn Asn Glu	
105 110 115	
ccc ggc agc gta gcg ctg gtt ccc acc gga cca ctg acc aac atc gcg	499
Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro Leu Thr Asn Ile Ala	
120 125 130	
ctg gca gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt	547
Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val	
135 140 145	
gtc ctc atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct	595
Val Leu Met Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala	
150 155 160 165	
gaa ttc aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac	643
Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn	
170 175 180	
gaa aag tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg	691
Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala	
185 190 195	
ctc gca aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac	739
Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp	
200 205 210	
gtc gcc gac ttc gtc gtc gcg ctt ttc gac gct ttc cgc aag aat tac	787
Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala Phe Arg Lys Asn Tyr	
215 220 225	
cag gac gca cag ggt ttt gat aac cca cca gta cac gac cct tgt gct	835
Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val His Asp Pro Cys Ala	
230 235 240 245	
gtt gca tac ctt gtt gac cca acc gta ttc acc acc cgc aaa gca cca	883

Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro
 250 255 260

ctc gat gtg gag ctg tac ggc gca ctc acc aca ggc atg acc gtt gct 931
 Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala
 265 270 275

gat ttc cgc gca ccg gct cca gca gat tgc acc acc caa gta gct gtt 979
 Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val
 280 285 290

gac ctg gac ttt gat aaa ttc tgg aac atg gtg atc gat gca gta aag
 1027
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 295 300 305

cgc atc gga tagacctgtt cacaagggttg tta
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 Arg Ile Gly
 310

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 35 40 45
 Thr Gln Val Val Ala Thr Ile Ala Asp Ile Asn Ala Pro Ile Tyr Arg
 50 55 60
 Gly Val Thr Arg Pro Leu Val Arg Pro Val Glu Val Ala Glu Asp Ile
 65 70 75 80
 His Gly Asp Thr Gly Met Glu Ile His Lys Tyr Glu Leu Pro Glu Pro
 85 90 95
 Thr Lys Gln Val Glu Asp Thr His Ala Val Asp Phe Ile Ile Asp Thr
 100 105 110
 Ile Met Asn Asn Glu Pro Gly Ser Val Ala Leu Val Pro Thr Gly Pro
 115 120 125
 Leu Thr Asn Ile Ala Leu Ala Val Arg Lys Glu Pro Arg Ile Ala Glu
 130 135 140
 Arg Val Lys Glu Val Val Leu Met Gly Gly Gly Tyr His Val Gly Asn
 145 150 155 160
 Trp Thr Ala Val Ala Glu Phe Asn Ile Lys Ile Asp Pro Glu Ala Ala
 165 170 175

His Ile Val Phe Asn Glu Lys Trp Pro Leu Thr Met Val Gly Leu Asp
 180 185 190
 Leu Thr His Gln Ala Leu Ala Thr Pro Glu Ile Glu Ala Lys Phe Asn
 195 200 205
 Glu Leu Gly Thr Asp Val Ala Asp Phe Val Val Ala Leu Phe Asp Ala
 210 215 220
 Phe Arg Lys Asn Tyr Gln Asp Ala Gln Gly Phe Asp Asn Pro Pro Val
 225 230 235 240
 His Asp Pro Cys Ala Val Ala Tyr Leu Val Asp Pro Thr Val Phe Thr
 245 250 255
 Thr Arg Lys Ala Pro Leu Asp Val Glu Leu Tyr Gly Ala Leu Thr Thr
 260 265 270
 Gly Met Thr Val Ala Asp Phe Arg Ala Pro Ala Pro Ala Asp Cys Thr
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 <223> FRXA01940

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 gtc cgg aaa gaa cca cgc atc gcc gag cga gtc aag gaa gtt gtc ctc 96
 Val Arg Lys Glu Pro Arg Ile Ala Glu Arg Val Lys Glu Val Val Leu
 20 25 30
 atg ggc ggg ggc tac cac gta gga aac tgg acc gcc gta gct gaa ttc 144
 Met Gly Gly Gly Tyr His Val Gly Asn Trp Thr Ala Val Ala Glu Phe
 35 40 45
 aac atc aag atc gac ccc gaa gca gcc cac atc gta ttc aac gaa aag 192
 Asn Ile Lys Ile Asp Pro Glu Ala Ala His Ile Val Phe Asn Glu Lys
 50 55 60
 tgg cca ctg act atg gtc ggc ctc gac ctt acc cac cag gcg ctc gca 240
 Trp Pro Leu Thr Met Val Gly Leu Asp Leu Thr His Gln Ala Leu Ala
 65 70 75 80
 aca cct gag atc gaa gcc aag ttc aac gag ctg ggc acc gac gtc gcc 288
 Thr Pro Glu Ile Glu Ala Lys Phe Asn Glu Leu Gly Thr Asp Val Ala

85								90				95				
gac	ttc	gtc	gtc	gcg	ctt	ttc	gac	gct	ttc	cgc	aag	aat	tac	cag	gac	336
Asp	Phe	Val	Val	Ala	Leu	Phe	Asp	Ala	Phe	Arg	Lys	Asn	Tyr	Gln	Asp	
			100					105					110			
gca	cag	ggt	ttt	gat	aac	cca	cca	gta	cac	gac	cct	tgt	gct	ggt	gca	384
Ala	Gln	Gly	Phe	Asp	Asn	Pro	Pro	Val	His	Asp	Pro	Cys	Ala	Val	Ala	
		115					120					125				
tac	ctt	ggt	gac	cca	acc	gta	ttc	acc	acc	cgc	aaa	gca	cca	ctc	gat	432
Tyr	Leu	Val	Asp	Pro	Thr	Val	Phe	Thr	Thr	Arg	Lys	Ala	Pro	Leu	Asp	
	130					135					140					
gtg	gag	ctg	tac	ggc	gca	ctc	acc	aca	ggc	atg	acc	ggt	gct	gat	ttc	480
Val	Glu	Leu	Tyr	Gly	Ala	Leu	Thr	Thr	Gly	Met	Thr	Val	Ala	Asp	Phe	
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Arg	Ala	Pro	Ala	Pro	Ala	Asp	Cys	Thr	Thr	Gln	Val	Ala	Val	Asp	Leu	
				165				170						175		
gac	ttt	gat	aaa	ttc	tgg	aac	atg	gtg	atc	gat	gca	gta	aag	cgc	atc	576
Asp	Phe	Asp	Lys	Phe	Trp	Asn	Met	Val	Ile	Asp	Ala	Val	Lys	Arg	Ile	
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Gly																

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<211> 193

<212> PRT

<213> Corynebacterium glutamicum

<400> 1060

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			20					25					30			
Met	Gly	Gly	Gly	Tyr	His	Val	Gly	Asn	Trp	Thr	Ala	Val	Ala	Glu	Phe	
		35					40					45				
Asn	Ile	Lys	Ile	Asp	Pro	Glu	Ala	Ala	His	Ile	Val	Phe	Asn	Glu	Lys	
	50					55					60					
Trp	Pro	Leu	Thr	Met	Val	Gly	Leu	Asp	Leu	Thr	His	Gln	Ala	Leu	Ala	
65				70					75					80		
Thr	Pro	Glu	Ile	Glu	Ala	Lys	Phe	Asn	Glu	Leu	Gly	Thr	Asp	Val	Ala	
			85						90					95		
Asp	Phe	Val	Val	Ala	Leu	Phe	Asp	Ala	Phe	Arg	Lys	Asn	Tyr	Gln	Asp	
			100					105					110			
Ala	Gln	Gly	Phe	Asp	Asn	Pro	Pro	Val	His	Asp	Pro	Cys	Ala	Val	Ala	
		115					120					125				

Tyr Leu Val Asp Pro Thr Val Phe Thr Thr Arg Lys Ala Pro Leu Asp
 130 135 140
 Val Glu Leu Tyr Gly Ala Leu Thr Thr Gly Met Thr Val Ala Asp Phe
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 Arg Ala Pro Ala Pro Ala Asp Cys Thr Thr Gln Val Ala Val Asp Leu
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 Asp Phe Asp Lys Phe Trp Asn Met Val Ile Asp Ala Val Lys Arg Ile
 180 185 190

Gly

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 <223> RXA02559

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 Met Ile Pro Val Leu
 1 5

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 Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ile Tyr Leu
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gtt gct ttg cat aaa cgt ggt gaa atc caa ctt ttt gga gca acg acc 211
 Val Ala Leu His Lys Arg Gly Glu Ile Gln Leu Phe Gly Ala Thr Thr
 25 30 35

acc gca gga aat gtt gat gtg aaa caa acc gcc atc aat acc agg tgg 259
 Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala Ile Asn Thr Arg Trp
 40 45 50

gtg ttg gat cag tgt gga tta gcg gac atc ccg gtc ctc gca gga caa 307
 Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro Val Leu Ala Gly Gln
 55 60 65

cct gaa cca aag cac gtg ccg cta gtg act act cca gaa aca cac ggc 355
 Pro Glu Pro Lys His Val Pro Leu Val Thr Thr Pro Glu Thr His Gly
 70 75 80 85

gac cat ggc ctt ggt tat ata aac cca ggt cac gtc gaa att cca gaa 403
 Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His Val Glu Ile Pro Glu
 90 95 100

ggt gac tgg aag cag ctg tgg aaa gaa cac ctc agt aac cca gaa act 451
 Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu Ser Asn Pro Glu Thr
 105 110 115


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aag ctg att gtc acc ggg ccc gcc acc aac ctt gcg gaa ttc ggg cca 499
Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu Ala Glu Phe Gly Pro
      120                      125                      130

gtg gaa aac gtc acg ctg atg ggt ggc acc tac ctt tat cca ggc aac 547
Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr Leu Tyr Pro Gly Asn
      135                      140                      145

acc act cca acg gca gaa tgg aat acc tgg gtt gat cca cac gga gct 595
Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val Asp Pro His Gly Ala
      150                      155                      160                      165

aaa gaa gca ttc gcg gca gcc caa aag ccc att acg gtg tgt tcc ttg 643
Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile Thr Val Cys Ser Leu
      170                      175                      180

ggc gtg acc gag cag ttt acg ctg aac ccg gac atc ctt tct aca ctt 691
Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp Ile Leu Ser Thr Leu
      185                      190                      195

atc aac acg ctt ggc agc caa ccc atc gca gag cat tta cct gag atg 739
Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu His Leu Pro Glu Met
      200                      205                      210

ctg cgc ttt tac ttt gaa ttt cac gaa gtg cag ggc gaa ggt tac ctt 787
Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln Gly Glu Gly Tyr Leu
      215                      220                      225

gct caa att cat gac ctg ctg acc tgc atg att gcc ttg gat aaa atc 835
Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile Ala Leu Asp Lys Ile
      230                      235                      240                      245

cca ttt tca ggc cgt gaa gta acc gtg gac gtg gag gct gat tcg ccc 883
Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val Glu Ala Asp Ser Pro
      250                      255                      260

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Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg Gly His Trp Gly Lys
      265                      270                      275

cca gct aac gca ttt ctt gtg gaa acc gca gac att gag gcc gcc cac 979
Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp Ile Glu Ala Ala His
      280                      285                      290

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1026
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      295                      300

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<210> 1062

<211> 301

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1062

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Met Ile Pro Val Leu Ile Asp Cys Asp Thr Gly Ile Asp Asp Ala Leu
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Ala Leu Ile Tyr Leu Val Ala Leu His Lys Arg Gly Glu Ile Gln Leu
      20           25           30

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Phe Gly Ala Thr Thr Thr Ala Gly Asn Val Asp Val Lys Gln Thr Ala
    35          40          45

Ile Asn Thr Arg Trp Val Leu Asp Gln Cys Gly Leu Ala Asp Ile Pro
    50          55          60

Val Leu Ala Gly Gln Pro Glu Pro Lys His Val Pro Leu Val Thr Thr
    65          70          75          80

Pro Glu Thr His Gly Asp His Gly Leu Gly Tyr Ile Asn Pro Gly His
    85          90          95

Val Glu Ile Pro Glu Gly Asp Trp Lys Gln Leu Trp Lys Glu His Leu
   100          105          110

Ser Asn Pro Glu Thr Lys Leu Ile Val Thr Gly Pro Ala Thr Asn Leu
   115          120          125

Ala Glu Phe Gly Pro Val Glu Asn Val Thr Leu Met Gly Gly Thr Tyr
   130          135          140

Leu Tyr Pro Gly Asn Thr Thr Pro Thr Ala Glu Trp Asn Thr Trp Val
   145          150          155          160

Asp Pro His Gly Ala Lys Glu Ala Phe Ala Ala Ala Gln Lys Pro Ile
   165          170          175

Thr Val Cys Ser Leu Gly Val Thr Glu Gln Phe Thr Leu Asn Pro Asp
   180          185          190

Ile Leu Ser Thr Leu Ile Asn Thr Leu Gly Ser Gln Pro Ile Ala Glu
   195          200          205

His Leu Pro Glu Met Leu Arg Phe Tyr Phe Glu Phe His Glu Val Gln
   210          215          220

Gly Glu Gly Tyr Leu Ala Gln Ile His Asp Leu Leu Thr Cys Met Ile
   225          230          235          240

Ala Leu Asp Lys Ile Pro Phe Ser Gly Arg Glu Val Thr Val Asp Val
   245          250          255

Glu Ala Asp Ser Pro Leu Met Arg Gly Thr Thr Val Ala Asp Ile Arg
   260          265          270

Gly His Trp Gly Lys Pro Ala Asn Ala Phe Leu Val Glu Thr Ala Asp
   275          280          285

Ile Glu Ala Ala His Ala Glu Leu Leu Arg Ala Val Glu
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<210> 1063

<211> 1050

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1027)

<223> RXA02497

<400> 1063

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 Val Arg Leu Gly Val
 1 5

tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt 163
 Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg
 10 15 20

ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc 211
 Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp Arg Thr Pro Leu Arg
 25 30 35

ctt gtt gag ctt ctt gat gac tcc ggg gcg atc tcc gaa aag ggc atc 259
 Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile Ser Glu Lys Gly Ile
 40 45 50

aac aaa ctc acc tca gca gtc ggg gaa gca gca gac cta gcg aaa acg 307
 Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala Asp Leu Ala Lys Thr
 55 60 65

ctc ggc tgc gct gaa ctg atg cca ttt gct aca tcg gca gtc cgc tcc 355
 Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr Ser Ala Val Arg Ser
 70 75 80 85

gcc acc aac agc gag gca gtg ctc gac cac gtg gag aag gaa acc ggc 403
 Ala Thr Asn Ser Glu Ala Val Leu Asp His Val Glu Lys Glu Thr Gly
 90 95 100

gtc cgc ctg tcc atc ctt tcc ggt gaa gac gaa gca cgc caa act ttc 451
 Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu Ala Arg Gln Thr Phe
 105 110 115

ctc gca gtt cga cgt tgg tat gga tgg tcc gca ggg cgc ata act aac 499
 Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala Gly Arg Ile Thr Asn
 120 125 130

ctc gac atc ggt ggc ggc tcc ctg gaa cta tcc tcc gga acc gac gaa 547
 Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser Ser Gly Thr Asp Glu
 135 140 145

tcc cca gac ctc gcg ttc tca ctg gat ctg ggt gcg ggc cgc ttg acc 595
 Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly Ala Gly Arg Leu Thr
 150 155 160 165

cac aac tgg ttc gac acc gat cca ccg gca cgt aag aaa atc aac ctc 643
 His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg Lys Lys Ile Asn Leu
 170 175 180

ctg cgc gat tat atc gat gcg gaa ctt gca gaa ccc gcc cgc cag atg 691
 Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu Pro Ala Arg Gln Met
 185 190 195

cgc acc cta ggg ccc gcg cgc ctg gca gtg gga aca tcc aaa act ttc 739
 Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly Thr Ser Lys Thr Phe
 200 205 210

cgc acc ctg gca cga ctg act ggt gct gcg ccc tca tcc gca gga cca 787
 Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro Ser Ser Ala Gly Pro
 215 220 225

cac gtc acc cga acc ctg acc gcg ccg ggt ctg cgc cag ctg atc gca 835
 His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu Arg Gln Leu Ile Ala
 230 235 240 245

ttt atc tca cga atg act gcg gcg gac cgc gct gag ctg gaa ggt atc 883
 Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala Glu Leu Glu Gly Ile
 250 255 260

agc tcg gat cgg tca cat cag atc gtg gca ggt gcg cta gtt gcg gaa 931
 Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly Ala Leu Val Ala Glu
 265 270 275

gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg 979
 Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp
 280 285 290

gca ctt cgt gaa ggt gtg atc ctg acc agg atc gac aaa gga ctg gag
 1027
 Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile Asp Lys Gly Leu Glu
 295 300 305

taacatttac ccggaagga gtt
 1050

<210> 1064

<211> 309

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 1064

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Ala Val Asp Ala Arg Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp
 20 25 30

Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile
 35 40 45

Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala
 50 55 60

Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr
 65 70 75 80

Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val
 85 90 95

Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu
 100 105 110

Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala
 115 120 125

Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser
 130 135 140

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly
 145 150 155 160
 Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg
 165 170 175
 Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu
 180 185 190
 Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly
 195 200 205
 Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro
 210 215 220
 Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu
 225 230 235 240
 Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala
 245 250 255
 Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly
 260 265 270
 Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val
 275 280 285
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 290 295 300
 Asp Lys Gly Leu Glu
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 <211> 2226
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2203)
 <223> RXN01079

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 Met Asp Phe His Ala
 1 5
 ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163
 Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe
 10 15 20
 gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211
 Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn
 25 30 35
 cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259

Gln	Asn	Thr	Val	Phe	Phe	His	Asn	Leu	Gln	Glu	Lys	Ile	Asp	Tyr	Leu	
		40					45					50				
gtt	gaa	aac	aag	tac	tat	gac	cca	atc	gtt	ctg	gac	aag	tac	gac	ttc	307
Val	Glu	Asn	Lys	Tyr	Tyr	Asp	Pro	Ile	Val	Leu	Asp	Lys	Tyr	Asp	Phe	
	55					60					65					
cag	ttc	atc	aag	gac	ctc	ttc	aag	cgc	gca	tac	gga	ttc	aag	ttc	cgc	355
Gln	Phe	Ile	Lys	Asp	Leu	Phe	Lys	Arg	Ala	Tyr	Gly	Phe	Lys	Phe	Arg	
70					75					80					85	
ttc	cag	tcc	ttc	ctc	ggc	gca	tac	aag	tac	tac	act	tcc	tac	acc	ctg	403
Phe	Gln	Ser	Phe	Leu	Gly	Ala	Tyr	Lys	Tyr	Tyr	Thr	Ser	Tyr	Thr	Leu	
				90					95					100		
aag	acc	ttc	gac	ggc	cgc	cgc	tac	ctc	gag	cgt	ttc	gaa	gac	cgt	gtc	451
Lys	Thr	Phe	Asp	Gly	Arg	Arg	Tyr	Leu	Glu	Arg	Phe	Glu	Asp	Arg	Val	
			105					110					115			
tgc	atg	gtc	gcc	ctc	acc	ctc	gct	gac	ggc	gac	cgc	gca	ttg	gcc	gag	499
Cys	Met	Val	Ala	Leu	Thr	Leu	Ala	Asp	Gly	Asp	Arg	Ala	Leu	Ala	Glu	
		120					125					130				
aac	ctg	gtc	gat	gag	atc	atg	tct	ggc	cgt	ttc	caa	cca	gca	acc	cca	547
Asn	Leu	Val	Asp	Glu	Ile	Met	Ser	Gly	Arg	Phe	Gln	Pro	Ala	Thr	Pro	
	135					140					145					
acc	ttc	ctg	aac	tcc	ggc	aag	gca	cag	cgc	ggc	gag	cca	gta	tcc	tgc	595
Thr	Phe	Leu	Asn	Ser	Gly	Lys	Ala	Gln	Arg	Gly	Glu	Pro	Val	Ser	Cys	
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ttc	ctc	ctg	cgt	atc	gaa	gac	aac	atg	gag	tcc	atc	gga	cgt	tcc	atc	643
Phe	Leu	Leu	Arg	Ile	Glu	Asp	Asn	Met	Glu	Ser	Ile	Gly	Arg	Ser	Ile	
				170					175					180		
aac	tct	gct	ctt	cag	ctg	tcc	aag	cgt	ggc	ggc	gta	gca	ttg	ctg		691
Asn	Ser	Ala	Leu	Gln	Leu	Ser	Lys	Arg	Gly	Gly	Gly	Val	Ala	Leu	Leu	
			185					190				195				
ctg	tcc	aac	ctt	cgt	gaa	gcc	ggc	gca	ccg	att	aag	aag	att	gaa	aac	739
Leu	Ser	Asn	Leu	Arg	Glu	Ala	Gly	Ala	Pro	Ile	Lys	Lys	Ile	Glu	Asn	
		200					205					210				
cag	tct	tcc	ggc	gtt	atc	cca	gtg	atg	aaa	ctt	ctg	gaa	gat	gct	ttc	787
Gln	Ser	Ser	Gly	Val	Ile	Pro	Val	Met	Lys	Leu	Leu	Glu	Asp	Ala	Phe	
	215					220					225					
tcc	tac	gct	aac	cag	ctg	ggc	gct	cgt	cag	ggc	gca	ggc	gct	gtg	tac	835
Ser	Tyr	Ala	Asn	Gln	Leu	Gly	Ala	Arg	Gln	Gly	Ala	Gly	Ala	Val	Tyr	
230					235					240					245	
ctc	aac	gct	cac	cac	cca	gat	atc	ctg	tcc	ttc	ctg	gat	acc	aag	cgt	883
Leu	Asn	Ala	His	His	Pro	Asp	Ile	Leu	Ser	Phe	Leu	Asp	Thr	Lys	Arg	
				250					255					260		
gag	aac	gcc	gat	gag	aag	atc	cgc	atc	aag	acc	ctg	tcc	ctg	ggc	gtt	931
Glu	Asn	Ala	Asp	Glu	Lys	Ile	Arg	Ile	Lys	Thr	Leu	Ser	Leu	Gly	Val	
			265					270					275			
gtg	att	ccg	gac	atc	acc	ttc	gag	ctg	gct	aag	cgc	aac	gat	gac	atg	979
Val	Ile	Pro	Asp	Ile	Thr	Phe	Glu	Leu	Ala	Lys	Arg	Asn	Asp	Asp	Met	

280	285	290
tac ctg ttc tcc cca tac gat gtg gag cgc att tac ggc aag cct ttc 1027		
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gca gac gtc tca atc acc gag cac tac gac gag atg gtg gat gat gac 1075		
Ala Asp Val Ser Ile Thr Glu His Tyr Asp Glu Met Val Asp Asp Asp 310 315 320 325		
cgc atc cgc aag acc aag atc aac gcg cgt cag ttc ttc cag acc ctg 1123		
Arg Ile Arg Lys Thr Lys Ile Asn Ala Arg Gln Phe Phe Gln Thr Leu 330 335 340		
gca gaa atc cag ttc gag tcc ggt tac cca tac atc atg tat gaa gac 1171		
Ala Glu Ile Gln Phe Glu Ser Gly Tyr Pro Tyr Ile Met Tyr Glu Asp 345 350 355		
acc gtg aat gca tcc aac cca atc gaa ggt cgc atc acc cac tca aac 1219		
Thr Val Asn Ala Ser Asn Pro Ile Glu Gly Arg Ile Thr His Ser Asn 360 365 370		
ctg tgc tct gag atc ctt cag gtg tcc acc cca tct gaa ttc aac gat 1267		
Leu Cys Ser Glu Ile Leu Gln Val Ser Thr Pro Ser Glu Phe Asn Asp 375 380 385		
gac ctg act tac gca gag gtc ggc gaa gac att tct tgt aac ttg ggt 1315		
Asp Leu Thr Tyr Ala Glu Val Gly Glu Asp Ile Ser Cys Asn Leu Gly 390 395 400 405		
tcc ctc aac gtt gca atg gct atg gat gca cca aac ttt gag aag acc 1363		
Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro Asn Phe Glu Lys Thr 410 415 420		
atc gaa acc gaa atc cgc ggc tta act gca gtg cct gag cag acc agc 1411		
Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val Pro Glu Gln Thr Ser 425 430 435		
atc gat tcc gtg cct tcc atc cgt aag ggc aac gaa gca gct cac gcc 1459		
Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn Glu Ala Ala His Ala 440 445 450		
atc ggc ctt ggc cag atg aac ctt cac ggc tac ttc ggt cgc gag cac 1507		
Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr Phe Gly Arg Glu His 455 460 465		
atg cac tac ggc tcc gag gaa gcc ctg gac ttc acc aac gca tac ttt 1555		
Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe Thr Asn Ala Tyr Phe 470 475 480 485		

gct gcc gtg ctg tac cag tgc ctg cgt gca tcc aac cag atc gct act
1603

Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser Asn Gln Ile Ala Thr
490 495 500

gag cgt gga gag cgt ttc aag aac ttc gaa aac tcc aag tat gca acc
1651

Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn Ser Lys Tyr Ala Thr
505 510 515

ggt gag tac ttc gat gat ttc gat gca aac gac ttc gca cca aag tcc
1699

Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp Phe Ala Pro Lys Ser
520 525 530

gac aag gtc aag gaa ctc ttt gcc aag tcg aac atc cac acc cca acc
1747

Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn Ile His Thr Pro Thr
535 540 545

gtt gag gac tgg gct gcg ctg aag gcc gac gtg atg gag cac ggt ctg
1795

Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val Met Glu His Gly Leu
550 555 560 565

ttc aac cgt aac ctg caa gcg gtt cca cca acc ggt tcg atc tcc tac
1843

Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr Gly Ser Ile Ser Tyr
570 575 580

atc aac aac tcc acc tcg tcg atc cac cca atc gca tcc aag att gag
1891

Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile Ala Ser Lys Ile Glu
585 590 595

atc cgc aag gaa ggc aag atc ggc cgc gtt tac tac cca gct cca cac
1939

Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr Tyr Pro Ala Pro His
600 605 610

atg gac aat gac aac ctt gag tac ttc gag gac gcc tac gaa atc ggc
1987

Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp Ala Tyr Glu Ile Gly
615 620 625

tac gag aag atc att gac acc tac gct gtg gca acc aag tac gtt gac
2035

Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala Thr Lys Tyr Val Asp
630 635 640 645

cag ggc ctg tca ctg acc ttg ttc ttc aag gac act gcc acc acc cgt
2083

Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp Thr Ala Thr Thr Arg
650 655 660

gac atc aac cgt gcg cag atc tac gca tgg cgc aag ggc atc aag acc
2131

Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg Lys Gly Ile Lys Thr
665 670 675

ttg tac tac att cgc ctg cgc cag gtt gct ctg gaa ggc act gaa gtt
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 Leu Tyr Tyr Ile Arg Leu Arg Gln Val Ala Leu Glu Gly Thr Glu Val
 680 685 690

gac ggc tgc gtc agc tgc atg ctg taaaagcact taaaaatatc ccc
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 Asp Gly Cys Val Ser Cys Met Leu
 695 700

<210> 1066
 <211> 701
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1066
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Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu
 35 40 45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu
 50 55 60

Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr
 65 70 75 80

Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr
 85 90 95

Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg
 100 105 110

Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp
 115 120 125

Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe
 130 135 140

Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly
 145 150 155 160

Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser
 165 170 175

Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly
 180 185 190

Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile
 195 200 205

Lys Lys Ile Glu Asn Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu
 210 215 220

Leu Glu Asp Ala Phe Ser Tyr Ala Asn Gln Leu Gly Ala Arg Gln Gly
 225 230 235 240

Ala Gly Ala Val Tyr Leu Asn Ala His His Pro Asp Ile Leu Ser Phe
 245 250 255
 Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile Lys Thr
 260 265 270
 Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu Ala Lys
 275 280 285
 Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu Arg Ile
 290 295 300
 Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr Asp Glu
 305 310 315 320
 Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala Arg Gln
 325 330 335
 Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr Pro Tyr
 340 345 350
 Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu Gly Arg
 355 360 365
 Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser Thr Pro
 370 375 380
 Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu Asp Ile
 385 390 395 400
 Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp Ala Pro
 405 410 415
 Asn Phe Glu Lys Thr Ile Glu Thr Glu Ile Arg Gly Leu Thr Ala Val
 420 425 430
 Pro Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys Gly Asn
 435 440 445
 Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His Gly Tyr
 450 455 460
 Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu Asp Phe
 465 470 475 480
 Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg Ala Ser
 485 490 495
 Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe Glu Asn
 500 505 510
 Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala Asn Asp
 515 520 525
 Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys Ser Asn
 530 535 540
 Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala Asp Val
 545 550 555 560

Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro Pro Thr
 565 570 575

Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His Pro Ile
 580 585 590

Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg Val Tyr
 595 600 605

Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe Glu Asp
 610 615 620

Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala Val Ala
 625 630 635 640

Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe Lys Asp
 645 650 655

Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala Trp Arg
 660 665 670

Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val Ala Leu
 675 680 685

Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu
 690 695 700

<210> 1067

<211> 790

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(790)

<223> FRXA01079

<400> 1067

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 Met Asp Phe His Ala
 1 5

ctt aac gcg ttg ctc aac ctt tac gat gac aac ggc aag atc cag ttt 163
 Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn Gly Lys Ile Gln Phe
 10 15 20

gag aaa gac cgt gaa gct gca aac cag tac ttc ctg cag cac gtc aac 211
 Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe Leu Gln His Val Asn
 25 30 35

cag aac acc gtc ttc ttc cac aac ctg cag gaa aag atc gac tac ctg 259
 Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu Lys Ile Asp Tyr Leu
 40 45 50

gtt gaa aac aag tac tat gac cca atc gtt ctg gac aag tac gac ttc 307
 Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu Asp Lys Tyr Asp Phe
 55 60 65

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cag ttc atc aag gac ctc ttc aag cgc gca tac gga ttc aag ttc cgc 355
Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr Gly Phe Lys Phe Arg
70 75 80 85

ttc cag tcc ttc ctc ggt gca tac aag tac tac act tcc tac acc ctg 403
Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr Thr Ser Tyr Thr Leu
90 95 100

aag acc ttc gac ggt cgc cgc tac ctc gag cgt ttc gaa gac cgt gtc 451
Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg Phe Glu Asp Arg Val
105 110 115

tgc atg gtc gcc ctc acc ctc gct gac ggc gac cgc gca ttg gcc gag 499
Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp Arg Ala Leu Ala Glu
120 125 130

aac ctg gtc gat gag atc atg tct ggc cgt ttc caa cca gca acc cca 547
Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe Gln Pro Ala Thr Pro
135 140 145

acc ttc ctg aac tcc ggc aag gca cag cgc ggc gag cca gta tcc tgc 595
Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly Glu Pro Val Ser Cys
150 155 160 165

ttc ctc ctg cgt atc gaa gac aac atg gag tcc atc gga cgt tcc atc 643
Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser Ile Gly Arg Ser Ile
170 175 180

aac tct gct ctt cag ctg tcc aag cgt ggc ggt ggc gta gcg ttg ctg 691
Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly Gly Val Ala Leu Leu
185 190 195

ctg tcc aac ctt cgt gaa gcc ggt gca ccg att aag aag att gaa atc 739
Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile Lys Lys Ile Glu Ile
200 205 210

cag tct tcc ggt gtt atc cca gtg atg aaa ctt ctg gaa gat gct ttc 787
Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu Leu Glu Asp Ala Phe
215 220 225

tcc 790
Ser
230

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<210> 1068

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 1068

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Met Asp Phe His Ala Leu Asn Ala Leu Leu Asn Leu Tyr Asp Asp Asn
1 5 10 15

Gly Lys Ile Gln Phe Glu Lys Asp Arg Glu Ala Ala Asn Gln Tyr Phe
20 25 30

Leu Gln His Val Asn Gln Asn Thr Val Phe Phe His Asn Leu Gln Glu
35 40 45

Lys Ile Asp Tyr Leu Val Glu Asn Lys Tyr Tyr Asp Pro Ile Val Leu

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50		55		60	
Asp Lys Tyr Asp Phe Gln Phe Ile Lys Asp Leu Phe Lys Arg Ala Tyr					
65		70		75	80
Gly Phe Lys Phe Arg Phe Gln Ser Phe Leu Gly Ala Tyr Lys Tyr Tyr					
		85		90	95
Thr Ser Tyr Thr Leu Lys Thr Phe Asp Gly Arg Arg Tyr Leu Glu Arg					
		100		105	110
Phe Glu Asp Arg Val Cys Met Val Ala Leu Thr Leu Ala Asp Gly Asp					
		115		120	125
Arg Ala Leu Ala Glu Asn Leu Val Asp Glu Ile Met Ser Gly Arg Phe					
		130		135	140
Gln Pro Ala Thr Pro Thr Phe Leu Asn Ser Gly Lys Ala Gln Arg Gly					
145		150		155	160
Glu Pro Val Ser Cys Phe Leu Leu Arg Ile Glu Asp Asn Met Glu Ser					
		165		170	175
Ile Gly Arg Ser Ile Asn Ser Ala Leu Gln Leu Ser Lys Arg Gly Gly					
		180		185	190
Gly Val Ala Leu Leu Leu Ser Asn Leu Arg Glu Ala Gly Ala Pro Ile					
		195		200	205
Lys Lys Ile Glu Ile Gln Ser Ser Gly Val Ile Pro Val Met Lys Leu					
		210		215	220
Leu Glu Asp Ala Phe Ser					
225		230			

<210> 1069

<211> 1364

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1341)

<223> FRXA01084

<400> 1069

tcc ttt ctg gat acc aag cgc gag aac gcc gat gag aag atc cgc atc	48
Ser Phe Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile	
1	5 10 15
aag acc ctg tcc ctg ggt gtt gtg att ccg gac atc acc ttc gag ctg	96
Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu	
	20 25 30
gct aag cgc aac gat gac atg tac ctg ttc tcc cca tac gat gtg gag	144
Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu	
	35 40 45
cgc att tac ggc aag cct ttc gca gac gtc tca atc acc gag cac tac	192
Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr	

50	55	60	
gac gag atg gtg gat gat gac cgc atc cgc aag acc aag atc aac gcg Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala 65 70 75 80			240
cgt cag ttc ttc cag acc ctg gca gaa atc cag ttc gag tcc ggt tac Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr 85 90 95			288
cca tac atc atg tat gaa gac acc gtg aat gca tcc aac cca atc gaa Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu 100 105 110			336
ggt cgc atc acc cac tca aac ctg tgc tct gag atc ctt cag gtg tcc Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser 115 120 125			384
acc cca tct gaa ttc aac gat gac ctg act tac gca gag gtc ggc gaa Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu 130 135 140			432
gac att tct tgt aac ttg ggt tcc ctc aac gtt gca atg gct atg gat Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp 145 150 155 160			480
gca cca aac ttt gag aag acc atn gaa acc gaa atc cgc ggc tta act Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr 165 170 175			528
gca gtg nct gag cag acc agc atc gat tcc gtg cct tcc atc cgt aag Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys 180 185 190			576
ggc aac gaa gca gct cac gcc atc ggc ctt ggc cag atg aac ctt cac Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His 195 200 205			624
ggc tac ttc ggt cgc gag cac atg cac tac ggc tcc gag gaa gcc ctg Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu 210 215 220			672
gac ttc acc aac gca tac ttt gct gcc gtg ctg tac cag tgc ctg cgt Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg 225 230 235 240			720
gca tcc aac cag atc gct act gag cgt gga gag cgt ttc aag aac ttc Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe 245 250 255			768
gaa aac tcc aag tat gca acc ggt gag tac ttc gat gat ttc gat gca Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala 260 265 270			816
aac gac ttc gca cca aag tcc gac aag gtc aag gaa ctc ttt gcc aag Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys 275 280 285			864
tcg aac atc cac acc cca acc gtt gag gac tgg gct gcg ctg aag gcc Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala 290 295 300			912

gac gtg atg gag cac ggt ctg ttc aac cgt aac ctg caa gcg gtt cca 960
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro
 305 310 315 320

cca acc ggt tcg atc tcc tac atc aac aac tcc acc tcg tcg atc cac
 1008
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His
 325 330 335

cca atc gca tcc aag att gag atc cgc aag gaa ggc aag atc ggc cgc
 1056
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg
 340 345 350

gtt tac tac cca gct cca cac atg gac aat gac aac ctt gag tac ttc
 1104
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe
 355 360 365

gag gac gcc tac gaa atc ggc tac gag aag atc att gac acc tac gct
 1152
 Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala
 370 375 380

gtg gca acc aag tac gtt gac cag ggc ctg tca ctg acc ttg ttc ttc
 1200
 Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe
 385 390 395 400

aag gac act gcc acc acc cgt gac atc aac cgt gcg cag atc tac gca
 1248
 Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala
 405 410 415

tgg cgc aag ggc atc aag acc ttg tac tac att cgc ctg cgc cag gtt
 1296
 Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val
 420 425 430

gct ctg gaa ggc act gaa gtt gac ggc tgc gtc agc tgc atg ctg
 1341
 Ala Leu Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu
 435 440 445

taaaagcact taaaaatatc ccc
 1364

<210> 1070

<211> 447

<212> PRT

<213> Corynebacterium glutamicum

<400> 1070

Ser Phe Leu Asp Thr Lys Arg Glu Asn Ala Asp Glu Lys Ile Arg Ile
 1 5 10 15

Lys Thr Leu Ser Leu Gly Val Val Ile Pro Asp Ile Thr Phe Glu Leu
 20 25 30

Ala Lys Arg Asn Asp Asp Met Tyr Leu Phe Ser Pro Tyr Asp Val Glu
 35 40 45
 Arg Ile Tyr Gly Lys Pro Phe Ala Asp Val Ser Ile Thr Glu His Tyr
 50 55 60
 Asp Glu Met Val Asp Asp Asp Arg Ile Arg Lys Thr Lys Ile Asn Ala
 65 70 75 80
 Arg Gln Phe Phe Gln Thr Leu Ala Glu Ile Gln Phe Glu Ser Gly Tyr
 85 90 95
 Pro Tyr Ile Met Tyr Glu Asp Thr Val Asn Ala Ser Asn Pro Ile Glu
 100 105 110
 Gly Arg Ile Thr His Ser Asn Leu Cys Ser Glu Ile Leu Gln Val Ser
 115 120 125
 Thr Pro Ser Glu Phe Asn Asp Asp Leu Thr Tyr Ala Glu Val Gly Glu
 130 135 140
 Asp Ile Ser Cys Asn Leu Gly Ser Leu Asn Val Ala Met Ala Met Asp
 145 150 155 160
 Ala Pro Asn Phe Glu Lys Thr Xaa Glu Thr Glu Ile Arg Gly Leu Thr
 165 170 175
 Ala Val Xaa Glu Gln Thr Ser Ile Asp Ser Val Pro Ser Ile Arg Lys
 180 185 190
 Gly Asn Glu Ala Ala His Ala Ile Gly Leu Gly Gln Met Asn Leu His
 195 200 205
 Gly Tyr Phe Gly Arg Glu His Met His Tyr Gly Ser Glu Glu Ala Leu
 210 215 220
 Asp Phe Thr Asn Ala Tyr Phe Ala Ala Val Leu Tyr Gln Cys Leu Arg
 225 230 235 240
 Ala Ser Asn Gln Ile Ala Thr Glu Arg Gly Glu Arg Phe Lys Asn Phe
 245 250 255
 Glu Asn Ser Lys Tyr Ala Thr Gly Glu Tyr Phe Asp Asp Phe Asp Ala
 260 265 270
 Asn Asp Phe Ala Pro Lys Ser Asp Lys Val Lys Glu Leu Phe Ala Lys
 275 280 285
 Ser Asn Ile His Thr Pro Thr Val Glu Asp Trp Ala Ala Leu Lys Ala
 290 295 300
 Asp Val Met Glu His Gly Leu Phe Asn Arg Asn Leu Gln Ala Val Pro
 305 310 315 320
 Pro Thr Gly Ser Ile Ser Tyr Ile Asn Asn Ser Thr Ser Ser Ile His
 325 330 335
 Pro Ile Ala Ser Lys Ile Glu Ile Arg Lys Glu Gly Lys Ile Gly Arg
 340 345 350
 Val Tyr Tyr Pro Ala Pro His Met Asp Asn Asp Asn Leu Glu Tyr Phe

355	360	365
Glu Asp Ala Tyr Glu Ile Gly Tyr Glu Lys Ile Ile Asp Thr Tyr Ala 370 375 380		
Val Ala Thr Lys Tyr Val Asp Gln Gly Leu Ser Leu Thr Leu Phe Phe 385 390 395 400		
Lys Asp Thr Ala Thr Thr Arg Asp Ile Asn Arg Ala Gln Ile Tyr Ala 405 410 415		
Trp Arg Lys Gly Ile Lys Thr Leu Tyr Tyr Ile Arg Leu Arg Gln Val 420 425 430		
Ala Leu Glu Gly Thr Glu Val Asp Gly Cys Val Ser Cys Met Leu 435 440 445		

<210> 1071

<211> 1125

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1102)

<223> RXN01920

<400> 1071

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cgaaaagcaa aaaaatttgt agaagggaag agcgcaccta atg gct gct gat tct 115
Met Ala Ala Asp Ser
1 5

gat ctc agt gtt cac gat gct tac tta aag gag cat gtt gca cct gta 163
Asp Leu Ser Val His Asp Ala Tyr Leu Lys Glu His Val Ala Pro Val
10 15 20

aag gcg atc aac tgg aac tcc atc cca gat tcc aaa gat ctt gaa gtc 211
Lys Ala Ile Asn Trp Asn Ser Ile Pro Asp Ser Lys Asp Leu Glu Val
25 30 35

tgg gat cgt ctg acc ggt aac ttc tgg ctc cca gaa aag gtc cca gta 259
Trp Asp Arg Leu Thr Gly Asn Phe Trp Leu Pro Glu Lys Val Pro Val
40 45 50

tcc aac gac atc aag agc tgg gga acc ctc aac gag gtt gaa aaa gcc 307
Ser Asn Asp Ile Lys Ser Trp Gly Thr Leu Asn Glu Val Glu Lys Ala
55 60 65

gca acc atg cgc gtg ttc acc gga ctt acc ctg ctg gac acc att cag 355
Ala Thr Met Arg Val Phe Thr Gly Leu Thr Leu Leu Asp Thr Ile Gln
70 75 80 85

ggc act gtc ggc gca atc tcc ctg ctt cca gac gca gat tca ctg cac 403
Gly Thr Val Gly Ala Ile Ser Leu Leu Pro Asp Ala Asp Ser Leu His
90 95 100

gaa gaa gcg gtg cta acc aac att gcg ttc atg gaa tcc gtg cac gca 451
Glu Glu Ala Val Leu Thr Asn Ile Ala Phe Met Glu Ser Val His Ala

105				110				115								
aag	agt	tac	tcc	aac	atc	ttc	atg	act	ctg	gcc	tcc	acc	gcg	gaa	atc	499
Lys	Ser	Tyr	Ser	Asn	Ile	Phe	Met	Thr	Leu	Ala	Ser	Thr	Ala	Glu	Ile	
		120					125					130				
aac	gat	gcg	ttc	cgt	tgg	tct	gag	gaa	aat	gaa	aac	ctg	cag	cgc	aag	547
Asn	Asp	Ala	Phe	Arg	Trp	Ser	Glu	Glu	Asn	Glu	Asn	Leu	Gln	Arg	Lys	
	135					140					145					
gca	aag	atc	atc	ctg	tct	tac	tat	gag	ggc	gat	gat	cca	cta	aag	cgc	595
Ala	Lys	Ile	Ile	Leu	Ser	Tyr	Tyr	Glu	Gly	Asp	Asp	Pro	Leu	Lys	Arg	
150					155					160					165	
aag	atc	gcc	tcc	gtg	atc	ctg	gag	tcc	ttc	ctg	ttc	tac	tcc	ggc	ttc	643
Lys	Ile	Ala	Ser	Val	Ile	Leu	Glu	Ser	Phe	Leu	Phe	Tyr	Ser	Gly	Phe	
				170					175					180		
tac	ctc	cca	atg	tat	tgg	tcc	agc	cac	tcc	aag	ctg	gcc	aac	acc	gcc	691
Tyr	Leu	Pro	Met	Tyr	Trp	Ser	Ser	His	Ser	Lys	Leu	Ala	Asn	Thr	Ala	
			185					190					195			
gac	gtg	atc	cgc	ctg	atc	atc	cgc	gat	gag	gca	gtg	cac	ggc	tac	tac	739
Asp	Val	Ile	Arg	Leu	Ile	Ile	Arg	Asp	Glu	Ala	Val	His	Gly	Tyr	Tyr	
	200						205					210				
att	ggc	tac	aag	tat	caa	aag	gct	gtc	gcg	aag	gag	act	cca	gag	cgt	787
Ile	Gly	Tyr	Lys	Tyr	Gln	Lys	Ala	Val	Ala	Lys	Glu	Thr	Pro	Glu	Arg	
	215					220					225					
cag	gaa	gag	ctg	aag	gag	tac	acc	ttc	gat	ctg	ctc	tac	gat	ctt	tac	835
Gln	Glu	Glu	Leu	Lys	Glu	Tyr	Thr	Phe	Asp	Leu	Leu	Tyr	Asp	Leu	Tyr	
230					235					240					245	
gat	aac	gaa	act	cag	tac	tcc	gaa	gat	ctc	tac	gac	gat	ctt	gga	tgg	883
Asp	Asn	Glu	Thr	Gln	Tyr	Ser	Glu	Asp	Leu	Tyr	Asp	Asp	Leu	Gly	Trp	
				250					255					260		
acc	gag	gat	gtt	aag	cga	ttc	ctt	cgc	tac	aac	gcc	aac	aag	gcc	ctc	931
Thr	Glu	Asp	Val	Lys	Arg	Phe	Leu	Arg	Tyr	Asn	Ala	Asn	Lys	Ala	Leu	
			265					270					275			
aac	aac	ctt	ggc	tac	gaa	gga	ctc	ttc	cca	gcg	gat	gaa	acc	aag	gtg	979
Asn	Asn	Leu	Gly	Tyr	Glu	Gly	Leu	Phe	Pro	Ala	Asp	Glu	Thr	Lys	Val	
		280					285					290				
tcc	cca	aac	atc	ttg	tct	gcg	ctg	tca	cca	aac	gct	gat	gag	aac	cac	
1027																
Ser	Pro	Asn	Ile	Leu	Ser	Ala	Leu	Ser	Pro	Asn	Ala	Asp	Glu	Asn	His	
	295					300					305					
gac	ttc	ttc	tcc	ggc	tcc	ggc	tcc	tct	tac	gtt	att	ggc	aag	gca	gaa	
1075																
Asp	Phe	Phe	Ser	Gly	Ser	Gly	Ser	Ser	Tyr	Val	Ile	Gly	Lys	Ala	Glu	
310					315					320					325	
aac	acc	gag	gat	gat	gac	tgg	gac	ttc	taacttttaa	aaagctgaag						
1122																
Asn	Thr	Glu	Asp	Asp	Asp	Trp	Asp	Phe								
				330												

cgc
1125

<210> 1072
<211> 334
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 1072

Met	Ala	Ala	Asp	Ser	Asp	Leu	Ser	Val	His	Asp	Ala	Tyr	Leu	Lys	Glu	1	5	10	15
His	Val	Ala	Pro	Val	Lys	Ala	Ile	Asn	Trp	Asn	Ser	Ile	Pro	Asp	Ser	20	25	30	
Lys	Asp	Leu	Glu	Val	Trp	Asp	Arg	Leu	Thr	Gly	Asn	Phe	Trp	Leu	Pro	35	40	45	
Glu	Lys	Val	Pro	Val	Ser	Asn	Asp	Ile	Lys	Ser	Trp	Gly	Thr	Leu	Asn	50	55	60	
Glu	Val	Glu	Lys	Ala	Ala	Thr	Met	Arg	Val	Phe	Thr	Gly	Leu	Thr	Leu	65	70	75	80
Leu	Asp	Thr	Ile	Gln	Gly	Thr	Val	Gly	Ala	Ile	Ser	Leu	Leu	Pro	Asp	85	90	95	
Ala	Asp	Ser	Leu	His	Glu	Glu	Ala	Val	Leu	Thr	Asn	Ile	Ala	Phe	Met	100	105	110	
Glu	Ser	Val	His	Ala	Lys	Ser	Tyr	Ser	Asn	Ile	Phe	Met	Thr	Leu	Ala	115	120	125	
Ser	Thr	Ala	Glu	Ile	Asn	Asp	Ala	Phe	Arg	Trp	Ser	Glu	Glu	Asn	Glu	130	135	140	
Asn	Leu	Gln	Arg	Lys	Ala	Lys	Ile	Ile	Leu	Ser	Tyr	Tyr	Glu	Gly	Asp	145	150	155	160
Asp	Pro	Leu	Lys	Arg	Lys	Ile	Ala	Ser	Val	Ile	Leu	Glu	Ser	Phe	Leu	165	170	175	
Phe	Tyr	Ser	Gly	Phe	Tyr	Leu	Pro	Met	Tyr	Trp	Ser	Ser	His	Ser	Lys	180	185	190	
Leu	Ala	Asn	Thr	Ala	Asp	Val	Ile	Arg	Leu	Ile	Ile	Arg	Asp	Glu	Ala	195	200	205	
Val	His	Gly	Tyr	Tyr	Ile	Gly	Tyr	Lys	Tyr	Gln	Lys	Ala	Val	Ala	Lys	210	215	220	
Glu	Thr	Pro	Glu	Arg	Gln	Glu	Glu	Leu	Lys	Glu	Tyr	Thr	Phe	Asp	Leu	225	230	235	240
Leu	Tyr	Asp	Leu	Tyr	Asp	Asn	Glu	Thr	Gln	Tyr	Ser	Glu	Asp	Leu	Tyr	245	250	255	
Asp	Asp	Leu	Gly	Trp	Thr	Glu	Asp	Val	Lys	Arg	Phe	Leu	Arg	Tyr	Asn	260	265	270	

Ala Asn Lys Ala Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala
 275 280 285

Asp Glu Thr Lys Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn
 290 295 300

Ala Asp Glu Asn His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val
 305 310 315 320

Ile Gly Lys Ala Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe
 325 330

<210> 1073

<211> 437

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (414)

<223> FRXA01920

<400> 1073

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Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr	
1 5 10 15	
tac att ggc tac aag tat caa aag gct gtc gcg aag gag act cca gag	96
Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu	
20 25 30	
cgt cag gaa gag ctg aag gag tac acc ttc gat ctg ctc tac gat ctt	144
Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu	
35 40 45	
tac gat aac gaa act cag tac tcc gaa gat ctc tac gac gat ctt gga	192
Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly	
50 55 60	
tgg acc gag gat gtt aag cga ttc ctt cgc tac aac gcc aac aag gcc	240
Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala	
65 70 75 80	
ctc aac aac ctt ggc tac gaa gga ctc ttc cca gcg gat gaa acc aag	288
Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys	
85 90 95	
gtg tcc cca aac atc ttg tct gcg ctg tca cca aac gct gat gag aac	336
Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn	
100 105 110	
cac gac ttc ttc tcc ggc tcc ggt tcc tct tac gtt att ggt aag gca	384
His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala	
115 120 125	
gaa aac acc gag gat gat gac tgg gac ttc taacttttaa aaagctgaag	434
Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe	
130 135	
cgc	437

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<210> 1074
<211> 138
<212> PRT
<213> Corynebacterium glutamicum
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<400> 1074
Ala Asp Val Ile Arg Leu Ile Ile Arg Asp Glu Ala Val His Gly Tyr
  1                               5                      10                15

Tyr Ile Gly Tyr Lys Tyr Gln Lys Ala Val Ala Lys Glu Thr Pro Glu
                20                               25                30

Arg Gln Glu Glu Leu Lys Glu Tyr Thr Phe Asp Leu Leu Tyr Asp Leu
          35                               40                45

Tyr Asp Asn Glu Thr Gln Tyr Ser Glu Asp Leu Tyr Asp Asp Leu Gly
  50                               55                      60

Trp Thr Glu Asp Val Lys Arg Phe Leu Arg Tyr Asn Ala Asn Lys Ala
  65                               70                75                80

Leu Asn Asn Leu Gly Tyr Glu Gly Leu Phe Pro Ala Asp Glu Thr Lys
          85                               90                95

Val Ser Pro Asn Ile Leu Ser Ala Leu Ser Pro Asn Ala Asp Glu Asn
          100                               105                110

His Asp Phe Phe Ser Gly Ser Gly Ser Ser Tyr Val Ile Gly Lys Ala
          115                               120                125

Glu Asn Thr Glu Asp Asp Asp Trp Asp Phe
  130                               135

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<210> 1075
<211> 567
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(544)  
<223> RXA01080
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<400> 1075
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ttgcgcacaa acggtattta gaagggaagt gagttcgagg atg cta atc gtg tat 115
Met Leu Ile Val Tyr
1 5

ttt tcc tcg gcc acc gac aac acg cat cgt ttt gta caa aag ctc gat 163
Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe Val Gln Lys Leu Asp
10 15 20

tta ccc aac gtg cgc atc ccc ctc act agg gtg gaa gaa ccg ctg aaa 211
Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val Glu Glu Pro Leu Lys
25 30 35

```

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atc aac gag ccc tac gtg cta atc acc ccg acc tat ggt ggt gga gtc 259
Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr Tyr Gly Gly Gly Val
      40                      45                      50

tcc atg act gga gaa aac tcc cgc ccg gtc cca cca caa gtc atc agg 307
Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro Pro Gln Val Ile Arg
      55                      60                      65

ttt tta aat gat gaa cac aac cgc agc ttc atc agg gca gtt gtt gca 355
Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile Arg Ala Val Val Ala
      70                      75                      80                      85

ggt gga aac tca aac ttc ggc tcc gat ttt ggg ttg gca ggc gag atc 403
Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly Leu Ala Gly Glu Ile
      90                      95                      100

att tcc aag aaa tgt aaa gtg ccc tat gtc tac cgt ttc gag ctc atg 451
Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr Arg Phe Glu Leu Met
      105                      110                      115

ggc aat gag gaa gat gta agt atc ctt cgt gga ggt ctt act caa aac 499
Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly Gly Leu Thr Gln Asn
      120                      125                      130

gcc caa gct ttg ggg ctg gaa cca caa gaa cca gtt acc tcg cga 544
Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro Val Thr Ser Arg
      135                      140                      145

taaaccttaa aacttaatca atc 567

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<210> 1076

<211> 148

<212> PRT

<213> Corynebacterium glutamicum

<400> 1076

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Met Leu Ile Val Tyr Phe Ser Ser Ala Thr Asp Asn Thr His Arg Phe
  1                      5                      10                      15

Val Gln Lys Leu Asp Leu Pro Asn Val Arg Ile Pro Leu Thr Arg Val
      20                      25                      30

Glu Glu Pro Leu Lys Ile Asn Glu Pro Tyr Val Leu Ile Thr Pro Thr
      35                      40                      45

Tyr Gly Gly Gly Val Ser Met Thr Gly Glu Asn Ser Arg Pro Val Pro
      50                      55                      60

Pro Gln Val Ile Arg Phe Leu Asn Asp Glu His Asn Arg Ser Phe Ile
      65                      70                      75                      80

Arg Ala Val Val Ala Gly Gly Asn Ser Asn Phe Gly Ser Asp Phe Gly
      85                      90                      95

Leu Ala Gly Glu Ile Ile Ser Lys Lys Cys Lys Val Pro Tyr Val Tyr
      100                      105                      110

Arg Phe Glu Leu Met Gly Asn Glu Glu Asp Val Ser Ile Leu Arg Gly
      115                      120                      125

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Gly Leu Thr Gln Asn Ala Gln Ala Leu Gly Leu Glu Pro Gln Glu Pro
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Val Thr Ser Arg
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 <211> 650
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<220>
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 <222> (1)..(627)
 <223> RXA00867

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 Ala Leu Gln Leu Asp Thr Lys Leu Asp Gly Ile Pro Ser Lys Val Leu
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 tcc gat gcg ctt gag cag gca cgc gat gcc cga ctg acc atc ctg aac 144
 Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn
 35 40 45
 acc atg gct gat gtc atc aac gga cct gat gag atg agc aag ttc gct 192
 Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala
 50 55 60
 cct cgc atc acc acc gtg aag atc cca gtg gca aag atc ggt gag ctg 240
 Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu
 65 70 75 80
 atc gga cca aag ggt aag aac atc aac gct ctt acc gaa gag acc ggc 288
 Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly
 85 90 95
 gca aac atc tcc atc gaa gat gac ggc acc gtg ttc atc tct gca gct 336
 Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala
 100 105 110
 gac ggc gca tct gct gaa gcg gcg atc gaa aag atc aac gct ctg gcg 384
 Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala
 115 120 125
 aac cca cag ctg cca aag gtt ggc gag cgc ttc ctc gga acc gtc gtc 432
 Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val
 130 135 140
 aag acc acc gca ttc gga gca ttc gtt tcc ttg ctc cca ggc cgc gac 480
 Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp
 145 150 155 160
 ggc ctt gtt cac atc tcc aag ctg ggt aac ggc aag cga gta gaa aag 528
 Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys
 165 170 175

gtc gac gat gtg gtg aag gtt ggc gag aag att cag gtc gaa atc gct 576
 Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala
 180 185 190

gac atc gac aac cgc ggc aag atc tcc ttg gtc cca gtt gtt gaa gag 624
 Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu
 195 200 205

gac taattagttc tggctagatc ggg 650
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<210> 1078

<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 1078

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Ser Asp Ala Leu Glu Gln Ala Arg Asp Ala Arg Leu Thr Ile Leu Asn
 35 40 45

Thr Met Ala Asp Val Ile Asn Gly Pro Asp Glu Met Ser Lys Phe Ala
 50 55 60

Pro Arg Ile Thr Thr Val Lys Ile Pro Val Ala Lys Ile Gly Glu Leu
 65 70 75 80

Ile Gly Pro Lys Gly Lys Asn Ile Asn Ala Leu Thr Glu Glu Thr Gly
 85 90 95

Ala Asn Ile Ser Ile Glu Asp Asp Gly Thr Val Phe Ile Ser Ala Ala
 100 105 110

Asp Gly Ala Ser Ala Glu Ala Ala Ile Glu Lys Ile Asn Ala Leu Ala
 115 120 125

Asn Pro Gln Leu Pro Lys Val Gly Glu Arg Phe Leu Gly Thr Val Val
 130 135 140

Lys Thr Thr Ala Phe Gly Ala Phe Val Ser Leu Leu Pro Gly Arg Asp
 145 150 155 160

Gly Leu Val His Ile Ser Lys Leu Gly Asn Gly Lys Arg Val Glu Lys
 165 170 175

Val Asp Asp Val Val Lys Val Gly Glu Lys Ile Gln Val Glu Ile Ala
 180 185 190

Asp Ile Asp Asn Arg Gly Lys Ile Ser Leu Val Pro Val Val Glu Glu
 195 200 205

Asp

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 <223> RXA01416

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 Ala Pro Thr Glu Lys Ile Val Ser Asp Gly Leu Glu Ala Ala Lys Pro
 20 25 30
 ttc atc gac atc ctg tgc cgc gca cag gaa ggt ctg gca cag cgc gtt 144
 Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val
 35 40 45
 gga aac gca gcc aag gaa ttc cca ctg ttc cct cca tac acc gac gag 192
 Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu
 50 55 60
 gtg tac tcc gca gtg gag cgc aag gta tcc aag aag cta gct tct ttg 240
 Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu
 65 70 75 80
 ctg acc ctg aag gca aag caa gag cgc gac gac gct acc aac gcc tac 288
 Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr
 85 90 95
 atg gaa gaa atc gaa gcc gaa ctg ctt cca aag ttc gag gct tcc tac 336
 Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr
 100 105 110
 agc tca gca gct gaa gcg tcc aag gaa atc cgt gca gga tac aac gct 384
 Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala
 115 120 125
 gtc atg aag gcc atc gtg cgc cgc atg atc ctc acc gat cac ttc cgc 432
 Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg
 130 135 140
 atc gac ggc cgc gga gtc acc gac atc cgt gac ctg gca gta gaa gtt 480
 Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val
 145 150 155 160
 gag ctc atc cca cgt gcg cac ggt tcc tcc ctc ttc gag cgt ggc gag 528
 Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu
 165 170 175
 acc cag atc ctt ggt gtc acc acc ctg gac atg ctc aag atg gaa cag 576
 Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln
 180 185 190

caa atc gac tcc ctg gca cca ggc gat gcg aag cgc tac atg cac cac 624
 Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His
 195 200 205

tac aac 630
 Tyr Asn
 210

<210> 1080
 <211> 210
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1080
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Phe Ile Asp Ile Leu Cys Arg Ala Gln Glu Gly Leu Ala Gln Arg Val
 35 40 45

Gly Asn Ala Ala Lys Glu Phe Pro Leu Phe Pro Pro Tyr Thr Asp Glu
 50 55 60

Val Tyr Ser Ala Val Glu Arg Lys Val Ser Lys Lys Leu Ala Ser Leu
 65 70 75 80

Leu Thr Leu Lys Ala Lys Gln Glu Arg Asp Asp Ala Thr Asn Ala Tyr
 85 90 95

Met Glu Glu Ile Glu Ala Glu Leu Leu Pro Lys Phe Glu Ala Ser Tyr
 100 105 110

Ser Ser Ala Ala Glu Ala Ser Lys Glu Ile Arg Ala Gly Tyr Asn Ala
 115 120 125

Val Met Lys Ala Ile Val Arg Arg Met Ile Leu Thr Asp His Phe Arg
 130 135 140

Ile Asp Gly Arg Gly Val Thr Asp Ile Arg Asp Leu Ala Val Glu Val
 145 150 155 160

Glu Leu Ile Pro Arg Ala His Gly Ser Ser Leu Phe Glu Arg Gly Glu
 165 170 175

Thr Gln Ile Leu Gly Val Thr Thr Leu Asp Met Leu Lys Met Glu Gln
 180 185 190

Gln Ile Asp Ser Leu Ala Pro Gly Asp Ala Lys Arg Tyr Met His His
 195 200 205

Tyr Asn
 210

<210> 1081
 <211> 757
 <212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(757)

<223> RXA01486

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				Met	Ser	Asp	Val	Lys	
				1				5	

gac	ttc	gaa	gac	acc	gaa	ttt	ggc	ctg	atc	gag	gcc	gtc	gca	acc	atc	163
Asp	Phe	Glu	Asp	Thr	Glu	Phe	Gly	Leu	Ile	Glu	Ala	Val	Ala	Thr	Ile	
				10					15					20		

gac	aac	ggt	gac	ttc	gga	acc	cgc	acc	atc	cgt	ttt	gaa	acc	ggc	caa	211
Asp	Asn	Gly	Asp	Phe	Gly	Thr	Arg	Thr	Ile	Arg	Phe	Glu	Thr	Gly	Gln	
			25					30					35			

ctt	gcc	cgc	cag	gca	gat	ggt	gca	gtg	acc	acc	tac	ctc	gac	gat	gac	259
Leu	Ala	Arg	Gln	Ala	Asp	Gly	Ala	Val	Thr	Thr	Tyr	Leu	Asp	Asp	Asp	
			40				45					50				

acg	atg	ctg	ctg	gca	acc	acc	acc	gca	tcc	aac	cag	cca	cgc	gag	ggc	307
Thr	Met	Leu	Leu	Ala	Thr	Thr	Thr	Ala	Ser	Asn	Gln	Pro	Arg	Glu	Gly	
	55					60				65						

ttt	gac	ttc	ttc	cca	ctg	acc	gtg	gac	gtt	gaa	gag	cgt	atg	tac	gca	355
Phe	Asp	Phe	Phe	Pro	Leu	Thr	Val	Asp	Val	Glu	Glu	Arg	Met	Tyr	Ala	
70					75					80					85	

gct	ggt	cgc	atc	cct	ggc	tct	ttc	ttc	cgt	cgg	gag	ggt	cgc	cca	tcc	403
Ala	Gly	Arg	Ile	Pro	Gly	Ser	Phe	Phe	Arg	Arg	Glu	Gly	Arg	Pro	Ser	
				90					95					100		

acc	gaa	gct	atc	ctg	gct	tgc	cgt	ctc	atc	gac	cgc	cca	ctg	cgc	cca	451
Thr	Glu	Ala	Ile	Leu	Ala	Cys	Arg	Leu	Ile	Asp	Arg	Pro	Leu	Arg	Pro	
			105					110					115			

acc	ttt	gtt	aag	ggc	ctg	cgc	aat	gag	gtt	cag	atc	gtt	gtc	acc	gtc	499
Thr	Phe	Val	Lys	Gly	Leu	Arg	Asn	Glu	Val	Gln	Ile	Val	Val	Thr	Val	
		120					125					130				

atg	tcc	atg	aac	cct	gag	gat	tac	tac	gat	gtc	gta	gca	atc	aac	gga	547
Met	Ser	Met	Asn	Pro	Glu	Asp	Tyr	Tyr	Asp	Val	Val	Ala	Ile	Asn	Gly	
	135					140					145					

gct	tcc	gca	gca	acc	cgc	atc	tcc	gga	ctt	cct	gtc	tcc	ggc	gct	gtc	595
Ala	Ser	Ala	Ala	Thr	Arg	Ile	Ser	Gly	Leu	Pro	Val	Ser	Gly	Ala	Val	
150					155					160					165	

ggt	ggc	gtt	cgc	atg	gca	ctg	gtt	ggt	gat	gaa	aag	cac	cca	gaa	ggc	643
Gly	Gly	Val	Arg	Met	Ala	Leu	Val	Gly	Asp	Glu	Lys	His	Pro	Glu	Gly	
				170				175						180		

caa	tgg	gtt	gca	ttc	cca	acc	cac	gct	caa	cat	gag	cag	tcc	gta	ttt	691
Gln	Trp	Val	Ala	Phe	Pro	Thr	His	Ala	Gln	His	Glu	Gln	Ser	Val	Phe	
			185					190					195			

gaa atc gtt gtg gct ggt cgc ctc gtc gag cgc aag cgc ggc aac aag 739
 Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg Lys Arg Gly Asn Lys
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acc ttc tcc gac gtc gca 757
 Thr Phe Ser Asp Val Ala
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<210> 1082

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 1082

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 20 25 30

Phe Glu Thr Gly Gln Leu Ala Arg Gln Ala Asp Gly Ala Val Thr Thr
 35 40 45

Tyr Leu Asp Asp Asp Thr Met Leu Leu Ala Thr Thr Thr Ala Ser Asn
 50 55 60

Gln Pro Arg Glu Gly Phe Asp Phe Phe Pro Leu Thr Val Asp Val Glu
 65 70 75 80

Glu Arg Met Tyr Ala Ala Gly Arg Ile Pro Gly Ser Phe Phe Arg Arg
 85 90 95

Glu Gly Arg Pro Ser Thr Glu Ala Ile Leu Ala Cys Arg Leu Ile Asp
 100 105 110

Arg Pro Leu Arg Pro Thr Phe Val Lys Gly Leu Arg Asn Glu Val Gln
 115 120 125

Ile Val Val Thr Val Met Ser Met Asn Pro Glu Asp Tyr Tyr Asp Val
 130 135 140

Val Ala Ile Asn Gly Ala Ser Ala Ala Thr Arg Ile Ser Gly Leu Pro
 145 150 155 160

Val Ser Gly Ala Val Gly Gly Val Arg Met Ala Leu Val Gly Asp Glu
 165 170 175

Lys His Pro Glu Gly Gln Trp Val Ala Phe Pro Thr His Ala Gln His
 180 185 190

Glu Gln Ser Val Phe Glu Ile Val Val Ala Gly Arg Leu Val Glu Arg
 195 200 205

Lys Arg Gly Asn Lys Thr Phe Ser Asp Val Ala
 210 215

<210> 1083

<211> 651

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(628)

<223> RXA01678

<400> 1083

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cggctatatc tctgcaactg cagctcaccc cgggtgcagca atg ctg aaa tgt gca 115
 Met Leu Lys Cys Ala
 1 5

gtc gat gaa gcc gct ggc gga cgc gcc caa gct ttc gta tcc tca ggc 163
 Val Asp Glu Ala Ala Gly Gly Arg Ala Gln Ala Phe Val Ser Ser Gly
 10 15 20

gat aac att ggt ggc agc ccg ttc caa tcc tcc att ctt ggt gat gaa 211
 Asp Asn Ile Gly Gly Ser Pro Phe Gln Ser Ser Ile Leu Gly Asp Glu
 25 30 35

ccc acc ttg gaa gca ctc aac caa atg ggt ctt gat tac tca gca gtg 259
 Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu Asp Tyr Ser Ala Val
 40 45 50

ggc aac cac gaa ttt gat aaa ggc tac gca gac tta agc agt cga gtc 307
 Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp Leu Ser Ser Arg Val
 55 60 65

gct gac ctt gct gat ttt gat tat ctc ggc gca aac gtt gag ggc gaa 355
 Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala Asn Val Glu Gly Glu
 70 75 80 85

aac cca gat ctt gca cca tat gga att tct cac ctt gat ggt gtg aag 403
 Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His Leu Asp Gly Val Lys
 90 95 100

gtt gct ttc gta ggc acc gta tcc caa gaa act ccg atg ttg gtc aat 451
 Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr Pro Met Leu Val Asn
 105 110 115

tct gaa ggc att gag gga atc acg ttt act gac cca ctt gaa gca acc 499
 Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp Pro Leu Glu Ala Thr
 120 125 130

aac cgt gta gct gat gaa ctc gtg gga agt ggc gca gca gat gtt gtc 547
 Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly Ala Ala Asp Val Val
 135 140 145

gtt gcg ctt tac cac gaa ggc att acc ggc acc gaa gca tgg tca gaa 595
 Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr Glu Ala Trp Ser Glu
 150 155 160 165

aat atc gac gtt gtt ttc gca ggt cac acc cac taagtctgtg atctaggaac 648
 Asn Ile Asp Val Val Phe Ala Gly His Thr His
 170 175

cga

651

<210> 1084
 <211> 176
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 1084

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          20          25          30

Ile Leu Gly Asp Glu Pro Thr Leu Glu Ala Leu Asn Gln Met Gly Leu
          35          40          45

Asp Tyr Ser Ala Val Gly Asn His Glu Phe Asp Lys Gly Tyr Ala Asp
          50          55          60

Leu Ser Ser Arg Val Ala Asp Leu Ala Asp Phe Asp Tyr Leu Gly Ala
          65          70          75          80

Asn Val Glu Gly Glu Asn Pro Asp Leu Ala Pro Tyr Gly Ile Ser His
          85          90          95

Leu Asp Gly Val Lys Val Ala Phe Val Gly Thr Val Ser Gln Glu Thr
          100          105          110

Pro Met Leu Val Asn Ser Glu Gly Ile Glu Gly Ile Thr Phe Thr Asp
          115          120          125

Pro Leu Glu Ala Thr Asn Arg Val Ala Asp Glu Leu Val Gly Ser Gly
          130          135          140

Ala Ala Asp Val Val Val Ala Leu Tyr His Glu Gly Ile Thr Gly Thr
          145          150          155          160

Glu Ala Trp Ser Glu Asn Ile Asp Val Val Phe Ala Gly His Thr His
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 <222> (101)..(1336)
 <223> RXA01679

<400> 1085

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                Met Gln Ser Gly Asn
                1          5

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Tyr Gly His Ala Leu Ala Asp Val Asp Phe Ser Phe Asn His Asp Thr	
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ggg gag ctc acc gta gat gat gcc cgc atg ctc gga gtc gac gat atc	211
Gly Glu Leu Thr Val Asp Asp Ala Arg Met Leu Gly Val Asp Asp Ile	
25 30 35	
aac gcg tgt gaa aac cca gat gac acc att gca gat att gtt gct cag	259
Asn Ala Cys Glu Asn Pro Asp Asp Thr Ile Ala Asp Ile Val Ala Gln	
40 45 50	
gcg gaa ctt gat gct ggt gaa gcc ggc aaa gaa gta gta gcg acc atc	307
Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu Val Val Ala Thr Ile	
55 60 65	
gat ggc gat ttt ctc cgc gcc agc gac gaa gga gca gaa tct ggc tcc	355
Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly Ala Glu Ser Gly Ser	
70 75 80 85	
aac tac ggc gct gaa tcc cag ctc gtc aac atg att gcc agt gct gtg	403
Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met Ile Ala Ser Ala Val	
90 95 100	
cgt tgg tcc atg tcc acc aat acc gcc acc acc gca gac att ggg ctt	451
Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr Ala Asp Ile Gly Leu	
105 110 115	
atg aac gcc gga gga ctc cac act gac cta ttc agc ggc gat gtt acc	499
Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe Ser Gly Asp Val Thr	
120 125 130	
tac gcc gaa gct ttt gaa atc cag cct ttc tcc ggt gaa gat tca ttt	547
Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser Gly Glu Asp Ser Phe	
135 140 145	
gtc acc ctc aag gga tca gtc ttc aaa gat gcc ctt gac cag cag tgg	595
Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala Leu Asp Gln Gln Trp	
150 155 160 165	
gaa gaa ggt tct gca cga cca gtg gca gca ctt ggc gta tcc gac aac	643
Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu Gly Val Ser Asp Asn	
170 175 180	
gtt tcc tac acc tac gac atc aac cgt cca atc ggt gac cgc gtc act	691
Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile Gly Asp Arg Val Thr	
185 190 195	
tcc gtg acc att gat gat acc cca ctt gat ccg gaa cgc gac tac gtt	739
Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro Glu Arg Asp Tyr Val	
200 205 210	
gtt gca gct tcc ctg tac ctc cag tcc ggc aac gaa ggt atg acc gca	787
Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn Glu Gly Met Thr Ala	
215 220 225	
ctg acc cgc gga acc gca cct gca caa acc ggc atc gtg gat gta cag	835
Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly Ile Val Asp Val Gln	
230 235 240 245	
tcc acc atc gga tac ttg tcc aac aac aat gtc acc cca cgt act ggt	883

Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val Thr Pro Arg Thr Gly
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 caa gcc cag att tcc atc acc cca tcc ggt gag ttc aat gcg ggt gaa 931
 Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu Phe Asn Ala Gly Glu
 265 270 275
 acc atc acc ctt gac atg gca gga ctc cgc tac acc caa ggc gac act 979
 Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr Thr Gln Gly Asp Thr
 280 285 290
 gcc acg gaa gta act gtc agc ctt cga gaa gaa att gtt tca gca cca
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 Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu Ile Val Ser Ala Pro
 295 300 305
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 Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly Glu Ala Gly Thr Ala
 310 315 320 325
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 1123
 Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser Gly Thr Gln Asn Leu
 330 335 340
 gtt gtc acc acc gat acc ggc acc cgt att tcc atg cca gtt gag att
 1171
 Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser Met Pro Val Glu Ile
 345 350 355
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 1219
 Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala Gly Ser Ser Val Leu
 360 365 370
 gga act gga gtg ctc agt gga ctc ctc ggc att gtt gta gga att cta
 1267
 Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile Val Val Gly Ile Leu
 375 380 385
 gga atg gtc ggt ctg gtg aac tgg att gac cca agc ttc att caa cag
 1315
 Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro Ser Phe Ile Gln Gln
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 Ile Gln Gln Gln Ile Phe Ala
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<211> 412

<212> PRT

<213> Corynebacterium glutamicum

<400> 1086

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 35 40 45
 Asp Ile Val Ala Gln Ala Glu Leu Asp Ala Gly Glu Ala Gly Lys Glu
 50 55 60
 Val Val Ala Thr Ile Asp Gly Asp Phe Leu Arg Ala Ser Asp Glu Gly
 65 70 75 80
 Ala Glu Ser Gly Ser Asn Tyr Gly Ala Glu Ser Gln Leu Val Asn Met
 85 90 95
 Ile Ala Ser Ala Val Arg Trp Ser Met Ser Thr Asn Thr Ala Thr Thr
 100 105 110
 Ala Asp Ile Gly Leu Met Asn Ala Gly Gly Leu His Thr Asp Leu Phe
 115 120 125
 Ser Gly Asp Val Thr Tyr Ala Glu Ala Phe Glu Ile Gln Pro Phe Ser
 130 135 140
 Gly Glu Asp Ser Phe Val Thr Leu Lys Gly Ser Val Phe Lys Asp Ala
 145 150 155 160
 Leu Asp Gln Gln Trp Glu Glu Gly Ser Ala Arg Pro Val Ala Ala Leu
 165 170 175
 Gly Val Ser Asp Asn Val Ser Tyr Thr Tyr Asp Ile Asn Arg Pro Ile
 180 185 190
 Gly Asp Arg Val Thr Ser Val Thr Ile Asp Asp Thr Pro Leu Asp Pro
 195 200 205
 Glu Arg Asp Tyr Val Val Ala Ala Ser Leu Tyr Leu Gln Ser Gly Asn
 210 215 220
 Glu Gly Met Thr Ala Leu Thr Arg Gly Thr Ala Pro Ala Gln Thr Gly
 225 230 235 240
 Ile Val Asp Val Gln Ser Thr Ile Gly Tyr Leu Ser Asn Asn Asn Val
 245 250 255
 Thr Pro Arg Thr Gly Gln Ala Gln Ile Ser Ile Thr Pro Ser Gly Glu
 260 265 270
 Phe Asn Ala Gly Glu Thr Ile Thr Leu Asp Met Ala Gly Leu Arg Tyr
 275 280 285
 Thr Gln Gly Asp Thr Ala Thr Glu Val Thr Val Ser Leu Arg Glu Glu
 290 295 300
 Ile Val Ser Ala Pro Ile Asp Pro Gln Leu Gly Glu Ala Gly Phe Gly
 305 310 315 320
 Glu Ala Gly Thr Ala Thr Val Ser Leu Asp Ile Pro Ala Thr Leu Ser
 325 330 335
 Gly Thr Gln Asn Leu Val Val Thr Thr Asp Thr Gly Thr Arg Ile Ser

340	345	350
Met Pro Val Glu Ile Val Gly Ala Glu Gln Pro Ala Pro Gln Pro Ala		
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Gly Ser Ser Val Leu Gly Thr Gly Val Leu Ser Gly Leu Leu Gly Ile		
370	375	380
Val Val Gly Ile Leu Gly Met Val Gly Leu Val Asn Trp Ile Asp Pro		
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<211> 1071

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1048)

<223> RXN01488

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 Met Ser Lys Lys Ala
 1 5

atc ctt gat atc gac acc ggc atc gat gat gcc ctc gca ctt gcc tac 163
 Ile Leu Asp Ile Asp Thr Gly Ile Asp Asp Ala Leu Ala Leu Ala Tyr
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gca ctg ggc tca cct gaa cta gag ctc att ggt gtc acc acc acc tac 211
 Ala Leu Gly Ser Pro Glu Leu Glu Leu Ile Gly Val Thr Thr Thr Tyr
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ggt aac gtg cta ctc gaa acc ggt gca gtc aat gac ctg gca ctg ctt 259
 Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn Asp Leu Ala Leu Leu
 40 45 50

gat ctg ttc ggt gca cca gaa gta cct gtg tac ttg ggt gag cca cac 307
 Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr Leu Gly Glu Pro His
 55 60 65

gca cag acc aag gat ggc ttt gaa gtt ctt gag atc tcc gcg ttc att 355
 Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu Ile Ser Ala Phe Ile
 70 75 80 85

cac gga caa aac ggc atc ggc gaa gtc gag ctg cca gca agc gag tca 403
 His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu Pro Ala Ser Glu Ser
 90 95 100

aag gca ctc ccc ggc gca gtg gat ttc ctc att gat tcc gtc aac acc 451
 Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile Asp Ser Val Asn Thr
 105 110 115

cac ggc gat gac ctg gtg atc atc gca act ggt ccc atg acc aac ctg 499

His	Gly	Asp	Asp	Leu	Val	Ile	Ile	Ala	Thr	Gly	Pro	Met	Thr	Asn	Leu		
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Ser	Ala	Ala	Ile	Ala	Lys	Asp	Pro	Ser	Phe	Ala	Ser	Lys	Ala	His	Val		
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gtc	atc	atg	ggg	ggc	gcc	ttg	act	gtc	cca	ggc	aac	gtc	agc	aca	tgg	595	
Val	Ile	Met	Gly	Gly	Ala	Leu	Thr	Val	Pro	Gly	Asn	Val	Ser	Thr	Trp		
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gca	gaa	gca	aac	atc	aac	cag	gac	cca	gat	gca	gca	aac	gat	ctg	ttc	643	
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Arg	Ser	Gly	Ala	Asp	Val	Thr	Met	Ile	Gly	Leu	Asp	Val	Thr	Leu	Gln		
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acc	ctt	ctt	acc	aag	aag	cac	act	gcg	cag	tgg	cgc	gaa	ctg	ggc	act	739	
Thr	Leu	Leu	Thr	Lys	Lys	His	Thr	Ala	Gln	Trp	Arg	Glu	Leu	Gly	Thr		
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cca	gct	gct	atc	gca	ctg	gcc	gac	atg	act	gat	tac	tac	atc	aag	gca	787	
Pro	Ala	Ala	Ile	Ala	Leu	Ala	Asp	Met	Thr	Asp	Tyr	Tyr	Ile	Lys	Ala		
	215					220					225						
tat	gag	acc	acc	gca	cca	cac	ctg	ggc	ggg	tgc	ggc	ctg	cac	gac	cca	835	
Tyr	Glu	Thr	Thr	Ala	Pro	His	Leu	Gly	Gly	Cys	Gly	Leu	His	Asp	Pro		
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Leu	Ala	Val	Gly	Val	Ala	Val	Asp	Pro	Ser	Leu	Val	Thr	Leu	Leu	Pro		
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Ile	Asn	Leu	Lys	Val	Asp	Ile	Glu	Gly	Glu	Thr	Arg	Gly	Arg	Thr	Ile		
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ggc	gat	gaa	gtc	cgc	ctc	aac	gat	cca	gtg	cgc	acc	tcc	cgc	gca	gct	979	
Gly	Asp	Glu	Val	Arg	Leu	Asn	Asp	Pro	Val	Arg	Thr	Ser	Arg	Ala	Ala		
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gtc	gcc	gta	gac	gtg	gat	cgt	ttc	ctt	tct	gaa	ttc	atg	acc	cgc	atc		
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Val	Ala	Val	Asp	Val	Asp	Arg	Phe	Leu	Ser	Glu	Phe	Met	Thr	Arg	Ile		
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Val Thr Thr Thr Tyr Gly Asn Val Leu Leu Glu Thr Gly Ala Val Asn	35	40	45
Asp Leu Ala Leu Leu Asp Leu Phe Gly Ala Pro Glu Val Pro Val Tyr	50	55	60
Leu Gly Glu Pro His Ala Gln Thr Lys Asp Gly Phe Glu Val Leu Glu	65	70	75
Ile Ser Ala Phe Ile His Gly Gln Asn Gly Ile Gly Glu Val Glu Leu	85	90	95
Pro Ala Ser Glu Ser Lys Ala Leu Pro Gly Ala Val Asp Phe Leu Ile	100	105	110
Asp Ser Val Asn Thr His Gly Asp Asp Leu Val Ile Ile Ala Thr Gly	115	120	125
Pro Met Thr Asn Leu Ser Ala Ala Ile Ala Lys Asp Pro Ser Phe Ala	130	135	140
Ser Lys Ala His Val Val Ile Met Gly Gly Ala Leu Thr Val Pro Gly	145	150	155
Asn Val Ser Thr Trp Ala Glu Ala Asn Ile Asn Gln Asp Pro Asp Ala	165	170	175
Ala Asn Asp Leu Phe Arg Ser Gly Ala Asp Val Thr Met Ile Gly Leu	180	185	190
Asp Val Thr Leu Gln Thr Leu Leu Thr Lys Lys His Thr Ala Gln Trp	195	200	205
Arg Glu Leu Gly Thr Pro Ala Ala Ile Ala Leu Ala Asp Met Thr Asp	210	215	220
Tyr Tyr Ile Lys Ala Tyr Glu Thr Thr Ala Pro His Leu Gly Gly Cys	225	230	235
Gly Leu His Asp Pro Leu Ala Val Gly Val Ala Val Asp Pro Ser Leu	245	250	255
Val Thr Leu Leu Pro Ile Asn Leu Lys Val Asp Ile Glu Gly Glu Thr	260	265	270
Arg Gly Arg Thr Ile Gly Asp Glu Val Arg Leu Asn Asp Pro Val Arg	275	280	285
Thr Ser Arg Ala Ala Val Ala Val Asp Val Asp Arg Phe Leu Ser Glu	290	295	300
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																Val	Ala	Arg	Val	Val							
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gtc	aat	gtc	atg	cct	aag	gct	gag	att	ctg	gat	ccc	cag	ggg	cag	gcg			163									
Val	Asn	Val	Met	Pro	Lys	Ala	Glu	Ile	Leu	Asp	Pro	Gln	Gly	Gln	Ala												
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gta	cac	cgc	gcc	ctc	gga	cgt	atc	gga	gtt	tct	ggc	gtt	tcc	gat	gtc			211									
Val	His	Arg	Ala	Leu	Gly	Arg	Ile	Gly	Val	Ser	Gly	Val	Ser	Asp	Val												
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cgt	cag	gga	aag	cgc	ttc	gag	ctt	gag	gta	gat	gat	tcc	gtc	acc	gaa			259									
Arg	Gln	Gly	Lys	Arg	Phe	Glu	Leu	Glu	Val	Asp	Asp	Ser	Val	Thr	Glu												
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gct	gac	cta	aag	aaa	att	gct	gaa	acc	ctc	ctc	gca	aac	acc	gtc	atc			307									
Ala	Asp	Leu	Lys	Lys	Ile	Ala	Glu	Thr	Leu	Leu	Ala	Asn	Thr	Val	Ile												
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gaa	gac	ttc	gat	gtg	gtg	gga	gtt	gag	gtc	gcg	aag	tgagcgccaa						353									
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Gly Val Ser Asp Val Arg Gln Gly Lys Arg Phe Glu Leu Glu Val Asp
          35          40          45

Asp Ser Val Thr Glu Ala Asp Leu Lys Lys Ile Ala Glu Thr Leu Leu
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Ala Asn Thr Val Ile Glu Asp Phe Asp Val Val Gly Val Glu Val Ala
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Lys

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 Met Arg Ile Asp Pro
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ctg gaa acc cgg caa gcc gta ttg gcc gtc aaa gac tgg att gaa ggg 163
 Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys Asp Trp Ile Glu Gly
 10 15 20

gag gga gac gtc aaa aag cct ggt cgt gcg gca ctt gcc gcc gca act 211
 Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala Leu Ala Ala Ala Thr
 25 30 35

cgc ctg agc gtc cga ctg ctc gcg caa cac gcg ccg gga aac agc gtg 259
 Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala Pro Gly Asn Ser Val
 40 45 50

gag gtg cgg gta ccc cca ttt gtt gcg gtg caa tgc ata gag ggg cca 307
 Glu Val Arg Val Pro Pro Phe Val Ala Val Gln Cys Ile Glu Gly Pro
 55 60 65

aaa cat aca cgc ggc aca cca ccc aac gtg gtg gag acc gac gcc aag 355
 Lys His Thr Arg Gly Thr Pro Pro Asn Val Val Glu Thr Asp Ala Lys
 70 75 80 85

acc tgg tta cgc tta gca cct ggg caa acc aca ttt gat gca gaa ttt 403
 Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr Phe Asp Ala Glu Phe
 90 95 100

gaa agc gga aaa att agc gca tca ggt acc cga gcc aaa gag att gcg 451
 Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg Ala Lys Glu Ile Ala
 105 110 115

gac tgg tta cca gtg gtc aaa ctt tagatttcct aatgctcatt agt 498
 Asp Trp Leu Pro Val Val Lys Leu
 120 125

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 <212> PRT
 <213> Corynebacterium glutamicum

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Asp Trp Ile Glu Gly Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala
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 Leu Ala Ala Ala Thr Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala
 35 40 45
 Pro Gly Asn Ser Val Glu Val Arg Val Pro Pro Phe Val Ala Val Gln
 50 55 60
 Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val Val
 65 70 75 80
 Glu Thr Asp Ala Lys Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr
 85 90 95
 Phe Asp Ala Glu Phe Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg
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 Ala Lys Glu Ile Ala Asp Trp Leu Pro Val Val Lys Leu
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 Met Gly Leu Trp Ile
 1 5
 gat gca acc gct ggc gtt gca ggg gat atg ttg ctg gga gca ctc att 163
 Asp Ala Thr Ala Gly Val Ala Gly Asp Met Leu Leu Gly Ala Leu Ile
 10 15 20
 gat gca ggt gca gaa cta gaa aaa atc caa cag gtt gtg gaa gca gtc 211
 Asp Ala Gly Ala Glu Leu Glu Lys Ile Gln Gln Val Val Glu Ala Val
 25 30 35
 atc ccc ggt gac gtg ctc ttg cgc acc gaa gag gta gtg cgc caa ggc 259
 Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu Val Val Arg Gln Gly
 40 45 50
 caa cga ggc atc aag ctg cat gtg gac gca caa cat gaa cac cat cat 307
 Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln His Glu His His His
 55 60 65
 cac cgc cac tta agc acc att aaa gaa ctg ctt gtc aat gct gac atc 355
 His Arg His Leu Ser Thr Ile Lys Glu Leu Leu Val Asn Ala Asp Ile
 70 75 80 85
 cct gaa caa acc aag cag gat gcc tta ggc gtt ttt gaa ctc atc gct 403

Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val Phe Glu Leu Ile Ala
90 95 100

atc gct gaa gga aaa gtc cac ggc atc gag ccg gag aaa atc cac ttc 451
Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro Glu Lys Ile His Phe
105 110 115

cat gag gta gga gct tgg gat tcc atc gca gac att gtg ggt gtg tgc 499
His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp Ile Val Gly Val Cys
120 125 130

gaa gcg atc agg cag ctt aac cca ggt ttg att gct gca tct ccg att 547
Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile Ala Ala Ser Pro Ile
135 140 145

gct tta gga ttc gga cgc atc aag gca gct cac gga gat att cca gtg 595
Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His Gly Asp Ile Pro Val
150 155 160 165

cca gtt cca gcc gtg gca gag ctg gtg aaa ggc tgg ccc acc caa acc 643
Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly Trp Pro Thr Gln Thr
170 175 180

gga gct ctt atg gag agc acc gaa cct gtt ggt gaa tta gcc acc cca 691
Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly Glu Leu Ala Thr Pro
185 190 195

act ggt gtt gcg ttg atc cgt cac ttt gcc acc caa gat ggc cct ttc 739
Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr Gln Asp Gly Pro Phe
200 205 210

cca ggt ggc atc atc aat gaa gtt ggc att ggt gca gga aca aaa gat 787
Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly Ala Gly Thr Lys Asp
215 220 225

aca gaa ggc cgt cca aat ata gtg cgc gca att ttg ttc aac acc tct 835
Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile Leu Phe Asn Thr Ser
230 235 240 245

agg agt aac cca gat acc cgc aca ctg gtg caa tta gaa gcc aat gtt 883
Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln Leu Glu Ala Asn Val
250 255 260

gat gat caa gac cca cgg ctg tgg cca gga gta ata gag atc ctc ttt 931
Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val Ile Glu Ile Leu Phe
265 270 275

gcc gct ggc gca gta gat gca tgg ctg act cca att ttg atg aag aag 979
Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro Ile Leu Met Lys Lys
280 285 290

ggc cgt cct gca cat agg gtg tca gca ttg gtg gat agc tcc gag gtg
1027
Gly Arg Pro Ala His Arg Val Ser Ala Leu Val Asp Ser Ser Glu Val
295 300 305

gaa gca gtg aaa acc gca tta ttt gca gcc acc acg act ttt ggg atc
1075
Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr Thr Thr Phe Gly Ile
310 315 320 325

aga tca tgg gaa gtc gaa cga gaa ggc ttg gac cgt cgt ttc gaa caa
1123

Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp Arg Arg Phe Glu Gln
330 335 340

gtc gag gtg gac gga cac acc atc aac atc aaa atc ggt tcc cgt gat
1171

Val Glu Val Asp Gly His Thr Ile Asn Ile Lys Ile Gly Ser Arg Asp
345 350 355

gat caa gta atc agt gca cag tcc gag ttt gaa gat att cgg tct gca
1219

Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu Asp Ile Arg Ser Ala
360 365 370

gcg gtg gcc ttg gga att tca gag cgg gaa gtt gtg gca aga att ccg
1267

Ala Val Ala Leu Gly Ile Ser Glu Arg Glu Val Val Ala Arg Ile Pro
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1305

Gln Gly Thr Thr Glu
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<212> PRT

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<400> 1094

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Val Val Glu Ala Val Ile Pro Gly Asp Val Leu Leu Arg Thr Glu Glu
35 40 45

Val Val Arg Gln Gly Gln Arg Gly Ile Lys Leu His Val Asp Ala Gln
50 55 60

His Glu His His His His Arg His Leu Ser Thr Ile Lys Glu Leu Leu
65 70 75 80

Val Asn Ala Asp Ile Pro Glu Gln Thr Lys Gln Asp Ala Leu Gly Val
85 90 95

Phe Glu Leu Ile Ala Ile Ala Glu Gly Lys Val His Gly Ile Glu Pro
100 105 110

Glu Lys Ile His Phe His Glu Val Gly Ala Trp Asp Ser Ile Ala Asp
115 120 125

Ile Val Gly Val Cys Glu Ala Ile Arg Gln Leu Asn Pro Gly Leu Ile
130 135 140

Ala Ala Ser Pro Ile Ala Leu Gly Phe Gly Arg Ile Lys Ala Ala His
145 150 155 160

Gly Asp Ile Pro Val Pro Val Pro Ala Val Ala Glu Leu Val Lys Gly
 165 170 175
 Trp Pro Thr Gln Thr Gly Ala Leu Met Glu Ser Thr Glu Pro Val Gly
 180 185 190
 Glu Leu Ala Thr Pro Thr Gly Val Ala Leu Ile Arg His Phe Ala Thr
 195 200 205
 Gln Asp Gly Pro Phe Pro Gly Gly Ile Ile Asn Glu Val Gly Ile Gly
 210 215 220
 Ala Gly Thr Lys Asp Thr Glu Gly Arg Pro Asn Ile Val Arg Ala Ile
 225 230 235 240
 Leu Phe Asn Thr Ser Arg Ser Asn Pro Asp Thr Arg Thr Leu Val Gln
 245 250 255
 Leu Glu Ala Asn Val Asp Asp Gln Asp Pro Arg Leu Trp Pro Gly Val
 260 265 270
 Ile Glu Ile Leu Phe Ala Ala Gly Ala Val Asp Ala Trp Leu Thr Pro
 275 280 285
 Ile Leu Met Lys Lys Gly Arg Pro Ala His Arg Val Ser Ala Leu Val
 290 295 300
 Asp Ser Ser Glu Val Glu Ala Val Lys Thr Ala Leu Phe Ala Ala Thr
 305 310 315 320
 Thr Thr Phe Gly Ile Arg Ser Trp Glu Val Glu Arg Glu Gly Leu Asp
 325 330 335
 Arg Arg Phe Glu Gln Val Glu Val Asp Gly His Thr Ile Asn Ile Lys
 340 345 350
 Ile Gly Ser Arg Asp Asp Gln Val Ile Ser Ala Gln Ser Glu Phe Glu
 355 360 365
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<211> 1419

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1396)

<223> RXC02624

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Gly	Val	Ala	Val	Leu	Leu	Val	Ile	Ile	Leu	Ala	Val	Ala	Ser	Leu	Met	
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ttc	acc	aat	tct	tca	atg	gtg	aat	ctt	tcg	gca	acg	att	gca	cag	ctg	211
Phe	Thr	Asn	Ser	Ser	Met	Val	Asn	Leu	Ser	Ala	Thr	Ile	Ala	Gln	Leu	
			25					30					35			
tgg	ctt	tcc	cta	aat	ctc	ggc	gcg	gtg	gac	ggc	agt	ggg	gaa	gtg	atc	259
Trp	Leu	Ser	Leu	Asn	Leu	Gly	Ala	Val	Asp	Gly	Ser	Gly	Glu	Val	Ile	
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Ser	Val	Leu	Pro	Thr	Leu	Pro	Gly	Phe	Ile	Phe	Leu	Trp	Ala	Ile	Ala	
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gcg	cgc	atc	cac	cgc	gca	gtc	aaa	gat	cgt	gtc	agc	atc	gcc	gac	tta	355
Ala	Arg	Ile	His	Arg	Ala	Val	Lys	Asp	Arg	Val	Ser	Ile	Ala	Asp	Leu	
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ggc	gtc	ctc	gca	gca	ctc	gtc	ctc	ggc	atc	ccg	ctt	gcg	ctc	acc	gcc	403
Gly	Val	Leu	Ala	Ala	Leu	Val	Leu	Gly	Ile	Pro	Leu	Ala	Leu	Thr	Ala	
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atc	gca	gcg	ttc	atg	ctt	ttc	gac	gcc	tcc	agc	gtc	ctc	aac	gtc	gag	451
Ile	Ala	Ala	Phe	Met	Leu	Phe	Asp	Ala	Ser	Ser	Val	Leu	Asn	Val	Glu	
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gcc	ctc	ttc	ctc	ggc	atg	ggg	cca	cgc	ctg	tgg	cag	gcg	ttg	gcg	cgc	547
Ala	Leu	Phe	Leu	Gly	Met	Gly	Pro	Arg	Leu	Trp	Gln	Ala	Leu	Ala	Arg	
	135					140					145					
cgc	tac	ggc	gct	cca	gaa	tgg	ctt	atc	gac	gcc	atc	acc	caa	gct	ttc	595
Arg	Tyr	Gly	Ala	Pro	Glu	Trp	Leu	Ile	Asp	Ala	Ile	Thr	Gln	Ala	Phe	
150					155					160					165	
cgc	ttc	ctc	atc	gca	ttt	gga	aca	gtc	tcc	ttg	ggt	tcc	gtg	ctc	gtg	643
Arg	Phe	Leu	Ile	Ala	Phe	Gly	Thr	Val	Ser	Leu	Val	Ser	Val	Leu	Val	
				170					175					180		
atg	acc	gcg	atc	aac	cac	agt	gca	ttc	acc	gcg	acc	atg	cag	ggc	tac	691
Met	Thr	Ala	Ile	Asn	His	Ser	Ala	Phe	Thr	Ala	Thr	Met	Gln	Gly	Tyr	
			185					190					195			
gac	gac	tcc	gcc	tct	gtt	gtg	gcc	ttg	atc	gtc	ctg	agc	att	ctg	tat	739
Asp	Asp	Ser	Ala	Ser	Val	Val	Ala	Leu	Ile	Val	Leu	Ser	Ile	Leu	Tyr	
		200					205					210				
ctg	ccc	aac	atg	atg	atc	ttt	gcg	atg	ggc	aat	ctg	atc	ggc	tca	ccc	787
Leu	Pro	Asn	Met	Met	Ile	Phe	Ala	Met	Gly	Asn	Leu	Ile	Gly	Ser	Pro	
	215					220					225					
ctt	tac	ttc	ggc	gac	gcc	tcc	atc	agc	gtc	ttc	agc	gtg	cat	tcc	gtt	835
Leu	Tyr	Phe	Gly	Asp	Ala	Ser	Ile	Ser	Val	Phe	Ser	Val	His	Ser	Val	

230	235	240	245	
cca ttg cca ccg ctt ccc atc ctc gca gct ctc ccc agc gaa gcc ctc				883
Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu Pro Ser Glu Ala Leu				
	250	255	260	
tca tgg gca gtg gcc tta ctg gtc atc cct gca att att gcc acc tgg				931
Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala Ile Ile Ala Thr Trp				
	265	270	275	
gtc tgc gtg aga aac ccc atg cgc ctt gcc gtg aac aca aca gca gca				979
Val Cys Val Arg Asn Pro Met Arg Leu Ala Val Asn Thr Thr Ala Ala				
	280	285	290	
gtc att tca gca ctg tgt ttc ctc gtc ctg gca gtt ttc gcc ggc gga				
1027 Val Ile Ser Ala Leu Cys Phe Leu Val Leu Ala Val Phe Ala Gly Gly				
	295	300	305	
acc ttg ggc gta tac aac tac gtc gga ctc aac ctc ctg gcg tca gtt				
1075 Thr Leu Gly Val Tyr Asn Tyr Val Gly Leu Asn Leu Leu Ala Ser Val				
	310	315	320	325
ggc cta gtt ttc gtc tat ttc gcc ctc gtt gga ctc ctc atc gcc gga				
1123 Gly Leu Val Phe Val Tyr Phe Ala Leu Val Gly Leu Leu Ile Ala Gly				
	330	335	340	
atc gac aag ctg cgc aac cct gta gaa gtt aag tct gtt aag gct gtg				
1171 Ile Asp Lys Leu Arg Asn Pro Val Glu Val Lys Ser Val Lys Ala Val				
	345	350	355	
gct gtt gtg gag ccc gag cct gaa gaa gtt gaa gag gac gaa gag gag				
1219 Ala Val Val Glu Pro Glu Pro Glu Glu Val Glu Glu Asp Glu Glu Glu				
	360	365	370	
cat gtt gaa gaa gaa gta gat gag gag gaa gag gaa gtt gag gaa ggg				
1267 His Val Glu Glu Glu Val Asp Glu Glu Glu Glu Glu Val Glu Glu Gly				
	375	380	385	
gta gaa gag gtc gaa gaa gac gac gca gag gat cct gaa gag aat cct				
1315 Val Glu Glu Val Glu Glu Asp Asp Ala Glu Asp Pro Glu Glu Asn Pro				
	390	395	400	405
gaa gag gaa gaa tcc gac gaa gaa att gag aca gaa act gag gct gaa				
1363 Glu Glu Glu Glu Ser Asp Glu Glu Ile Glu Thr Glu Thr Glu Ala Glu				
	410	415	420	
gaa acc aat gat ggt tcc gag gcc gaa gac cgt taacatatct gttgtgaatt				
1416 Glu Thr Asn Asp Gly Ser Glu Ala Glu Asp Arg				
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ctg				
1419				

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<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 1096

Val Leu Ile Pro His Gly Val Ala Val Leu Leu Val Ile Ile Leu Ala
 1 5 10 15

Val Ala Ser Leu Met Phe Thr Asn Ser Ser Met Val Asn Leu Ser Ala
 20 25 30

Thr Ile Ala Gln Leu Trp Leu Ser Leu Asn Leu Gly Ala Val Asp Gly
 35 40 45

Ser Gly Glu Val Ile Ser Val Leu Pro Thr Leu Pro Gly Phe Ile Phe
 50 55 60

Leu Trp Ala Ile Ala Ala Arg Ile His Arg Ala Val Lys Asp Arg Val
 65 70 75 80

Ser Ile Ala Asp Leu Gly Val Leu Ala Ala Leu Val Leu Gly Ile Pro
 85 90 95

Leu Ala Leu Thr Ala Ile Ala Ala Phe Met Leu Phe Asp Ala Ser Ser
 100 105 110

Val Leu Asn Val Glu Val Pro Pro Ile Thr Arg Leu Leu Arg Val Met
 115 120 125

Leu Phe His Leu Ser Ala Leu Phe Leu Gly Met Gly Pro Arg Leu Trp
 130 135 140

Gln Ala Leu Ala Arg Arg Tyr Gly Ala Pro Glu Trp Leu Ile Asp Ala
 145 150 155 160

Ile Thr Gln Ala Phe Arg Phe Leu Ile Ala Phe Gly Thr Val Ser Leu
 165 170 175

Val Ser Val Leu Val Met Thr Ala Ile Asn His Ser Ala Phe Thr Ala
 180 185 190

Thr Met Gln Gly Tyr Asp Asp Ser Ala Ser Val Val Ala Leu Ile Val
 195 200 205

Leu Ser Ile Leu Tyr Leu Pro Asn Met Met Ile Phe Ala Met Gly Asn
 210 215 220

Leu Ile Gly Ser Pro Leu Tyr Phe Gly Asp Ala Ser Ile Ser Val Phe
 225 230 235 240

Ser Val His Ser Val Pro Leu Pro Pro Leu Pro Ile Leu Ala Ala Leu
 245 250 255

Pro Ser Glu Ala Leu Ser Trp Ala Val Ala Leu Leu Val Ile Pro Ala
 260 265 270

Ile Ile Ala Thr Trp Val Cys Val Arg Asn Pro Met Arg Leu Ala Val
 275 280 285